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(71) Applicant (for all designated States except US): UNIVER-SITY OF SOUTH FLORIDA [US/US]; 4202 East Fowler Avenue, FAO 126, Tampa, FL 33620-7900 (US).

(72) Inventor; and

(75) Inventor/Applicant (for US only): SESHI, Beerelli [US/US]; 9128 Highland Ridge Way, Tampa, 11. 33647 (US).

(74) Agent: RINALDO, Amy, E.; Kohn & Associates, PLLC, 30500 Northwestern Highway, Suite 410, Farmington Hills, MI 48334 (US). (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, VN, YU, ZA, ZM, ZW.

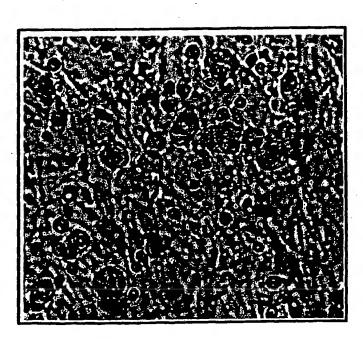
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(54) Title: HUMAN MESENCHYMAL PROGENITOR CELL



(57) Abstract: Pluri-differentiated human mesenchymal progenitor cells (MPCs) are isolated. A method isolates and purifies human mesenchymal progenitor cells from Dexter-type cultures for characterization of and uses, particularly therapeutic uses for such cells. Specifically, isolated MPCs can be used for diagnostic purposes, to enhance the engraftment of hematopoietic progenitor cells, enhance bone marrow transplantation, or aid in the treatment or prevention of graft versus host disease.

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HUMAN MESENCHYMAL PROGENITOR CELL FIELD OF THE INVENTION

The present invention generally relates to pluri-differentiated mesenchymal progenitor cells and therapeutic uses for the same. More specifically, the isolated mesenchymal progenitor cells are isolated from hematopoietic cells and macrophages in Dexter-type cultures cells.

BACKGROUND OF THE INVENTION

Bone marrow, the site of blood cell production and home to various leukemia and lymphoma cells, comprises a complex cellular population including hematopoietic progenitor or stem cells and the stromal cells that support them. Hematopoietic stem cells have the capacity for self-regeneration and for generating all blood cell lineages while stromal stem cells have the capacity for self-renewal and for producing the hematopoietic microenvironment.

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Two bone-marrow culture systems introduced in the mid-1970's have evolved as favored media for the *in vitro* analysis of mesengenesis and hematopoiesis. The Friedenstein culture system was introduced in 1976 as a media for the analysis and study of mesengenesis. (Friedenstein, et al, in *Exp Hematol* 4,267-74 (1976). In order to obtain mesenchymal stem cells (MSCs) for expansion in the culture medium, it is necessary to first isolate rare pluripotant mesenchymal stem cells from other cells in the bone marrow. In the Friedenstein culture system, isolating the nonhematopoietic cells is achieved by utilizing their tendency to adhere to plastic. Once isolated, a monolayer of homogeneous, undifferentiated stromal cells is then grown in the culture medium, in the <u>absence</u> of hematopoietic cells. The stromal cells from this system have the potential to differentiate into discrete mesenchymal tissues, namely bone, cartilage, adipose tissue and muscle depending on specific growth supplements. These MSCs have been the target of extensive investigation including exploration of their potential clinical utility in repair or replacement of genetically damaged mesenchymal tissues.

In 1977, Dexter, *et al.* developed another bone marrow culture system for the study of hematopoiesis. (Dexter et al. *J Cell Physiol 91*, 335-44 (1977). The Dexter culture does not require isolation of the mesenchymal cells before culturing. Thus, the monolayer of stromal cells is grown in the <u>presence</u> of hematopoietic cells. Greenberger later modified the Dexter system by the addition of hydrocortisone to

for matched sibling donors to 50% in the cases of matched, unrelated donors and un-matched donors from the patient's family.

The potential benefits of bone marrow transplantation have stimulated research on the cause and prevention of GvHD. The removal of T cells from the bone marrow obtained from matched unrelated or unmatched sibling donors results in a decreased incidence of graft versus host reactions, but an increased incidence of rejection of the allogeneic bone marrow graft by the patient.

Current therapy for GvHD is imperfect, and the disease can be disfiguring and/or lethal. Thus, risk of GvHD restricts the use of bone marrow transplantation to patients with otherwise fatal diseases, such as severe immunodeficiency disorders, severe aplastic anemia, and malignancies.

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The potential to enhance engraftment of bone marrow or stem cells from antigenically mis-matched donors to patients without graft rejection or GvHD would greatly extend the availability of bone marrow transplantation to those patients without an antigenically matched sibling donor.

Thus, it would be useful to develop methods of improving and/or enhance bone marrow transplantation by enhancing the engraftment of bone marrow or hematopoietic progenitor cells and/or decreasing the occurrence of graft rejection or GvHD in allogenic transplants.

Studies of hematopoiesis and mesengenesis and the urgent need for improved methods of treatment in the field of bone marrow transplants have led to the isolation of MSCs from bone marrow stroma. These MSCs are the same pluripotential cells that result from expansion in Friedenstein type cultures. Several patents describe the isolation and therapeutic uses of these MSCs.

U.S. Patent No. 5,486,359, to Caplan, et al., discloses isolated human MSCs, and a method for their isolation, purification, and culturing. Caplan, et al. also describes methods for characterizing and using the purified mesenchymal stem cells for research, diagnostic, and therapeutic purposes. The invention in `359, to Caplan, et al., describes pluri-potential cells that remain pluri-potential, even after cultural expansion. Caplan, et al. also teaches that it is necessary to first isolate the pluri-potent MSCs from other cells in the bone marrow and then, in some applications, uses culture medium to expand the population of the isolated MSCs. The Caplan et al. patent fails to disclose the use of Dexter-type cultures, pluri-

cell culture preparation by the Dexter method, treating the cells to obtain a cell suspension, removing macrophages, fractionating the cells, and collecting the fraction of pluri-differentiated mesenchymal progenitor cells.

The present invention also provides a method for enhancing bone marrow engraftment in a mammal in need thereof which includes administering to the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) a bone marrow graft, wherein the pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the bone marrow in the mammal.

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The present invention provides a method for enhancing engraftment of hematopoietic progenitor cells in a mammal in need thereof which includes the step of administering to the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) hematopoietic progenitor cells, wherein the pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the hematopoietic progenitor cells in the mammal.

Another embodiment of the present invention provides a method for treating graft-versus-host disease (GvHD) in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation, by administering to the mammal an effective amount of isolated pluri-differentiated mesenchymal progenitor cells.

Yet another embodiment of the present invention provides a method for diagnosing a disease state by: a) establishing gene expression patterns of normal state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells; b) establishing gene expression patterns of various leukemic state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells; c) identifying gene sets that are unique to a given state; and d) comparing a profile of bone marrow derived isolated mesenchymal progenitor cell of unknown state to the gene sets.

Additionally, the present invention provides a method for identifying therapeutic targets for treatment of hematopoietic function by: a) determining the median gene expression profile of bone marrow isolated pluri-differentiated mesenchymal progenitor cells associated with each disease state of interest; b)

Vectastain Elite ABC Kit). (Figure 4C) Immunostain using anti-CD45 antibody (Dako, Clone PD7/26 & 2B11; ABC Kit). (Figure 4D) Periodic acid-Schiff (Sigma). (Figure 4E) Nile Red (Sigma), counterstained with DAPI (Vector). (Figure 4F) Alkaline phosphatase (Sigma Kit No. 85), counterstained with Nuclear Fast Red (Baker). (Figure 4G) Immunostain using antibody to fibronectin (Immunotech, Clone 120.5; ABC Kit). (Figure 4H) Immunostain using anti-muscle actin antibody (Ventana, clone HUC 1-1; Ventana system using a section of formalin-fixed, paraffin-embedded cell block, instead of a cytospin). Appropriate positive controls and isotype-matched negative controls were employed to ascertain antibody staining-specificity. All parts of figure as shown, except 4E and 4H, have clearly identifiable built-in cell controls. The morphological features of the cells are listed in row 1 of Table 1.

Figure 5 is a photograph which shows a transmission electron micrograph of an MPC of the present invention bearing microvilli, irregular nucleus, and pools of glycogen (6) in the ectoplasm (x 4,600).

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Figure 6A-M are photographs which show Northern blot analysis of bone marrow stromal cell RNAs for expression of genes specific for multiple mesenchymal cell lineages. Figures 6A-M represent different gene probes used for hybridization. The following outlines the sources of the gene probes employed and the approximate sizes of the major transcripts observed (shown in parentheses): Figure 6A) CD68 (Clone ID 3176179, Genome Systems, Inc (GSI); 2-3 kb); Figure 6B) Cathepsin B (Clone ID 2806166, GSI; 2-3 kb); Figure 6C) GAPDH probe (generated using PCR primers from R&D Systems, Inc; ~2 kb) hybridized to same blot as A and B; Figure 6 D) Adipsin (probe generated using PCR primers as described, Ref 20; 0.5-1 kb); Figure 6E) Osteoblast-specific cadherin-11 (Clone ID 434771, GSI; ~3 kb); Figure 6F) Chondroitin sulfate proteoglycan 2 (Clone ID 1623237, GSI; >10 kb); Figure 6G) Collagen type I alpha 1 (Clone ID 782235, GSI; >10 kb); Figure 6H) Decorin (Clone ID 3820761, GSI; 2-3 kb); Figure 6I) GAPDH probe hybridized to same blot as D-H; Figure 6J) Fibronectin (Clone ID 3553729, GSI; >10 kb); Figure 6K) Caldesmon (Clone ID 1319608, GSI; ~4 kb); Figure 6L) Transgelin (Clone ID 4049957, GSI; ~1.5 kb); and Figure 6M) GAPDH probe hybridized to same blot as J-L.

Figure 7 is a photograph which shows RT-PCR analysis for expression of representative hematopoietic growth factors (G-CSF and SCF) and extracellular

(arrow; autoradiogram exposed for only 45 minutes). Figure 12B shows EcoR1 digest of thymic genomic DNA from SCID mice. Figure 12C shows EcoR1 digest of lymph node genomic DNA from SCID mice. Figure 13A and Figure 13 B show graphs comparing the survival rate and engraftment of human hematopoietic cells in SCID mice cotransplanted with the purified bone marrow MPCs of the present invention vs. unpurified bone marrow stromal cells. In the line graphs provided the line with diamonds represents MPCs and bone marrow mononuclear cells, squares represents bone marrow mononuclear cells only, triangles represents unfractionated bone marrow stromal cells, the Xs represent MPCs only, and the circles represent the control. In the bar graphs, the gray bars represent mice that survived and the black bars represent mice with engraftment. Figures 14A-C are photographs which demonstrate apoptosis by TUNEL assay in organs of SCID mice that died after transplantation. Figure 14A shows a serial section of the liver of the mouse that survived. Figure 14B shows a serial section of the liver of the mouse that died. Figure 14C shows a serial section of the spleen of the mouse that survived. Figure 14D shows a serial section of the spleen of the mouse that died.

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Figure 15 shows photomicrographs of single-cell MPCs that were isolated by laser capture microdissection (LCM) and subsequently targeted for microarray analysis.

Figure 16 shows a Venn diagram displaying the stromal-cell gene-list. Stromal cell genes are operationally defined as being active in at least 9 out of 10 single cell MPCs AND 4 out of 5 collective MPC samples AND 7 out of 8 collective USC samples, i.e., 20 of 23 samples tested. This criterion was very stringent and automatically excluded the outliers, independently of filtering for genes with weak expressions on the basis of control strength (referred to as C or CS). The stromal cell gene list of 2755 includes 13 AFFX microarray-assay positive controls.

Figure 17 shows a two-dimensional hierarchical clustering of 2755 stromal cell genes based on the expression profiles of 23 samples. The gene tree is displayed on top and the experiment or sample tree is shown on left. Accordingly, each column represents a particular gene on the chip and each row represents a separate stromal cell sample.

Figure 18 shows composite gene-expression plots of 2755 stromal cell genes comparing collective purified stromal cell samples (cMPC), collective

Generally, the present invention provides isolated and purified mesenchymal progenitor cells that are pluri-differentiated. Also provided by the present invention is a therapeutic composition including an effective amount of isolated and purified pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier.

The terms "enhance" or "improve" as used herein are intended to indicate that the there is a more beneficial end result. In other words, the product provides a more effective result.

The term "pluri-differentiated" as used herein refers to cells that are a single cell type co-expressing genes specific for multiple lineages. The term "pluri-potential" as used herein refers to cells that are undifferentiated and have the potential to be differentiated into discrete mesenchymal tissues.

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Dexter-type cultures contain stromal cells that co-express multiple message lineage markers. These pluri-differentiated cells are referred to by the inventor as mesenchymal progenitor cells (MPCs). Disclosed herein is a process for isolating and purifying MPCs from Dexter-type cultures. Purified MPCs provide a sufficiently defined system to permit detailed elucidation of the role of bone marrow in normal and leukemic hematopoiesis.

The present invention also provides various methods for using MPCs to enhance bone marrow transplantation, enhance hematopoietic progenitor cell engraftment, for diagnostic purposes, or for the treatment of GvHD.

The exact cell types in Dexter cultures have been identified. No evidence was found for the existence of discrete cellular populations, such as adipocytes, osteoblasts, fibroblasts, smooth muscle cells and endothelial cells, notwithstanding the abundance of literature and wide spread belief (*See*, J.L. Liesveld *et al.*, *Blood* 73, 1794 (1989); A.K. Sullivan, D. Claxton, G. Shematek *et al.*, *Lab Invest* 60, 667 (1989); K. Dorshlind, *Ann Rev Immunol* 8, 126 (1990); S. Perkins, R.A. Fleischman, *Blood* 75, 620 (1990); I.A. Denkers, R.H. Beelen, G.J. Ossenkoppele *et al.*, *Ann Hematol* 64, 210 (1992); P.E. Penn, D.Z. Jiang, R.G. Fei *et al.*, *Blood* 81, 1205 (1993); E. de Wynter *et al.*, *J Cell Sci* 106, 761 (1993); A. Ferrajoli *et al.*, *Stem Cells (Dayt)* 12, 638 (1994); B.R. Clark, A. Keating, *Ann NY Acad Sci* 770, 70 (1995); B.S. Wilkins, D.B. Jones, *Br J Haematol* 90, 757 (1995); S. Gronthos, P.J. Simmons, *J Hematother* 5, 15 (1996); D. Soligo *et al.*, Abstract

The MPCs in Dexter type cultures were characterized using a variety of techniques. Cytospins were prepared using aliquots of unfractionated cells for performance of various cytological, cytochemical and immunocytochemical stains. Reactivity patterns of the bone marrow culture cells are outlined in Table 1. Figures 4A-E illustrate morphologic and phenotypic characteristics, as uncovered by staining for representative cell lineage markers.

Only rarely have investigators in this field taken the approach of preparing a cell suspension and staining cells on cytospins as was done to characterize the cells of the present invention (Simmons, et al., Nature 328, p429-32 (1987)) and no other group has used this method to address the issue of pluridifferentiation by bone marrow stromal cells. Almost all of the published studies in the field, with a rare exception (Simmons, et al., Nature, 328, p429-32 (1987)), conducted cytochemical and immunocytochemical staining on layers of stromal cells grown to confluence on coverslips. In this situation, the stromal cultures appear very complex especially in the areas of hematopoietic activity, so-called "cobblestones" with macrophages and hematopoietic cells enmeshed in them. Macrophages and nonhematopoietic cells spread themselves and assume varied shapes when they adhere to and grow on plastic or glass. This spreading further contributes to the The complexity precludes a clear perceived heterogeneity and complexity. morphological visualization of the nonhematopoietic cells and consequently interferes with the determination of what percent of what cell type is positive for any given marker.

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In terms of lineage markers, up to 100% of the nonhematopoietic cells or MPCs of the present invention expressed two fat cell markers (Nile Red (Figure 4E) and Oil Red O); an osteoblast marker (alkaline phosphatase (Figure 4F)); and two fibroblast markers (fibronectin (Figure 4G) and prolyl-4-hydroxylase). Greater than 85% of the MPCs were also positive for a muscle marker, actin (Figure 4H). There was no evidence of expression of endothelial cell differentiation, as judged by immunohistochemical staining for CD34 and CD31.

In addition, the Dexter type stromal cells had not previously been subjected to Periodic Acid-Schiff (PAS) staining, which revealed a strong and uniform positivity by almost 100% of the MPCs studied. This indicates the presence of large stores of glycogen (Figure 4D). The presence of glycogen (6) was confirmed

Percoll gradient centrifugation (Figure 2). The isolated MPCs were then collected and washed.

The purity of the nonhematopoietic cells was demonstrated by a near complete absence of two macrophage markers, CD68 and cathepsin B (as shown by Northern blotting data, Figure 6A and 6B). As a positive control, bone marrow mononuclear cells rich in myelomonocytic cells abundantly expressed CD68 (lanes 5 & 6, Figure 6A). The Northern blot results are consistent with a purity estimate of ~95% (vs. 60% in unfractionated samples) based on morphology and immunocytochemical staining for CD68.

A purified source of MPCs is desirable for a number of reasons. The relative ease with which large numbers of the MPCs can be purified and their distinctive phenotypic characteristics make them valuable targets for future investigations. Purified MPCs provide a sufficiently defined system to permit detailed elucidation of the role of bone marrow in normal and leukemic hematopoiesis in addition to aiding in bone marrow transplantation.

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Another major reason that purified cells are desirable is that Dexter cultures also contain a significant percentage of highly immunogenic macrophages that can cause onset of GvHD after transplantation. The MPCs of the present invention are purified to ~95% free of macrophages and hematopoietic cells. Note the increased survival rate in Severe Combined Immunodeficiency Disease (SCID) mice that received purified MPCs versus those that received unfractionated bone marrow stromal cells in Figure 13B. This data establishes that stromal cells in combination with engraftment or other similar procedures enhances the effectiveness of the treatment.

The present invention also provides methods of enhancing the engraftment of hematopoietic cells and of enhancing the engraftment of bone marrow. The hematopoietic support capacity of the Dexter-type cultures has been repeatedly demonstrated by a number of investigators. RT-PCR analysis showed that Dexter cultures and Friedenstein cultures expressed a similar pattern of cytokine and growth factor mRNAs; yet, Dexter cultures were found to be more efficient than Friedenstein cultures in achieving preservation of hematopoietic progenitors (Majumdar, et al., J.Cell.Physiol., 176, 57-66.). The pluri-differentiated MPC is capable of supporting hematopoiesis, as shown by its ability to express

invention represent a single pluridifferentiated MPC which allows for genomic study of the stromal cells and the development of new, more objective diagnostic tools for patients suffering from leukemia conditions.

The present invention provides a comprehensive phenotype of cultured bone marrow stromal cells at single cell level for the first time. These findings pave the road for ultimate identification and investigation of these cells in fresh samples of marrow, normal as well as diseased, in which they occur at a low frequency and are extremely difficult to study at the present time. The development of this phenotype forms the basis for various diagnostic tests including a comprehensive test that can be used to screen for different abnormalities of bone marrow stromal cells in various hematologic diseases and other diseases effecting stromal cells.

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Results show that isolated single stromal cells simultaneously express transcripts for osteoblasts, fibroblasts, muscle cells and adipocytes. Furthermore, there is shown that isolated single stromal cells simultaneously express transcripts for epithelial cells and neural/glial cells as well as transcripts for CD45, CD19, CD10, CD79a, and representative proto-oncogenes and transcription factors, typically known to be affiliated with normal and neoplastic hematopoietic cells. These findings are evidence of existence of a progenitor cell that is common to nonhematopoietic mesenchymal cells and hematopoietic cells, particularly B-lymphocytes. "Lineage burst" characterized by simultaneous activation of diverse differentiation pathways within the same cell appears to be the signature profile of a stromal cell, indicating that a "pluripotent" cell is "pluridifferentiated" at the molecular level. That is, prior to a selective and full-fledged lineage differentiation, progenitors express genes associated with multiple lineages to which they might possibly commit, thus providing insight into the molecular basis of cellular plasticity.

Transcriptomic analysis has been undeniably contributing to the molecular definition of new disease categories with demonstrable therapeutic benefit. The present invention contributes to the further definition of the stromal cell by refining its molecular signature. The *in vivo* identification of the stromal cell and its possible ontogenic variants as they might occur in different hematological diseases and subsequent targeting of these cells holds the key to ultimately treating some, if not all, of these diseases.

The present invention also provides for a method of preventing or treating GvHD. The highest mortality rate, Figure 13B, was observed in mice receiving the unpurified whole marrow stroma and the bone marrow mononuclear cells. The increased mortality observed is related to the presence of highly immunogenic macrophages and consequent GvHD. The mice with the highest survival rate, shown in Figure 13A, were the mice receiving purified MPCs and bone marrow mononuclear cells.

Notably, there is discrete TUNEL-positive nuclei in the liver of the expired mouse in Figure 14B and complete absence of staining in the liver of the surviving mouse (see Figure 14A). While some ill-defined globules of staining are observed in the spleen of the mouse that survived, the nuclear integrity of most of the cells is well preserved suggesting minimal or no apoptosis (Figure 14C). In contrast, the dead mouse spleen (Figure 14D) showed extensive TUNEL positivity precluding accurate interpretation. Control mouse liver and spleen showed results similar to those of the mouse that survived.

The above results indicate that purified MPCs can support human hematopoiesis in SCID mice as effectively as whole marrow stroma. Equally important is that the purified MPCs increased the survival rate. The evidence shows that the increased survival is due to a reduction in GvHD.

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Allogeneic bone marrow transplantation is the preferred method of treatment for a variety of malignant and genetic diseases of the blood and blood forming cells. However, failure of hematopoietic cell engraftment can occur for a number of reasons. These include, microenvironmental defects as part of the underlying disease itself (e.g., aplastic anemia), and/ or stromal cell damage caused by chemoradiotherapy and/ or microenvironmental damage as part of GvHD which is a dreaded complication following bone marrow transplantation. In GvHD, donor T cells present in the hematopoietic cell graft destroy host tissues. GvHD can involve multiple organs such as skin, liver, GI system etc. The current treatment modalities for preventing or treating graft failure or GvHD are cumbersome, costly and involve some form of immunosuppression. Stromal cell lesions, either primary to the disease process or secondarily induced by allogeneic bone marrow transplantation, play a prominent role in the success or failure of the hematopoietic cell graft. Cotransplantation of MPC not only enhances hematopoietic cell engraftment but

administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition can also include a local anesthetic to ameliorate any pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a cryopreserved concentrate in a hermetically sealed container such as an ampoule indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients can be mixed prior to administration.

The present invention paves the way for applications of mesenchymal progenitor cells in the field of transplantation with respect to hematopoietic support, immunoregulation, and graft facilitation. MPCs can be used as a supporting cell type in bone marrow transplantation, particularly in diseases where defects in the hematopoietic stromal microenvironment are believed to prevail, such as aplastic anemia, myelofibrosis, and bone marrow failure following high dose chemotherapy and radiation therapy.

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Another aspect of the invention provides a method for diagnosing various disease states in mammals by identifying new diagnostic markers, specifically the classification and diagnosis of leukemia. Prior to the present invention, stromal cells were not carefully investigated in terms of genomics because of the widespread belief that they represent a heterogeneous mixture of cell types and cellular heterogeneity presents significant challenges for the application of genetic analysis such as microarray technology. The isolated MPCs of the present invention represent a single cell type and allow for genomic study of the stromal cells.

Using the methods of the present invention, it has been determined that bone marrow stromal cells in leukemia patients are functionally and structurally defective regardless of the damage caused by chemotherapy and radiation therapy. Given the almost 25 year history and intense interest in bone marrow stromal cell cultures, previous documentation of stromal cell abnormalities has been disappointingly low (Martinez & Martinez, Exp. Hematol 11:522-26 (1983); Budak-Alpdogan, et al., Am.J.Hematol, 62:212-20 (1999); Nagao, et al., Blood, 61:589-92

(1983); Peled, et al., Exp.Hematol 24:728-37 (1996); Bhatia, et al., Blood 85:3636-45 (1995); Agarwal, et al., Blood 85:1306-12 (1995); Diana, et al., Blood 96:357a(2000)). By identifying gene sets that are unique to a given state, these differences in the stromal cells can be utilized for diagnostic purposes.

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In one embodiment of the invention, isolated MPCs from a patient are assayed for expression of a large number of genes. The gene expression profile is projected into a profile of gene set expression values according to the definition of gene sets. A reference database containing a number of reference projected profiles is also created from the isolated MPCs of patients with known states, such as normal and various leukemic disease states. The projected profile is then compared with the reference database containing the reference projected profiles. If the projected profile of the patient matches best with the profile of a particular disease state in the database, the patient is diagnosed as having such disease state. Various computer systems and software (see Example 5) can be utilized for implementing the analytical methods of this invention and are apparent to one of skill in the art. Some of these software programs include Cluster & TreeView (Stanford, URLs: rana.lbl.gov or www.microarray.org), GeneCluster (MIT/Whitehead Institute, URL: MPR/GeneCluster/GeneCluster.html), Array Explorer (SpotFire Inc, URL: http://www.spotfire.com/products/scicomp.asp#SAE) and GeneSpring (Silicon Genetics Inc, URL: http://www.sigenetics.com/Products/GeneSpring/index.html) (for computer systems and software, see also U.S. Patent No. 6,203,987).

The methods of the present invention can also be useful for monitoring the progression of diseases and the effectiveness of treatments. For example, by comparing the projected profile prior to treatment with the profile after treatment.

One aspect of the present invention provides methods for therapeutic and drug discovery utilizing bone marrow derived isolated mesenchymal progenitor cells. The present invention can be utilized to identify stromal cell genes that can be therapeutic targets for improvement of normal hematopoietic function, which is constantly compromised, in leukemic patients. In one embodiment, gene sets are defined using cluster analysis. The genes within a gene set are indicated as potentially co-regulated under the conditions of interest. Co-regulated genes are further explored as potentially being involved in a regulatory pathway. Identification

of genes involved in a regulatory pathway provides useful information for designing and screening new drugs.

Some embodiments of the present invention employ gene set definition and projection to identify drug action pathways. In one embodiment, the expression changes of a large number of genes in response to the application of a drug are measured. The expression change profile is projected into a gene set expression change profile. In some cases, each of the gene sets represents one particular pathway with a defined biological purpose. By examining the change of gene sets, the action pathway can be deciphered. In some other cases, the expression change profile is compared with a database of projected profiles obtained by perturbing many different pathways. If the projected profile is similar to a projected profile derived from a known perturbation, the action pathway of the drug is indicated as similar to the known perturbation. Identification of drug action pathways is useful for drug discovery. See, Stoughton and Friend, Methods for Identifying pathways of Drug Action, U.S. patent application Ser. No. 09/074,983.

The present invention provides a genomics strategy method for identifying genes differentially expressed in MPCs. The method begins with the preparation of total RNA from MPC samples, which leads to the generation of cDNA. From the cDNA, ds DNA can be prepared for *in vitro* transcription into cRNA. The cRNA is then fragmented for the hybridization of target RNA to a microarray of known genes (Affymetrix genechip containing DNA from ~12,000 known human genes, e.g., U95A oligonucleotide microarray). Finally, analysis of differentially expressed genes is accomplished using appropriate software (GeneSpring) to discern the patterns of gene expression or genomic signatures by a given MPC type (e.g., up-regulation or down-regulation).

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Up-regulated and down-regulated gene sets for a given disease-associated or cytokine-stimulated MPC are combined. The combination enables those of skill in the art to identify gene sets with minimal number of elements that are unique to a given MPC type with a capability to discriminate one MPC type from another (this can be accomplished by means of a series of Venn diagrams and lists of required genes obtained via GeneSpring). Such gene sets are of immense diagnostic value as they can be routinely used in assays that are simpler than microarray analysis (for example "real-time" quantitative PCR). Such gene sets also

provide insights into pathogenesis and targets for design of new drugs. For example, the method allows one to establish transcriptional profiles of MPC genes that are pathologically altered.

Those of skill in the art can use the data and methods contained herein for the following: a) study select gene or sets of genes that are relevant to hematopoietic disease conditions by using relatively inexpensive but low-throughput technologies such as Northern blotting, RNase protection assays and/or PCR intended for gene expression analysis; b) identify newer drug targets and diagnostic markers relevant to specific diseases, such as MM or CML etc depending on the research interests of the individual investigators.

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The present invention also provides a large-format 2-D gel electrophoretic system for the reproducible separation of MPC proteins and for preparing 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g., TNF- α and/or IL-4) and for MPCs derived from patients with representative pre-leukemic/ premalignant and leukemic/ malignant conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lyinphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples consist of culture supernatants/secreted proteins, extracellular matrix (ECM) proteins, plasma membrane proteins solubilized using a three-step differential extraction protocol, employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

The 2-D system described herein utilizes an immobilized pH gradient gel (pH 4-7) in the first dimension and a mini non-denaturing but high-resolution lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDS-PAGE) in the second dimension. As identified by silver staining, this system has resolved greater than 800 protein spots in a pH interval of 2.5 units (4.25-6.75, the isoelectric pH range for most of plasma membrane proteins to migrate) and a molecular mass range of 10-150 kDa. Equally important, the system is compatible with high sample

loads (up to 1.5 to 2.0 mg of total protein in up to 350 µl sample volume). All the protein species identifiable by a silver stain that is compatible with subsequent mass spectrometric analysis have been analyzed by a 2-D gel software with respect to isoelectric point, molecular weight and mass abundance. The lectin-binding status of these proteins has also been determined by lectin blotting. Lectin blots and Western blots have subsequently been stained by a gold stain for detection of total proteins on the same PVDF membrane. Although gold-staining of the Western blot is not as sensitive as silver-staining of the gel, gold-staining of the Western blot generates the necessary landmarks for alignment with the silver stained gel, facilitating excision of spots of interest from the gel for identification by MALDI-MS. Representative protein spots were excised from gel and subjected to mass spectrometric profiling (MALDI-MS) and/or sequencing (Nano ESI MS/MS) with subsequent database searching, resulting in a productive identification of ten proteins.

The invention is further described in detail by reference to the following experimental examples. These examples are provided for the purpose of illustration only, and are not intended to be limiting unless otherwise specified. Thus, the invention should in no way be construed as being limited to the following examples, but rather, should be construed to encompass any and all variations which become evident as a result of the teaching provided herein.

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EXAMPLES

The examples presented herein can be summarized as follows. The data disclosed herein demonstrate that Dexter cultures consist of only three cell types macrophages (~35%), hematopoietic cells (~5%), and nonhematopoietic cells (~60%). Using a percoll gradient centrifugation technique, the nonhematopoietic mesenchymal progenitor cells were isolated, free of macrophages and hematopoietic cells. A variety of techniques were used to identify the isolated cells as a multi-differentiated mesenchymal cell lineage co-expressing genes specific for multiple mesenchymal cell lineages including adipocytes, osteoblasts, fibroblasts and muscle cells.

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Evidence that this multi- or pluri-differentiated mesenchymal progenitor cell is capable of supporting hematopoiesis is shown by the expression of a number of hematopoietic growth factors and extracellular matrix receptors. The SCID mouse experimental data provides evidence that since the MPCs can be purified to near

homogeneity (95%) with relative ease, MPCs can be of value for enhancing engraftment of hematopoietic stem cells and bone marrow transplants. Additionally, increased survival rate in the SCID mouse model indicates that isolated MPCs can also be useful for the treatment of GvHD. An example of the administration of bone marrow cells and MPCs to breast cancer patients treated with chemotherapy is also provided.

A stepwise genomics strategy and an example of the genomic changes observed in leukemia associated MPCs is also provided. Cluster analysis was performed to show gene expression patterns in isolated MPCs of a normal individual and individuals with different leukemic conditions. The approach presented provides the basis for a new more objective means to diagnose patients suffering from leukemic conditions.

EXAMPLE 1

Isolation and Characterization of MPCs from Dexter-Type Bone Marrow Stromal Cell Culture Systems

Bone marrow culture:

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Bone marrow samples were obtained from posterior superior iliac crest under general anesthesia for standard marrow transplantation. Marrow stromal cell cultures were set up using the residual cells recovered from the filters of Fenwal Bone Marrow Collection System after complete filtration of the marrow samples. The filters were rinsed with phosphate-buffered saline without Ca²⁺ and Mg²⁺ (PBS-CMF). The cell suspension was subjected to Ficoll gradient isolation of the mononuclear cells (bone marrow MNCs). The bone marrow MNCs were washed (x2) in PBS-CMF and suspended in McCoy's 5A with HEPES medium containing 12.5% fetal bovine serum (FBS), 12.5% horse serum, 1 µM/L hydrocortisone and 1% penicillin/streptomycin (for this study McCoy's complete medium) and cultured under standard stromal-cell culture conditions (Figure 1) (Seshi, *et al. Blood* 83, 2399 (1994) and Gartner, *et al. Proc Natl Acad Sci USA* 77, 4756 (1980). After two weeks, confluent stromal cell cultures were trypsinized (first passage), followed by splitting each T75 flask into two T150 flasks.

Morphologic and phenotypic characteristics of MPCs as uncovered by staining for representative mesenchymal cell lineage markers:

Two weeks after the first passage (above), confluent stromal cells were again trypsinized. Cytospins were prepared using aliquots of unfractionated cells for performance of various cytological, cytochemical and immunocytochemical stains.

Reactivity patterns of the bone marrow culture cells are outlined in Table 1. Figures 4A-E illustrate morphologic and phenotypic characteristics, as uncovered by staining for representative cell lineage markers. As illustrated in Table 1 and Figures 3 and 4A, Wright-Giemsa staining revealed three morphologically identifiable cell populations in Dexter type stromal cell cultures, macrophages, hematopoietic cells, and nonhematopoietic cells (labeled 4, 3, and 5, respectively).

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The identity of macrophages was confirmed by immunostain using anti-CD68 antibody (Figure 4B) and cytochemical stains for acid phosphatase and Sudan black. The identity of hematopoietic cells (including macrophages) was confirmed by immunostain using anti-CD45 antibody (Figure 4C).

The remaining nonhematopoietic cells stained intensely positive for Periodic acid-Schiff, which was diastase sensitive, signifying the presence of large stores of glycogen (Figure 4D). The presence of glycogen (6) was confirmed by electron microscopy (see Figure 5). In this respect, MPCs are reminiscent of the glycogen-laden reticular cells in the developing bone marrow of human fetuses (observed by L-T. Chen, L.Weiss, *Blood* 46, 389 (1975)). Glycogen deposition is viewed to be a developmentally regulated process during morphogenesis (H. Ohshima, J. Wartiovaara, I. Thesleff, *Cell Tissue Res.* 297, 271 (1999)).

In terms of lineage markers, up to 100% of the nonhematopoietic cells expressed two fat cell markers (Nile Red (Figure 4E) and Oil Red O); an osteoblast marker (alkaline phosphatase (Figure 4F)); and two fibroblast markers (fibronectin (Figure 4G) and prolyl-4-hydroxylase). Greater than 85% of the nonhematopoietic cells were also positive for a muscle marker, actin (Figure 4H). There was no evidence of expression of endothelial cell differentiation, as judged by immunohistochemical staining for CD34 and CD31 (data not shown).

The results indicate that the nonhematopoietic cells of the Dexter cultures are in fact a single, pluri-differentiated cell type co-expressing multiple mesenchymal cell lineage markers. The pluri-differentiated mesenchymal progenitor cells reported here are to be distinguished from the pluri-potential, but

undifferentiated, MSCs that are generated in the absence of hematopoietic cells, such as in Friedenstein-type cultures.

Table 1. Reactivity patterns of bone marrow stromal cells based on cytological, cytochemical and immunocytochemical stains*,***

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Hematopoietic Mesenchymal Test **Figure** Macrophages cells Utilized progenitor cells Small cells with Large cells with a Wright-Large cells with a 3 and 4A relatively irregular small round minimal amount of Giemsa nucleus & cytoplasm nucleus & foamy cytoplasm: (Harleco) 5% of total cells compartmentalized into cytoplasm: 35% ectoplasm and of total cells endoplasm: 60% of total cells 4D Periodic ō ō ~100% MPCs: staining 2 acid-Schiff restricted to ectoplasm in a ring-like fashion; (PAS) and completely (Sigma) abolished by diastase digestion 100% HCs 0 4C CD45 100% (Dako, macrophages (M PD7/26 & Φ) 2B11) 0 4B **CD68** 100% MΦ 0 (Immunotec h, clone PG-M1) 0 Sudan 0 5 ~100% MΦ Black (Sigma) 100% MPCs; positive 100% MΦ; 0 Acid 6 granules in moderate phosphatas positive granules e (Sigma Kit packed amounts; staining restricted to No. 387) throughout cytoplasm endoplasm Nile Red 0 ~100% MPCs; staining 4E 0 restricted to (Sigma) endoplasm ~ 95% MPCs: Oil Red O 0 0 8 variable number of (Sigma) positive granules; staining preferentially in the endoplasm Alkaline ō ~100% MPCs: variable 4F 9 phosphatas number of positive e (Sigma Kit granules; staining restricted to No. 85) endoplasm & plasma membrane** ~100% MPCs: staining 0 4G Fibronectin restricted to (Immunotec 0 endoplasm h, clone 120.5) ~100% MPCs: staining 0 Prolyl-4-1 preferentially in the hydroxylase 1 endoplasm (Dako.

		clone 5B5)			
1 2	4H	Muscle actin (Ventana, clone HUC 1-1)	0	0	> 85% MPCs: variable staining restricted to ectoplasm

*The lineages of the markers tested above are: 3, hematopoietic cell marker; 4, 5 and 6, monocyte/macrophage markers; 7 and 8, adipocyte markers; 9, osteoblast marker; 10 and 11, fibroblast markers; 12 muscle marker.

**One earlier study (Simmons, et al., Nature 328, 429-432) interpreted the localization of alkaline phosphatase staining as confined to the plasma membrane when in fact it is predominately present within the endoplasm (compare Figure 1C of this reference with Figure 4F).

*** While well-accepted mesenchymal lineage markers were used, these markers do not necessarily lend themselves to simultaneous assessment of the same cell. For example, muscle-specific actin antibody worked only on formalin-fixed, paraffin embedded material, whereas stains like alkaline phosphatase, Oil Red and Nile Red are not anti-body based and involve varying fixing and staining conditions. Thus, the evidence shows that close to 100% of members of a morphologically distinct population express multiple lineage markers of interest.

Bone marrow mesenchymal progenitor cell (MPC) purification:

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To further investigate the characteristics of the MPCs, the nonhematopoietic stromal cells were then purified from the macrophages (–95% pure), the dominant "contaminating" cell type using the following method. Confluent monolayers of stromal cells resulting from first passage, above, were washed for three minutes in Ca²⁺/Mg²⁺ free Hanks' balanced salt solution. Cells were incubated at room temperature for 45 minutes with intermittent mixing in serum-free McCoy's medium containing 10 mM L-leucine methyl ester (LME, Sigma). LME is a lysosomotropic agent that selectively kills and detaches macrophages. The detached macrophages were removed by washing the monolayers twice in McCoy's complete medium, followed by trypsinization of the monolayers. The resulting single cell suspensions were fractionated by discontinuous Percoll gradient (70%, 50%, 30%, 20%, 10%) centrifugation at 800xG for 15 minutes at 4°C in a fixed angle rotor (Avanti-J25 Beckman centrifuge) (Figure 2). Low-density cells representing the

macrophages resistant to detachment by LME separate as a band at the interface of serum and 10% Percoll and were discarded (1). High-density nonhematopoietic cells representing MPCs form a layer in the region of 30-50% Percoll (2). These were collected and washed twice by centrifugation through PBS-CMF. This protocol is conservatively expected to yield, >2.5x10⁶ MPCs per T-150 flask (i.e., >50x10⁶ MPCs per batch of 20 flasks). The purity of these preparations, typically about 95%, was routinely monitored by Wright-Giemsa staining.

Northern Blotting:

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Additional sets of multiple mesenchymal lineage markers were assessed by Northern blotting to eliminate any observer bias that might be inherent in morphological assessment. Figures 6A-M represent different gene probes used for hybridization. The sources of the gene probes employed and the major transcripts observed are outlined in the brief description of the figures.

Total RNA was prepared by dissolving the high-density cell pellets in Trizol (Life-Technologies). Total RNA samples from unfractionated stromal cells and BM MNCs were similarly prepared. The RNA samples were electrophoresed in a standard 1% agarose gel containing 2% formaldehyde in MOPS/EDTA buffer and blotted onto Immobilon-Ny+ membrane. Probes were labeled using Prime-A-Gene Kit (Promega) and a³²P dCTP (NEN). Hybridization was performed at 65°C in modified Church's hybridization solution using 3x10⁶ counts/ml in 10 ml (Millipore, 1998).

In Figures 6A-M, Northern blot analysis was performed side-by-side on fractionated stromal cells, non-hematopoietic cells freed of macrophages, and initial bone marrow mononuclear cell samples. Lanes 1 and 2 represent total RNA samples (10µg each) from unfractionated stromal cells (subjects S1 and S2, respectively). Lanes 3 and 4 represent total RNA samples (10µg each) from purified stromal MPCs (subjects S1 and S2, respectively). Lanes 5 and 6 represent total RNA samples (10µg each) from bone marrow mononuclear cells, the starting cells for bone marrow cell cultures (subjects S3 and S4, respectively).

The large transcripts, especially of collagen (lane 1, Figure 6G) and fibronectin (lane 1, Figure 6J), in RNA extracted from unfractionated stromal cells of subject 1 showed difficulty migrating into the gel. This observation correlates with the presence of an artifact of unresolved positive material in lane 1, Figure 6A. Since

the RNA extracted from unfractionated stromal cells of the subject 2 did not present this problem (lane 2, Figure **6G**, Figure **6J** and Figure **6A**), the observation does not impact on the overall interpretation of the results (see text). The lineages of markers tested were: monocyte/macrophage markers, CD68 and cathepsin B; adipocyte marker, adipsin; osteoblast markers, osteoblast-specific cadherin-11, chondroitin sulfate proteoglycan 2, collagen type I alpha 1 and decorin; fibroblast marker, fibronectin; muscle markers, caldesmon and transgelin. Marker signals were normalized to the amount of RNA loaded, which was based on densitometry of the GAPDH signals on the corresponding blot (Bio-Rad Model GS-700 Imaging Densitometer). Attenuation or enhancement of the marker signals in the purified stromal MPCs (i.e., lanes 3 and 4) relative to unfractionated stromal cells (i.e., lanes 1 and 2, respectively) is shown as fold Δ (decrease/increase) underneath the lanes 3 and 4; ND, means not determined.

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The purity of the nonhematopoietic cells was demonstrated by a near complete absence of two macrophage markers, CD68 and cathepsin B (as shown by Northern blotting data, Figure 6A and 6B). As a positive control, bone marrow mononuclear cells rich in myelomonocytic cells abundantly expressed CD68 (lanes 5 & 6, Figure 6A). The Northern blot results are consistent with a purity estimate of ~95% (vs. 60% in unfractionated samples) based on morphology and immunocytochemical staining for CD68.

Compared to unfractionated cells, the purified nonhematopoietic cells expressed significantly higher levels of markers representing fat cells (adipsin, Figure 6D); osteoblasts (osteoblast-specific cadherin-11, chondroitin sulfate, collagen type 1 and decorin, Figures 6E-H); fibroblasts (fibronectin, Figure 6J); and smooth muscle cells (caldesmon and transgelin, Figures 6K-L).

No trace of osteoblast, fibroblast, or smooth muscle cell markers were detected in the bone marrow mononuclear cells, suggesting a less than detectable level of stromal cells or their precursors in bone marrow mononuclear cells. However, the fat cell marker, adipsin, was detected in all samples including the bone marrow mononuclear cells.

Taken together, the morphologic, cytochemical and immunocytochemical results (Figure 4A-H and Table 1), and the Northern blotting data (Figure 6A-M) indicate that the nonhematopoietic stromal cells of the Dexter

cultures co-express markers specific for at least four different mesenchymal cell lineages.

This finding is especially intriguing because pluri-differentiation is often a feature of neoplastic cells (Brambilia and Brambilia, *Rev. Mal. Respir.* 3,235 (1986); Pfeifer et al., *Cancer Res.* 51, 3793-3801 (1991); Tolmay *et al.*, *Virchow's Arch* 430, 209-12 (1997). However, a cytogenetic analysis of the Percoll-gradient purified MPCs showed a normal GTW banding pattern.

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RT-PCR Analysis for expression of representative hematopoietic growth factors and extracellular matrix receptors by MPCs

RT-PCR was conducted in a total reaction volume of 100 μl using 2 μg each of total RNA; corresponding primers; and a master mix of the PCR reagents. The RT conditions included sequential incubations at 42°C for 15 minutes, 99°C for five minutes, and 5°C for five minutes. The PCR conditions included: initial melting at 94°C for four minutes; and cyclical melting at 94°C for 45 seconds, annealing at 55°C for 45 seconds and extension at 72°C for 45 seconds with 34 cycles. PCR was terminated after final extension at 72°C for ten minutes. Reaction products (G-CSF, SCF, each 25 μl; VCAM-1, ALCAM, each 50 μl; ICAM-1, 75 μl) were concentrated as necessary; electrophoresed along with a 100-bp DNA ladder (GIBCO-BRL) in a standard agarose (1%) gel in TAE buffer; and stained with ethidium bromide.

PCR products, shown in Figure 7 lanes labeled 1-2, were generated using aliquots of the same RNA samples from purified stromal MPCs, as used for Northern blotting shown under Figure 6 lanes 3 and 4 respectively. The gene transcripts amplified were as follows: G-CSF (granulocyte-colony stimulating factor); (Tachibana et al., Br. J. Cancer, 76, 163-74 (1997); SCF (stem cell factor, i.e., c-Kit ligand); (Saito et al., Biochem, Biophys. Res. Commun., 13, 1762-69 (1994); ICAM-1 (intercellular adhesion molecule-1, CD54) and VCAM-1 (vascular cell adhesion molecule-1, CD106) (primers from R&D); and ALCAM (activated leukocyte cell adhesion molecule, CD166) (Bruder et al., J. Bone Miner. Res., 13, 655-63 (1998)).

The observed PCR products for G-CSF (600 bp, i.e., the top bright band) and ALCAM (175 bp) were significantly different from the expected sizes (278 bp; 372 bp, respectively). However, sequencing of the gel-purified PCR bands and subsequent BLAST search showed a 99-100% identity with respective members. Attempts to detect c-Kit (i.e., SCF receptor) using primers as described (Saito *et al.*,

Biochem, Biophys. Res. Commun., 13, 1762-69 (1994)) amplified a PCR product of ~300 bp with no homology to c-Kit (data not shown). The observed product sizes for SCF (~730 bp); ICAM-1 (~750 bp); and VCAM-1 (~500 bp) were as expected.

As illustrated in Figure 7, RT-PCR analysis showed that purified, multidifferentiated MPCs express both critical hematopoietic growth factor/cytokines, such as G-CSF and SCF as well as matrix receptors/hematopoietic cell adhesion molecules, i.e. ICAM-1, VCAM-1, and ALCAM.

EXAMPLE 2

Comparison of the Ability to Support in vitro Hematopoiesis by Purified MPCs vs.

Unfractionated Bone Marrow Stromal Cells

CD34+ positive cells (hematopoietic progenitor cells) were purified (Dynal kit) and cocultured with irradiated stromal monolayers for five weeks, followed by performance of standard colony assays for hematopoietic progenitors using methylcellulose medium supplemented with colony stimulating factors (using MethoCult medium from Stem Cell Technologies, Inc, Canada). Unfractionated bone marrow stromal cells and purified MPCs were prepared in the same manner as in Example 1. Data in Figure 8 represents results from three experiments. Purified MPC provides increased preservation of hematopoietic progenitor cells compared to unfractionated stromal cells.

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EXAMPLE 3

Animal Model for Enhanced Engraftment Capacity of MPCs

The Severe Combined Immunodeficiency Disease (SCID) mouse model is an ideal system in which to investigate MPC function. Engraftment of human hematopoietic progenitors in SCID mice requires either coadministration of exogenous human cytokines, or cotransplantation of human bone marrow plugs or bone fragments.

There has been discovered a convenient, new source for human bone marrow stromal cells for enhancing transplantation that does not require cytokines, bone fragment, or marrow. Unlike prior methods, the isolated cells of the present invention support human hematopoiesis in the SCID mouse model as effectively as whole marrow stroma. The transplantation of human marrow mononuclear cells combined with purified MPCs results in dramatically vigorous engraftment of human cells in spleen, bone marrow, liver, pancreas, lungs, stomach, and paravertebral

neuronal ganglia of SCID mice. By contrast, mice receiving human bone marrow mononuclear cells alone or MPCs alone expectedly showed no detectable evidence of human hematopoietic cell engraftment. Also notably, the mortality rate was highest in mice that received unfractionated whole marrow stroma whereas purified MPC increased the survival rate which can be due to reduction in GvHD.

Transplantation of human cells in SCID mice:

Homozygous CB-17 scid/scid mice, six to eight weeks of age, were used. Lyophilized anti-asialo GM1 rabbit antibody (Wako Chemicals) was suspended in 1 ml sterile ddH₂O, followed by pretreatment of mice with an IP injection of 20 ml (600 mg) ASGM1 antibody (to specifically deplete mouse macrophages and NK cells). Alternatively, one could use NOD/SCID mice lacking NK cell function, however, in light of highly promising preliminary results it was elected to continue use of scid/scid mice. The antibody treatment schedule included four-hour pre-engraftment and every seven days thereafter for the duration of the experiment. On the day of transplantation, the mice were irradiated with 200 or 300 cGy gamma-irradiation from a ¹³⁷Cs source. Approximately 2.5 x 10⁶ MPCs suspended in 0.5 ml McCoy's medium and/ or 25x10⁶ MNCs suspended in 0.2 ml were injected per mouse, intraperitoneally. Hematopoietic cell engraftment was assessed after five weeks by harvesting and analyzing representative hematopoietic and nonhematopoietic organs including blood, spleen, bone marrow (from two femurs and tibia) from euthanized mice.

Flow Cytometric Evidence

Figure **9A** and **9B** are flow cytometric evidence of human hemopoietic cells in a SCID mouse cotransplanted with marrow MPC. Figure **9A** shows the presence of CD45+/CD34+ progenitors in the marrow. Figure **9B** shows CD45/CD34- mature hematopoietic cells circulating in the mouse's blood.

Photomicrographs of Cells

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Figures 10A-H shows engraftment of human hematopoietic cells in a SCID mouse cotransplanted with the purified marrow MPCs of the present invention. Figure 10A shows a serial section of a mouse spleen stained with H & E. Figure 10B shows a serial section of a mouse spleen stained with immunoperoxidase stain for CD45. Figure 10C shows bone marrow stained for CD45. Figure 10D shows a serial section of the mouse liver stained with H&E depicting involvement of periportal

areas. Figure 10E shows a serial section of the mouse stomach stained with H&E showing transmural infiltration. Figure 10F shows a serial section of the mouse lung stained with H&E showing involvement of peribronchial area. Figure 10G shows a serial section of the mouse pancreas stained with H&E. Figure 10H shows a serial section of the mouse paravertebral ganglia stained with H&E.

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Figure 11A is a photomicrograph of a serial section of the spleen of a normal BALB/C mouse showing white pulp populated by darkly staining lymphocytes (H&E). Figure 11B is a photomicrograph of the spleen of a SCID mouse showing white pulp largely consisting of lightly staining stromal framework (H&E). Figure 11C is a photomicrograph of the spleen of a SCID mouse cotransplanted with human bone marrow MNC and the purified bone marrow MPCs of the present invention showing homing (engraftment) of human B cells to white pulp.

Southern Blotting Data

Hybridization of sample DNA using a DNA probe specific for human chromosome 17 alpha satellite DNA (p17H8) shows linear signal intensity with a 2.7 Kb band (arrow; autoradiogram exposed for only 45 minutes) (Figure 12A). Lanes 1-10 contain human DNA starting 1000 ng to 100 ng admixed with 0 ng 900 ng of mouse DNA, total amount DNA loaded in each lane being 1 ug, allowing construction of a standard curve. The reported limit of detection with this technique is 0.05% human cells, which is more reliable than flow cytometry in detecting very low levels of human cell engraftment.

Figure 12B is a Southern blot of EcoR1 digest of thymic genomic DNA from SCID mice. Lanes 1-5 were loaded with 500 through 100 ng human DNA. Lanes 6, 9-11 were loaded with DNA from mice which received unfractionated bone marrow stroma plus bone marrow mononuclear cells. Lanes 7, 8, 14, 15 were loaded with DNA from mice that received MPCs plus bone marrow mononuclear cells. Lanes 12, 13 were loaded with DNA from mice that received bone marrow mononuclear cells only. There is evidence of human cell engraftment in the mouse thymus in lanes 9 and 11 and lanes 14 and 15 evidenced by the 2.7 Kb band. There was no evidence of engraftment in mice that only received only bone marrow mononuclear cells, lanes 12 and 13.

Figure 12C isEcoR1 digest of Lymph Node genomic DNA from SCID mice. Lanes 1-5 were loaded with 500 through 100 ng human DNA. Lanes 6, 9-11 were loaded with DNA from mice which received unfractionated bone marrow stroma plus bone marrow mononuclear cells. Lanes 7, 8, 14, 15 were loaded with DNA from mice that received MPCs plus bone marrow mononuclear cells. Lanes 12, 13 were loaded with DNA from mice that received bone marrow mononuclear cells only. While there was evidence of engraftment of human cells in the mouse lymph nodes for mice that received unfractioned bone marrow stromal cells and MPCs, there was no evidence of engraftment in mice that only received only bone marrow mononuclear cells, lanes 12 and 13.

Increased Survival and Evidence of MPC Effect on GvHD

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Figure 13A and Figure 13 B show graphs comparing the survival rate and engraftment of human hematopoietic cells in SCID mice cotransplanted with the purified bone marrow MPCs of the present invention versus unpurified bone marrow stromal cells. Mice in Figure 13A received 300 cGy irradiation dose and mice in Figure 13B received 200 cGY of irradiation. Figure 13A and Figure 13B show comparable engraftment of human hematopoietic cells in SCID mice cotransplanted with purified MPCs versus unpurified bone marrow stromal cells and the markedly enhanced survival of mice receiving purified MPCs. Notably, no engraftment was observed in mice receiving bone marrow mononuclear cells alone.

The highest mortality rate, Figure 13B, was observed in mice receiving the unpurified stromal cells and the bone marrow mononuclear cells. The increased mortality observed can be related to the presence of highly immunogenic macrophages and consequent GvHD. The mice with the highest survival rate, as shown in Figure 13A, were the mice receiving purified MPCs and bone marrow mononuclear cells.

Figures 14A-C demonstrate apoptosis by TUNEL assay in organs of SCID mice that died after transplantation with human bone marrow mononuclear cells and unpurified bone marrow stromal cells. Figure 14A shows a serial section of the liver of the mouse that survived. Figure 14B shows a serial section of the liver of the mouse that died. Figure 14C shows a serial section of the spleen of the mouse that survived. Figure 14D shows a serial section of the spleen of the mouse that died. Hematoxylin counterstain was applied to sections in Figure 14A and Figure

14C. Methylgreen counterstain was applied to sections in Figure 14B and Figure 14D.

Notably, there is discrete TUNEL-positive nuclei in the liver of the expired mouse in Figure 14B and complete absence of staining in the liver of the surviving mouse Figure 14A. While some ill-defined globules of staining are observed in the spleen of the mouse that survived, the nuclear integrity of most of the cells is well preserved suggesting minimal or no apoptosis (Figure 14C). By contrast, the dead mouse spleen (Figure 14D) showed extensive TUNEL positivity precluding accurate interpretation. Control mouse liver and spleen showed results similar to those of the mouse that survived.

The size of the spleens from the mice that survived and the mice that died were compared. The dead mice were observed to have small and atrophic spleens correlating with lymphoid cell depletion and apoptosis.

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The above results indicate that purified MPC can support human hematopoiesis in SCID mice as effectively as whole marrow stroma. Equally important is that the purified MPCs increased the survival rate. Evidence suggests that the increased survival can be due to a reduction in GVHD.

EXAMPLE 4

Administration of Bone Marrow Cells and Mesenchymal Progenitor Cells to Breast Cancer Patients Treated with Chemotherapy

A breast cancer patient undergoes a diagnostic posterior iliac crest bone marrow aspiration and biopsy using a local anesthetic. A small portion (2 to 3 ml) of the aliquot (10 to 20 ml) of marrow is submitted for routine histologic testing and determination of the presence of tumor cells using immunoperoxidase testing. The remainder of the cells are Dexter cultured for MPCs as described above in Example 1.

The patient also undergoes placement of a pheresis central venous catheter, and receives subcutaneous injections of G-CSF (filgrastin) 10µg/kg/day as described in Peters, et al, Blood, Vol. 81, pgs. 1709-1719 (1993); Chao, et al, Blood, Vol. 81, pgs. 2031-2035 (1993); Sheridan, et al, The Lancet, Vol. 2, pgs. 891-895 (1989); and Winter, et al, Blood, Vol. 82, pg. 293a (1993). G-CSF injections begin at least three days before the first pheresis is initiated. G-CSF therapy is withheld if the

white blood cell count rises above $40,000/\mu L$ and is resumed once the white blood cell count drops to less than $20,000/\mu L$.

If the patient is receiving only G-CSF as the vehicle for "mobilization" of peripheral blood progenitor cells, the patient must not have received chemotherapy within four weeks of the planned pheresis. If the patient has received both conventional chemotherapy and G-CSF treatment for mobilization, the patient must not have received chemotherapy within ten days of the planned pheresis, and the white blood cell count must be at least $800/\mu L$ and the platelet count at least $30,000/\mu L$.

Daily pheresis procedures are performed using a Cobe Spectra instrument (Cobe, Lakewood, Col.), and each cellular collection is cryopreserved using a controlled-rate liquid nitrogen freezer, until at least 15x10⁸ mononuclear cells/kg are collected (Lazarus, et al., Bone Marrow Transplant, Vol. 7, pgs. 241-246 (1991)). Each peripheral blood progenitor cell is processed and cryopreserved according to previously published techniques. (Lazarus, et al., J. Clin, Oncol., Vol. 10, pgs, 1682-1689) (1992); Lazarus et al., (1991)).

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Eight days before the patient is infused with the autologous peripheral blood progenitor cells, the patient receives chemotherapy over a period of 96 hours (four days), with the following chemotherapy agents: 1) Cyclophosphamide in a total dosage of 6 g/m² (1.5 g/m 2/day for four days) is given via continuous intravenous infusion at 500 mg/m² in 1,000 ml normal saline every eight hours; 2) Thiotepa in a total dosage of 500 mg/ m² /day for four days) is given via continuous intravenous infusion at 125 mg/² in 1,000 ml normal saline every 24 hours; and 3) Carboplatin in a total dosage of 1,800 mg/m² (200 mg/m² /day for four days) is given via continuous intravenous infusion at 200 mg/m² in 1,000 ml of 5% dextrose in water every 24 hours.

The patient also receives 500 mg of Mesna in 50 ml normal saline IV over 15 minutes every four hours for six days (144 hours), beginning with the first dose of cyclophosphamide.

At least 72 hours after the completion of the chemotherapy, the MPCs are harvested from the Dexter culture(s). MPCs are collected and purified as described in Example 1. Cells are resuspended at approximately 10⁶ cells/ml, and

injected slowly intravenously over 15 minutes to provide a total dosage of from 10 to about 5x10⁶ cells.

MPCs can also be frozen and thawed to use when needed. For example, unfractionated cells from a Dexter culture are frozen. Upon thawing the cells are plated for about two days. The MPCs are then purified as in Example 1 above. The MPCs are then replated with serum or in a serum free media and can remain stable for up to six days.

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The day after the patient receives the MPCs, the frozen autologous peripheral blood progenitor cells are removed from the liquid nitrogen refrigerator, transported to the patient in liquid nitrogen, submersed in a 37°C to 40°C sterile water bath, and infused rapidly intravenously without additional filtering or washing steps. GM-CSF in an amount of 250 $\mu g/m^2$ then is given as a daily subcutaneous injection, beginning three hours after completion of the autologous blood progenitor cell infusion. The GM-CSF is given daily until the peripheral blood neutrophil count exceeds 1,000/ μ L for three consecutive days.

EXAMPLE 5

Genomic Changes Observed in Leukemia Associated MPCs

The following is one example of how normal hematopoiesis might be compromised in leukemic conditions. The cellular interactions that underlie leukemic bone marrow involve stromal cells, leukemia/ lymphoma cells, and normal hematopoietic pro`genitors (including those of myelopoiesis, erythropoiesis and megakaryocytopoiesis). In addition to displacing normal hematopoietic cells, the leukemia/ lymphoma cells can potentially cause direct damage to the hematopoietic supportive stromal cells by inducing unwanted gene expression profiles and adversely affecting the normal hematopoiesis. The cellular interactions can be schematized as:

Leukemia/lymphoma cells _____ stromal cells ____ normal hematopoietic progenitors.

The point of this scheme is that regardless of whether stromal cell lesions are primary or secondary to leukemogenesis, the normal hematopoietic function is invariably compromised in leukemic conditions, though different leukemias affect myelopoiesis, erythropoiesis and megakaryocytopoiesis differentially. Contrary to the prevailing notion (see Marini, F et al., Mesenchymal Stem Cells from Patients with Chronic Myelogenous Leukemia Patients can be

Transduced with Common Gene Transfer Vectors at High Efficiency, and are Genotypically Normal, 42nd Annual Meeting of the American Society of Hematology, Dec. 1-5, 2000 Poster # 665), there has been observed extensive and striking gene expression changes in leukemia-associated bone marrow MPCs by using high-resolution genomics. Therefore, one embodiment of the present invention is to use transplantation of tissue-culture expanded, purified normal MPCs to improve granulopoiesis, erythropoiesis and thrombopoiesis, in for example MDS (most of MDS patients do not die from blast transformation but from complications related to cytopenias, i.e., hematopoietic failure).

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The studies targeted acute myeloid leukemia (AML), chronic myeloid leukemia (CML) and multiple myeloma (MM), one case of each. The AML patient was a 57 year-old woman with 52% myeloblasts in the bone marrow with immunophenotype confirmed by flow cytometry and a karyotypic abnormality of 45, XX, -7(6)/46, XX [6]. Together with morphology, the diagnosis was AML arising in a background of myelodysplasia. The CML patient was a 35 year-old man with 2% blasts in the bone marrow and karyotypic abnormalities of Philadelphia chromosome and BCR/ABL gene rearrangement. Together with morphology, the diagnosis was CML in chronic phase. The MM patient was a 61 year-old woman with a IgA myeloma. The serum IgA level was 2.4 g/dl and the marrow plasma cell count was 37%. None of the patients was treated prior to obtaining marrow samples used in this study, to avoid any therapy-induced changes complicating the disease-associated changes.

The leukemic samples consisted of marrow aspirates that remained unused after clinical diagnostic studies were preformed. A bone marrow sample obtained from an adult healthy male who had consented to donate bone marrow for standard marrow transplantation was simultaneously studied. The normal bone marrow sample consisted of residual cells recovered from the filters after complete filtration of the marrow sample. Setting up of Dexter-type stromal cell cultures and isolation of MPC were as described in Example 1. The normal stromal cells were studied without and after stimulation with TNF α because TNF α (and IL-4) are regarded as negative regulators of hematopoiesis. Notably these cytokines, especially TNF α , are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and

thrombocytopenia (i.e., pancytopenia). TNF α and IL-4 are considered possible mediators of hematopoietic dysregulation typical of MDS.

A stepwise genomics strategy encompassed:

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Preparation of total RNA from MPC samples \rightarrow generation of cDNA \rightarrow preparation of ds DNA \rightarrow *in vitro* transcription into cRNA \rightarrow fragmentation of cRNA \rightarrow hybridization of target RNA to a microarray of known genes (Affymetrix genechip containing DNA from ~12,000 known human genes, e.g., U95A oligonucleotide microarray) \rightarrow analysis of differentially expressed genes using an appropriate software (GeneSpring) to discern the patterns of gene expression or genomic signatures by a given MPC type.

Cluster analysis showing gene expression patterns in bone marrow MPC isolated from a normal individual and patients with different leukemic conditions.

Genes with correlated expression across bone marrow MPC types: GeneSpring was used for cluster analysis. Prior to application of an agglomerative hierarchical clustering algorithm, microarray signals were normalized across experiments (i.e., from one MPC type to another) making the median value of all of measurements unity, so different experiments are comparable to one another. The signals were also normalized across genes in order to remove the differing intensity signals from multiple experimental readings. Genes that are inactive across all samples were eliminated from analysis. Notably, 7398 genes out of 12,626 genes (present on the Affymetrix genechip used) passed the filter of a normalized signal intensity of at least 0.1 across at least one of the five experiments performed. Cluster analysis was performed with standard correlation (same as Pearson correlation around zero) as the distance metric, a separation ratio of 0.5 and a minimum distance of 0.001 as provided by the software application. A closer relationship between CML- and MM-associated MPCs was observed, which in turn are related to AML-associated MPC, thus transforming global patterns of gene expression into potentially meaningful relationships.

Two-dimensional cluster analysis of tissue vs. gene expression vectors: A gene tree was constructed. Genes cluster near each other on the "gene tree" if they exhibit a strong correlation across MPC experiments and MPC tree branches move near each other if they exhibit a similar gene expression profile. The data indicated that the two-way clustering readjusted the location of a number of

genes resulting in accentuation of genomic signatures of each cell type. Investigators can usefully catalog genes composing any unique or signature cluster of interest by creating a gene list and disclosing their identities.

Self-organizing map (SOM) clusters (6x5) show differential gene expression in bone marrow MPC isolated from different hematopoietic conditions.

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Generation of SOM clusters involved prior normalization and filtering of the data. SOM algorithm was applied as provided by GeneSpring. Visualization of SOM clusters in combination with hierarchical clustering (i.e., MPC tree) revealed correlated meaningful patterns of gene expression. Predicated on the basis of SOM operating principle, the related SOM clusters tend to be located physically close to each other. For example, the juxtaposition of the SOM clusters with the common denominator containing genes that are up-regulated in AML/MDS-associated MPC. Whole or part of any SOM cluster can be selected to make a gene list providing the identities of the genes involved.

Genes highly expressed in normal MPC but absent or minimally expressed in leukemia-associated MPC

Lists of genes that are down-regulated in leukemia-associated MPC (AML/MDS, CML and MM) were created in comparison to normal MPC. A Venn diagram was made using these three gene lists. GeneSpring allows creation of sublists of genes corresponding to union, intersection and exclusion. Transcriptional profiles of any of these sublists of genes can be visualized across MPC samples of interest. The following is one such sublist of genes containing genes that are highly expressed in normal MPC and down-regulated in leukemia-associated MPCs revealing the identity of the subset of genes of interest: putative, wg66h09.x1 Soares Homo sapiens cDNA clone, Homo sapiens mRNA for CMP-Nacetylneuraminic acid hydroxylase, Homo sapiens cDNA clone DKFZp586G0421 (symptom: hute1), Human mRNA for histone H1x, Putative monocarboxylate transporterHomo sapiens gene for LD78 alpha precursor, Interacts with SH3 proteins; similar to c-cbl proto-oncogene product, wg82b12.x1 Soares Homo sapiens cDNA clone, Human atrial natriuretic peptide clearance receptor (ANP C-receptor) mRNA, Human 71 kDa 2'5' oligoadenylate synthetase (p69 2-5A synthetase) mRNA, Homo sapiens hMmTRA1b mRNA, Human G0S2 protein gene, Preproenkephalin, Human guanylate binding protein isoform I (GBP-2) mRNA, Human gene for

hepatitis C associated microtubular aggregate protein p44, 17-kDa protein, Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA, GS3686, Human monoamine oxidase B (MAOB) mRNA, Insulin-like growth factor II precursor, Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA, Similar to ribosomal protein L21, X-linked mental retardation candidate gene, and Homo sapiens mRNA; cDNA DKFZp434A202. Genes not expressed in normal MPC but highly expressed in leukemia-associated MPC

Lists of genes that are upregulated (instead of down-regulated) in leukemia-associated MPCs (AML/MDS, CML and MM) were created in comparison to normal MPC and a Venn diagram was made. The following is one such sublist of genes containing genes that are inactive in normal MPC but up-regulated in leukemia-associated MPCs revealing the identity of the subset of genes of interest: Beta- tropomyosin, Homo sapiens clone 24659 mRNA sequence, Human mRNA for DNA helicase Q1, OSF; contains SH3 domain and ankyrin repeat, ym22b12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone, Human mRNA for pre-mRNA splicing factor SRp20, Human mRNA for golgi alpha-mannosidasell, OSF-2os, Homo sapiens gene for Proline synthetase, hk02952 cDNA clone for KIAA0683, wi24g10.x1 Homo sapiens cDNA clone, Lysosomal enzyme; deficient in Sanfilippo B syndrome, CTP synthetase (AA 1-591), WD repeat protein; similar to petunia AN11, Human mRNA for 5'-terminal region of UMK, complete cds, Homo sapiens chemokine exodus-1 mRNA, complete cds, Human GPI-H mRNA, complete cds, Homo sapiens mRNA encoding RAMP1, Transforming growth factor-beta-2 precursor, and Homo sapiens mRNA for KIAA0763 protein.

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Visualizing expression of phenotypically & functionally relevant genes across samples of normal & disease-associated BM MPC.

Although GeneSpring is a highly flexible and user-friendly software application, it lacks the facility to create functionally relevant gene lists containing user-defined key words. This limitation was overcome by devising the following method via Microsoft Excel. A stepwise protocol to create such a gene list using Excel includes: Open the annotated microarray genome file (e.g., Affymetrix U95A) in Excel \rightarrow select the column with gene names \rightarrow select Data from pull-down menu \rightarrow Filter \rightarrow AutoFilter \rightarrow Custom \rightarrow enter key words (e.g., cell adhesion or cell cycle) \rightarrow OK \rightarrow generates a new Excel worksheet with the list of genes containing the key

words. Copy and paste the list of genes containing the key words into GeneSpring and save the gene list with a meaningful name. Twenty-two (22) such functionally relevant gene lists (Table 2) were created.

The resulting approach is a simple and powerful way to peer into the expression profiles of focused sets of functionally relevant genes across samples of interest. For example, the human vascular cell adhesion molecule-1 (VCAM-1) gene is completely down-regulated in AML/MDS and the human insulin-like growth factor binding protein (hIGFBP1) gene is up-regulated in AML compared to all other samples. Similarly, *Homo sapiens* gene for LD78 alpha precursor is down-regulated in all of leukemia-associated MPCs. Finally, the lineage markers CD45 and CD68 are essentially absent from the leukemia-associated MPCs attesting to the high degree of purity achieved by the sample preparation technique of the present invention.

Results

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The genomic changes observed in leukemia-associated MPCs are striking. As shown in Table 2, the changes (up-regulation and/ or down-regulation) involved hundreds of genes. These changes were most dramatic in MPC associated with AML arising in a background of MDS and involved multiple classes of genes (Tables 1-2). Expectedly, the TNFa-induced changes were extensive. Given the high level of purity of MPC preparations, the enormous genomic changes observed are reflective of the underlying pathologic lesions in the MPCs themselves (and not due to the contaminating leukemic cells and/ or macrophages). These studies strongly support the hypothesis that stromal cells in a leukemic patient are functionally defective and therefore purified MPCs are of value in restoring the loss of hematopoietic function in leukemic patients.

Table 2. Magnitude of global gene expression changes in leukemia-associated and TNFa-stimulated MPCs in comparison to normal MPC

	AML/MDS MPC	CML MPC	ММ МРС	TNFa MPC
# of genes up- regulated	234	112	108	279
# of genes down- regulated	379	208	251	164

Table 3. Functional classes of genes analyzed across normal and leukemiaassociated MPCs

Annexins (14) Caspases & apoptosis- related transcripts (33) Cadherins (50) Calmodulins/ calmodulin- dependent kinases (25) Cell adhesion molecules (20) Cathepsins (19) Collagens (71)	Cell division cycle-related transcripts (36) Cytokines (19) Epidermal growth factors and related transcripts (22) Fibroblast growth factors (21) Fibronectins (6) Galectins (6) Growth factors (136)	IGF system (24) Interleukins/ receptors (76) Integrins/ disintegrins (70) Lineage-related markers (19) Laminins (13) Platelet-derived growth factors & receptors (12) TNF alpha-related transcripts (29) TGF beta-related transcripts (25)
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The gene lists in Table 3 were created as described above and analyzed using GeneSpring. The numerical value in parenthesis refers to the number of transcripts in the corresponding class of genes analyzed.

Example 6

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The present invention provides the following benefits: a) identification and documentation of BM stromal cell gene expression patterns under varied, normal, and leukemic hematopoietic conditions; b) identification of stromal cell genes that can be therapeutic targets for improvement of normal hematopoietic function that is constantly compromised in leukemic patients, and identification of similar targets for arresting the growth and progression of neoplastic clones since stromal cells provide the necessary support for preferential growth of leukemic cells (CLL, MM) within BM and protect the leukemic cells from chemotherapy-induced death (MM); and c) identification of new biological bases and new diagnostic markers for refinement of the classification and diagnosis of leukemia. This present invention can also lead to important insights into the pathogenesis of leukemia. In broad terms, analysis of global gene expression or transcriptome (transcriptional profile composed of all transcribed regions of the genome) is considered a nonbiased discovery-driven (as opposed to hypothesis-driven) approach to the analysis of gene expression. A stepwise genomic strategy encompasses preparation of total RNA from cells of interest, to generation of cDNA, to preparation of ds DNA, to in vitro transcription into cRNA, to fragmentation of cRNA, to hybridization of target RNA, to a microarray of known genes (and/or ESTs), to analysis of

differentially expressed genes using an appropriate software to discern the patterns of gene expression or genomic signatures by a given disease-associated cell type.

Further test utility of sample preparation technology applied to normal EM-derived MPCs (untreated and treated with representative cytokines) and MPCs derived from patients with representative pre-leukemic and leukemic conditions for performance of high-resolution DNA microarray technology (Affymetrix genechip containing DNA from 12,000 known human genes, e.g., U95A oligonucleotide microarray).

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Representative cytokines which are pathologically altered in hematopoietic conditions and that can be used in this study include TNF- α , TGF- β and interferon- γ . The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), acute lymphocytic leukemia (ALL), and multiple myeloma (MM).

The front-end strategy of microarray analysis involves the use of Percoll-gradient purified MPCs. As a follow-up strategy, to validate the stromal cell origin of the differentially expressed genes, MPCs obtained from cytospins of BM stromal cells by laser-capture microdissection (LCM) selected on the basis of morphology (Figure 3) are used followed by "real-time" quantitative polymerase chain reaction (PCR). This can be performed with an LGM system as well as a "real-time" QPCR system. Validation can be performed on at least one sample from each of 6 normal BM M7NC/ MPC types and on one sample from each of 5 leukemia-associated MPC types. Validation is considered successful if the microarray results and PCR results on a given MPC sample match using a suite of 20 genes selected based on median pattern of microarray results for the given cell type. This approach not only validates the microarray results but also ascertains the stromal cell origin of the expressed genes. The standard published protocols involving LGM and "real-time" quantitative PCR and the instructions accompanying the equipment are used for performing the experiments.

Stepwise LCMJ real-time QPCR protocol entails the following. Cytospins are made from BM stromal cells. The cytospins are stained with hematoxylin and MPC is selected for based on morphology. Microdissect up to 1,000 MPC from each sample. RNA is extracted and reverse transcribed into cDNA.

The cDNA is amplified using gene-specific primers and "real-time" quantitative PCR.

By applying the combined power of different analytical techniques (such as hierarchical clustering and self-organizing maps) together with the recently developed sample preparation technology for stromal cells the present invention provides a molecular biological basis that can allow refinement of the classification and diagnosis of leukemias and lymphomas, uncovering the suspected disease heterogeneity. This enables the deciphering of the genomic expression profiles or signatures of bone marrow stromal cells in about 10 different physiologic states and about 20 different leukemic states. In addition to aiding in refinement of the classification and diagnosis of the hematopoietic malignancies, the data provides clues to potential novel drug targets and insights into pathogenesis.

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The present invention functions by identifying the MPC genes that are differentially expressed after stimulation with different hematopoietic cytokines implicated in the pathogenesis of pre-leukemic conditions (MDS); in actual pre-leukemic disorders (MDS); and in overt leukemias (CML, AML, CLL, ALL, MM) as well as in lymphomas that have a leukemic phase with involvement of BM.

The present invention is accomplished by first determining the median gene expression profiles for MPCs associated with each disease and stimulated by each cytokine of interest (this objective can be achieved by treating the gene expression vectors of individual cases in each MPC category as replicates; this capability is available in GeneSpring software application). Then the gene groups that are up regulated and down regulated and that are common to all the members in a given MPC category are identified (this is accomplished using a series of Venn diagrams and creating required gene lists via GeneSpring). Finally, the up-regulated and down-regulated gene sets for a given disease-associated or cytokine-stimulated MPC are combined. This allows the identification of gene sets with minimal number of elements that are unique to a given MPC type with a capability to discriminate one MPC type from another (this can also be accomplished by means of a series of Venn diagrams and lists of required genes obtained via GeneSpring). Such gene sets can be of immense diagnostic value as they can be routinely used in an assay simpler than microarray analysis (for example "real-time" quantitative PCR). Such gene sets can additionally provide insights into pathogenesis and possible targets for design of new drugs.

Determine expression profiles of MPC genes which are regulated as a result of exposure of normal MPCs to cytokines that are known to have a hematopoietic support role and/or are abnormally elevated in pre-leukemic/leukemic conditions, i.e., TNF α ; IL-4; TNF α + IL-4; interferon γ , TGF β ; PDGF; FGF; EGF; and calmodulin.

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TNF α , IL-4 and IFN γ are potent negative regulators of hematopoiesis. Notably these cytokines, especially TNF α , are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and thrombocytopenia (i.e., pancytopenia). TNF α and IL-4 are thus possible mediators of hematopoietic dysregulation typical of MDS. Studies regarding these regulators can uncover the molecular pathways leading to cytopenias in MDS patients. As indicated earlier, myeloproliferative disorders are another, in some ways similar, group of hematopoietic disorders that are clonal in origin but not overtly malignant clinically. These MPDs include polycythemia vera, essential thrombocythemia, idiopathic myelofibrosis (agnogenic myeloid metaplasia) and chronic myelogenous leukemia. These disorders have the potential to change from one to the other at any time, however the signals that trigger such conversion remain enigmatic. Idiopathic myelofibrosis (IMF), in which stromal cells seem to play a profound pathogenetic role, is characterized by fibrosis of the marrow cavity, extramedullary hematopoiesis, splenomegaly, and anemia and leukoerythroblastic features in the peripheral blood. While myeloproliferation is known to be a clonal process, the accompanying stromal cell proliferation and fibrosis are believed to be a polyclonal reactive process that is likely to be due to increased intramedullary activity of a number of cytokines including TGF β, PDGF, FGF, EGF and calmodulin, as shown by other investigators.

Cancer genomics is a rapidly expanding area of investigation. The focus is unique however in emphasizing not the leukemic cells themselves but rather BM stromal cells that provide a haven to various types of pre-leukemia and leukemia cells, non-Hodgkin's lymphomas (NHLs) and metastatic cancers (METs). Pre-leukemic clonal neoplastic conditions include myelodysplastic syndromes (MDSs) and myeloproliferative disorders (MPD5). Stromal cells are known to produce and/or respond to growth factors such as EGF, PDGF, FGF, VEGF, and cytokines such as IL-I or TNF a, partially explaining the interactive relationship between stromal cells

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and cancer cells, especially in MDS and CML.

Table 4, accounting for a total of 310 samples.

In spite of similarities between BM stroma and non-BM stroma, certain sharp distinctions do stand out. Non-BM stromal cells are terminally differentiated fibroblasts, while BM stromal cells represent a unique pluripotent or pluridifferentiated mesenchymal cell type, thus exhibiting preserved developmental "plasticity". Using 5-10 cc BM aspirate samples from adult leukemic patients and 3-5 cc BM samples from pediatric patients with ALL, the study can analyze the BM stroma. One cc of marrow sample can produce at least 1 T-150 flask of stromal cells. One concern is that it can be hard to obtain marrow samples from cases like CML and myelofibrosis. In such cases stromal cells are grown using peripheral blood samples as described in the prior art. At least one flask of stromal cells (i.e., 1 cc marrow) to yield the RNA required for analysis. About 10 cases of each type of leukemia/lymphoma were studied. The study provided important insights into the functioning of the BM microenvironment in normal and leukemic hematopoiesis.

A database including all of the above information and that can include age, gender and associated major illness in terms of clinical/pathologic diagnosis for each subject/patient can be created. This can also include information on cytogenetic, molecular and flow cytometric studies. Finally, also included can be the information on clinical course in terms of disease progression and response to treatment exercising adequate care to protect the identity of individual patients. The study analyzed genomic expression profiles or signatures of bone marrow stromal cells derived from about 12 different normal bone marrow states and about 19 different leukemia/lymphoma states, approximately 10 cases of each as shown in

Using the information of the present invention, those of skill in the art can: a) study select gene or sets of genes as relevant to hematopoietic disease conditions using relatively inexpensive but low-throughput technologies such as Northern blotting, RNase protection assays and/or PCR intended for gene expression analysis; b) reanalyze the primary data by using newer and more powerful bioinformatic tools as they become available; and/or c) identify newer drug targets and diagnostic markers relevant to specific diseases, such as MM or CML etc.

Table 4 Scope of human BM samples targeted for DNA microarray analysis (approximately 10 cases of each)

Normal BM mononuclear cells (NMNC)

Normal BM stromal cells, unfractionated and unstimulated (NBMS)

Normal purified mesenchymal progenitor cells, unstimulated (NMPC)

NMPC stimulated with 9 different cytokines:

5 NMPC stimulated with TNF α (TNF α MPC)

NMPC stimulated with TGFβ (TGFβ MPC)

NMPC stimulated with interferon y (IFNy MPC)

NMPC stimulated with 1L-4 (IL-4 MPC)

NMPC stimulated with TNF α + IL-4 (TNF α + IL-4 MPC)

10 NMPC stimulated with PDGF (PDGF MPC)

NMPC stimulated with EGF (EGF MPC)

NMPC stimulated with FGF (FGF MPC)

NMPC stimulated with calmodulin (calmodulin MPC)

MDS - Refractory anemia (MDS-RA MPC)

15 MDS - Refractory anemia with ringed sideroblasts (MDS-RARS MPC)

MDS - Refractory anemia with excess blasts (MDS-RAEB MPC)

MDS - Chronic myelomonocytic leukemia (M1)S-CMML MPC)

MPD - Polycytheniia vera (MPD-PV MPC)

MPD - Essential thrombocythemia (MPD-ET MPC)

20 MPD - Myelofibrosis (MPD-LMF MPC)

CML (CML MPC)

AML-MO/M1/M2 (AML-MOJM1JM2 MPC)

AML-M3 (APL) (AML-M3 MPC)

AML-M4/M5 (myelomonocytic) (AML-M4i'M5 MPC)

25 ALL-L1/L2 (lymphoblastic) (ALL-L1/L2 MPC)

ALL-L3 (Burkitt's) (ALL-L3 MPC)

Multiple myeloma (MM MPC)

CLLISLL (CLL/SLL MPC)

Follicle center cell lymphoma (FCL MPC)

30 Mantie cell lymphoma (MCL MPC)

Lymphoplasmacytic lymphoma (LPL MPC)

Marginal zone lymphoma (MZL MPC).

Human Subjects

This study involves the use of bone marrow (BM) samples from human subjects. BM samples can be obtained from normal subjects (male and female 20-45 years) as well as leukemic patients after informed consent is obtained. Leukemic cells can be obtained from diagnostic samples of BM of adult and pediatric patients (in those cases in which cells remain unused after clinical diagnostic studies are

preformed; i.e., about 90% of cases).

Example 7

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In broad terms, global gene expression analysis is considered a nonbiased discovery-driven (as opposed to hypothesis-driven) approach to the analysis of protein expression. A stepwise proteomics strategy encompasses: solubilization of proteins from cells of interest; 2-D gel electrophoresis (IPG DALT); staining and image analysis of gels; excision of protein spots of interest; trypsin digestion of proteins; mass spectrometry (MALDI-TOF MS and/or ESI MS/MS) performed on tryptic fragments; identification of proteins by database searching. The present invention provides a method to analyze the population of expressed proteins (i.e., proteome) of BM MPCs in relation to hematopoiesis in collaboration with a state-of-the-art mass spectrometry facility.

The large-format 2-D gel electrophoretic system is used for reproducible separation of MPC proteins and to prepare 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g., TNF α and/or IL-4) and for MPCs derived from patients with representative pre-leukemic/premalignant and leukemic/malignant conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples can consist of culture supernatants/secreted proteins; extracellular matrix (ECM) proteins; plasma membrane proteins solubilized using a three-step differential extraction protocol, employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

The system of the present invention can be used to differentially express MPC proteins (i.e., those that increased or decreased in intensity as compared to 2-D PAGE protein maps of normal, unstimulated MPCs) using mass spectrometry (MALDI-MS and/or nanoelectrospray ionization MS/MS) and/or Western blotting and/or Western-ligand blotting.

Using high-resolution proteomics with the added power of high-

throughput robotics, enables the system to identify on a larger (semi-comprehensive) scale the MPC proteins that are differentially expressed in conditions that simulate pre-leukemic bone marrow (following stimulation with different cytokines); and in actual pre-leukemic disorders (MDS) as well as in overt leukemias (CML, AML, CLL, ALL, MM).

The system of the present invention enables the identification of MPC proteins whose expression is regulated as a result of exposure of normal MPCs to cytokines that are known to have a hematopoietic support role and/or are abnormally elevated in pre-leukemic/leukemic conditions, i.e., TNF α ; IL-4; TNF α + IL-4; interferon γ , TGF β ; PDGF; FGF; EGF; and calmodulin.

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The system of the present invention also enables the identification of MPC proteins for which expression is altered as a result of exposure of normal MPCs to agents that are clinically used for mobilization of hematopoietic stem cells from BM into peripheral blood to facilitate easy collection and subsequent transplantation, e.g., G-CSF and G-CSF plus cyclophosphaniide.

Further, the system of the present invention enables the identification of Identify the MPC proteins whose expression is pathologically altered in hematopoietic disease states such as: MDS, CML, AML, CLL, ALL and MM by matching the 2-D PAGE protein maps of disease-associated MPCs with the 2-D PAGE database of normal MPCs. If a protein of interest does not exist in the normal MPC proteome, or if it exists in the normal MPC proteome but has not yet been characterized, then such proteins can be identified by MALDI-MS and/or Nano ESI MS/MS.

The system facilitates understanding of the pathogenetic mechanisms by identifying the phosphoproteins involved in cell signaling pathways. The systems immunoblots the whole cell lysate proteins of normal MPCs, untreated and treated with respective cytokines, using antibodies to phosphotyrosine, phosphoserine, and phosphothreonine. The system then locates the corresponding putative phosphoprotein spots on the gel and identifies the proteins by MALDI-MS and/or Nano ESI MS/MS. Similarly, the system can locate the altered phosphoproteins by immunoblotting the whole cell lysate proteins of untreated MPCs derived from leukemic patients. If a protein of interest does not exist in the normal MPC proteome, or if it exists in the normal MPC proteome but has not yet been identified,

then MALDI-MS and/or Nano ESI MS/MS can identify the protein.

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Bone marrow MPCs derived from a leukemia background express distinctively different patterns of cell adhesion molecules from normal MPCs.

BM stromal cells provide the background required for homing and subsequent proliferation and differentiation of hematopoietic stem cells. BM stromal cells also provide a rich microenvironment for metastases and growth of various leukemias. Based on the hypothesis that homing of normal hematopoietic cells and leukemic cells to marrow utilize the same adhesion mechanisms, it was questioned whether there are fine regulatory distinctions in terms of quantitative differences in the expression of the adhesion molecules in normal vs. leukemic BM microenvironments. In a pilot study 11 cell adhesion molecules (CAMs) and several lineage-associated markers for Northern blot analysis were targeted. Dexter-type cultures were grown under standard stromal cell culture conditions using bone marrow samples from a normal individual and from one patient diagnosed with and treated for acute myelogenous leukemia (AML). Representative cultures were treated with cytokines such as TNF α alone, IL-4 alone, and TNF α plus IL-4. MPCs from unstimulated and cytokine-treated cultures were purified using Percoll gradient techniques disclosed above. Total RNAs were extracted by a standard method and analyzed by Northern blotting. This study demonstrated expression by MPCs of several CAMs, heretofore unsuspected of expression by BM stroma. These include an embryonic endothelial cell protein Dell (developmental endothelial locus 1), galectin-I, human milk fat globule protein (RMFG, lactadherin), and epithelial membrane protein I (EMP 1). Secondly, MPCs from the AML patient expressed significantly lower levels of mRNA for three CAMs Del- 1, galectin- 1, and collagen type 1 as well as for the adipocyte marker adipsin, and to a minor degree the muscle-associated protein caldesmon. On the other hand, mRNA for CAMs like TGF beta-inducible BiGH3, HMFG, osteoblast-specific cadherin 11, and VCAM1 were dramatically increased in AML-associated MPCs. CAMs such as integrin beta 5, fibronectin, EMP 1 and the muscle-associated molecule transgelin are variably increased in diseased MPCs and appear to be unaffected by treatment with cytokines tested. ICAM I was undetectable at basal level in either patient or normal samples, but was slightly elevated by TNF α and markedly elevated by TNF α plus

IL-4. VCAM1 was mildly up regulated by TNF α alone or IL-4 alone, but markedly up regulated by TNF α /IL-4 in combination. Also, the MPCs from the patient were much more sensitive to stimulation by these inflammatory cytokines than were the normal MPCs. These studies establish that stromal cells in a leukemic patient are functionally defective.

Role of leptin receptor in hematopoiesis using human marrow stromal cells as a model.

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The receptor for the product of the obesity gene, leptin, is widely distributed in tissues ranging from central nervous system to reproductive system to hematopoietic system. Within hematopoietic system, OB-R is reportedly expressed on diverse cell types ranging from early CD 34+ hematopoietic stem cells to circulating monocytes. Leptin acts on monocytes to induce production of TNF α and IL-6, which are powerful regulators of hematopoiesis. However, literature reports on the expression of leptin or its receptor on stromal cells are infrequent. To date, one particular report suggests that leptin acts on the stromal cells to enhance their differentiation into osteoblasts and to inhibit differentiation into adipocytes. Because leptin is an adipocyte-generated hormone and because marrow stromal cells represent a unique pluridifferentiated mesenchymal cell type expressing some adipocytic features, the expression of the leptin receptor by these cells was investigated in the hope of revealing its role in hematopoiesis.

By Northern blotting marrow stromal cells showed abundant expression of OB-R, consistent with their adipocytic nature. In terms of regulation, exposure of the stromal cultures to different cytokines revealed an interesting pattern of OB-R. As shown, G-CSF and TNF α down-regulated OB-R while IL-4 upregulated OB-R expression by stromal cells. Simultaneous treatment of stromal cultures with TNF α and IL-4 nearly abolished OB-R expression. The expression of OB-R was also analyzed at the protein level by a high-resolution, high capacity 2-D PAGE system, followed by Western blotting.

More specifically, the method provides the identification of leptin receptor in human BM stromal cell membrane protein extracts using 2-D Western blotting. The expression of OB-R was investigated at protein level using 2-D PAGE, followed by Western blotting. Two isoforms differing in molecular weight of 2.2 kDa (60.2; 62) and an isoelectric point of 0.2 pH unit (5.78; 5.98, respectively) have been

identified (the pH was determined by using the values specified by the IPG strip manufacturer). The ability to subsequently stain the same Western blot with gold stain allowed precise localization of the immunoreactive protein spots of interest on the blot. The gold staining of the blot, by revealing other protein spots in addition to the immunoreactive spots, has provided the necessary landmarks in turn facilitating subsequent alignment with the silver-stained gel using an appropriate 2-D analysis software program (Melanie 3).

This technique has identified two OB-R isoforms that differ in molecular mass by 2.2 kDa (60.2; 62.4) and differ in their isoelectric point by 0.2 pH units (5.78; 5.98). The level of macrophage contamination is determined by two macrophage markers, CD68 and cathepsin B. The studies include the determination of OB-R expression in a) unfractionated stromal cells vs. isolated pluri-differentiated mesenchymal progenitor cells; b) unstimulated cultures vs. cultures stimulated with a variety of cytokine/hormones including leptin itself. The studies also include mass spectrometric characterization of the two OB-R isoforms detected by Western blotting in order to establish their exact structural differences.

Proteome analysis of 2-D PAGE separated human BM stromal cell membrane proteins.

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BM stromal cells support the growth and development of normal blood cells as well as providing a haven for malignant leukemia/lymphoma cells. Focusing on stromal cell-surface proteins as potentially playing a role in cell-to-cell communication in normal as well as in abnormal hematopoiesis, the mixtures of stromal-cell plasma membrane, and plasma membrane-associated proteins were analyzed by a high-resolution, high-capacity 2-D gel electrophoresis. The 2-D system described utilizes an immobilized pH gradient gel (pH 4-7) in the first dimension and a mini nondenaturing but high-resolution lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDS-PAGE) in the second dimension. As identified by silver staining, this system has resolved greater than 800 protein spots in a pH interval of 2.5 units (4.25-6.75, the isoelectric pH range for most of plasma membrane proteins to migrate) and a molecular mass range of 10-150 kDa. Equally important, the system is compatible with high sample loads (up to 1.5 — 2.0 mg of total protein in up to 350-μl sample volume). All the protein species identifiable by a silver stain that is compatible with subsequent mass spectrometric analysis have

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been analyzed by a 2-D gel software with respect to isoelectric point, molecular weight and mass abundance. The lectin-binding status of these proteins has also been determined by lectin blotting. Lectin blots and Western blots have subsequently been stained by a gold stain for detection of total proteins on the same PVDF membrane. Although gold-staining of the Western blot is not as sensitive as silver-staining of the gel, gold-staining of the Western blot generates the necessary landmarks for alignment with the silver stained gel, facilitating excision of spots of interest from the gel for identification by MALDI-MS. Representative protein spots were excised from gel and subjected to mass spectrometric profiling (MALDI-MS) and/or sequencing (Nano ESI MS/MS) with subsequent database searching. resulting in a productive identification of ten proteins. The protein digests are then submitted in a near-ready state for mass spectrometry. Upon receiving the MS data the group performs the database searching. MALDI/MS has been used, which identifies a protein on the basis of its characteristic mass sizes, as well as MS/MS studies that provide amino acid sequences of selected masses to identify proteins with enhanced specificity and confidence level. This work represents the first systematic attempt to analyze BM stromal cell proteins by high-resolution 2-D gel electrophoresis and provides the basis for a full-scale proteome mapping of the marrow stromal cells. The present work can facilitate the long-term goal of deciphering the hematopoietic support functions of BM stromal cells.

Modulation of stromal cell plasma membrane protein expression by TNF α /IL-4.

The effects of TNF α TM on bone marrow stromal cell plasma membrane protein expression has been tested using the described system. TNF α and IL-4 are regarded as negative regulators of hematopoiesis. Notably these cytokines, especially TNF α , are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and thrombocytopenia (i.e., pancytopenia). TNF α and IL-4 are thus possible mediators of hematopoietic dysregulation typical of MDS. TNF α IL-4 treatment of the stromal cultures induced dramatic changes in the protein profile. Initial studies using plasma membrane protein samples show reduced expression of at least 7 proteins and enhanced expression of 13 proteins.

Analyzing the insulin-like growth factor system in human marrow stromal cells

by 2-D PAGE analysis of BM stromal cell culture supernatants.

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Proliferation and development of normal and leukemic hematopoietic cells within bone marrow is regulated by interplay of various classes of molecules. These include cell adhesion molecules (CAMs), colony stimulating factors (CSFs), and cytokines as well as growth factors including insulin-like growth factors 1 and 2 (IGF 1 and IGF 2), which are small peptide homologs of prolinsulin. IGF 1 has known erythropoietic activity, whereas the function of IGF 2 is less clear. IGF 1 and 2 exert their activities through two types of receptors. The type I IGF receptor, a tyrosine kinase receptor highly homologous to the insulin receptor, binds to IGF 1 and IGF 2 with high affinity. The type II IGF receptor, a mannose 6-phosphate receptor that lacks intrinsic kinase activity, binds IGF 2 with high affinity and IGF I with low affinity. The type and number of receptors expressed on a target cell determine the strength of the IGF signal. One important key to understanding the IGFs' role in hematopoiesis is to appreciate how biological effects of receptors are modulated by larger soluble proteins, the IGF binding proteins (IGFBPs), which share no homology with the IGF receptors. Because IGFs and IGFBPs play important roles in cell growth and proliferation in many tissues, and because marrow stromal cells support hematopoietic growth and development, the patterns of expression of the IGF system components by marrow stromal cells cultured under serum-free conditions is necessary. To this end, unfractionated and purified stromal cells were analyzed, side-by-side, by Northern blotting, under varied stimulatory conditions for expression of IGFs and IGFBPs with surprising results. IGF 2 is constitutively expressed at a high level by macrophages in Dexter cultures; it is down regulated markedly by TNF α alone; moderately by TNF α plus IL-4; and unaffected by IL-4 alone. On the other hand, IGF 2 is minimally expressed by unstimulated MPCs, but is markedly up regulated by TNF α alone or IL-4 alone; and moderately up regulated by combined TNF α and IL-4. IGFBP4 is abundantly expressed both by macrophages and MPCs and is unaffected by cytokine treatment. In contrast, IGFBPs 5, 7, and 10, selectively expressed by MPCs, show no evidence of expression by macrophages and are unaffected by cytokine treatments. IGF 1 and the precursor to IOFBP 3 are not expressed in either macrophages or MPCs, either constitutively or after stimulation with TNF α , IL-4 or both. In initial studies, bone marrow mononuclear cells expressed none of the IGFs or IGFBPs tested. These

results provide important insights into the operation of the IGF system in stromal cells and it is likely that potentially novel IGFBPs can be uncovered by ligand blotting studies.

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The present invention provides a large-format 2-D gel electrophoretic system for reproducible separation of MPC proteins and to prepare 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g. TNF α or IL-4) and for MPCs derived from patients with representative pre-leukemic and leukemic conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples can consist of culture supernatants/secreted proteins; extracellular matrix (ECM) proteins; plasma membrane proteins solubilized using a three-step differential extraction protocol employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

Molecular analysis assay involving the high-resolution 2-D PAGE and mass spectrometric identification of gel-separated proteins.

The completion of human genome project has provided a huge proteome database including the theoretical mass databases generated on the basis of site-specific cleavage employing proteolytic enzymes, such as trypsin and others. The availability of highly sensitive biological mass spectrometers together with the capability of bioinformatics to search extremely large amounts of data and identify the relevant proteins matching the mass spectrometry data provides the basis for the current excitement in proteomics. The focus of the interest is the BM MPC proteome as expressed under varied functional and disease states. The goal of the present invention is to identify BM MPC proteins that have possible functional and/or pathologic significance, that is, those proteins that show altered levels of expression in response to cytokine treatments and various leukemic states.

Until recently, the focus of the laboratory has centered on isolation and characterization of BM stromal cell adhesion molecules using a novel 2-D cell

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blotting technique. For this purpose, applicants have established an analytical 2-D mini gel system that separates stromal cell plasma membrane proteins using 18-cm long 4-7 pH range IPG strips in the 1st D (Amersham Pharmacia Biotech). Subsequent to IEF, the IPG strip is cut into appropriately small pieces and subjected to 2 D separation using nondenaturing lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDSPAGE) and mini gels. The reason for using mini gels in the 2nd D is that they are compatible with a downstream functional assay involving cell adhesion. The stromal cell membrane proteins are blotted on to a PVDF membrane and assayed for hematopoietic cell-binding proteins directly on the blotting membrane. The system can be extended using 17-cm long 3-10 pH range IPG strips (Bio-Rad) for separation of stromal cell culture supernatants, ECM proteins, and whole cell lysates. As detected by silver staining of the gels, and analyzed by appropriate software (GelLab II or Melanie 3) this 2-D system has resolved greater than 800 membrane protein spots within a pH interval of 2.5 units (4.25-6.75) and a MW range of 10-150 kDa. Similarly, the ECM samples showed 475 spots; and conditioned media from BM stromal cell cultures grown under serum free conditions showed 524 spots. Not surprisingly, the total cell lysate of BM stromal cultures showed only 553 spots, most likely representing the abundant housekeeping proteins and masking detection of many functionally relevant proteins. These observations provide the rationale for the proposed subproteome approach involving the use of differential solubilization of sample proteins and multiple large gels. Membrane proteins thus far identified by mass spectrometry followed by database searching; proteins are identified by standard Western blotting. Select IGF binding proteins were identified by ligand Western blotting. The blotting shows the identification of IGF-binding proteins (IGFBPs) using 2-D ligand blotting. The conditioned media from BM stromal cultures grown under serum-free conditions were concentrated using Microcon concentrator, and proteins were fractionated using a high-resolution 2-D PAGE. The separated proteins were electroblotted onto PVDF membrane and subjected to Western ligand-blotting assays using 1-125 labeled IGF-2, resulting in the identification of a series of IGFBPs (up to 30 spots). Notably, TNF α treatment of the cultures down-regulated two LGFBPs and upregulated IGFBP labeled 6.

By necessity the protein work began on BM stromal cells using a

nondenaturing (LDS-PAGE) mini gel system that contained no reducing/alkylating agents. To preserve the function of 2-D gel separated proteins many otherwise powerful sample preparation methodologies designed for proteomic studies (such as multiple surfactant solution, MSS) were avoided. While mini gels are convenient and allow comparison and information transfer to large-format gels, they are less sensitive.

Subproteomes according to sample prefractionation.

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In order to be able to identify the low-abundance proteins implicated in the regulatory and pathologic processes, a number of approaches to prefractionation of the whole cell lysates have been described. Applicant studied the subproteomes of secreted proteins from BM stromal cell culture supernatants as well as ECM proteins. Notably, the ECM protein samples can be a rich source of functionally relevant cytokines and chemokines since the latter are known to mediate function by binding to ECM. In addition, the plasma membrane and whole cell samples were subjected to the 3-step sequential solubilization protocol shown. The solubilizing solutions can be prepared in-house or purchased commercially (Bio-Rad). The first step involves the use of Tris base, which can solubilize the peripheral membrane proteins and cytosolic proteins. These proteins are lyophilized and subsequently solubilized prior to 2-D PAGE in a standard solubilizing medium (the modified O'Farrell cell lysis solution containing urea, CHAPS, DII, Iris, ampholytes and appropriate protease inhibitors). The resulting pellet can also be solubilized in the standard 2-D solubilizing medium and subjected to 2-D PAGE. Because the standard solution cannot solubulize some proteins, the membrane-rich pellet is finally solubilized in a potent multiple surfactant solution (MSS) consisting of urea, thitheea, CI-LAPS, zwittergent 3-10 and tributyl phosphine (TBP) in addition to Iris base and ampholytes that is compatible with subsequent IEF. The MSS has been shown to solubilize the hydrophobic proteins with as many as 12 transmembrane regions (TMRs), facilitating their 2-D analysis. Another final step incorporating 1% SDS in boiling sample buffer can be used to test by 1-D SDS-PAGE if any proteins remained unsolubilized after these extractions (notably, SDS extract is unsuitable for 2-D PAGE analysis since SDS interferes with IEF). The prefractionation step clearly reduces the complexity of the sample. Thus, the serial extractions not only simplify the gel images and reduce spot overlapping frequently encountered in single-step

extractions but also correlate closely with the cellular location of specific proteins, providing clues to their function. The prefractionation strategy can be extended to enriching low-abundance proteins in culture supernatants by selective removal of contaminating albumin using an Albumin Depletion Kit (containing Cibachron Blue resins) (Genomic Solutions, mc). Similarly membrane glycoproteins can be enriched by a Glycoprotein Enrichment Kit (containing lectins) prior to 2-D PAGE analysis (Genomic Solutions, Inc.).

Subproteomes according to overlapping pH gradients.

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Using a series of medium-range and partially overlapping pH gradients (3-6, 5-8, 7-10, each 17-cm long) (Bio-Rad) can enhance reproducibility and resolution by creating "virtual" gels with up to 40 cm equivalent of PI separation across a pH 3-10 range. Alternatively, a combination of two pH gradients, pH 4-7 and pH 6-11, each 24 cm-long (Amersham Pharmacia Biotech) can be used, also providing a "virtual" separation distance of 40 cm across a pH range of 4-11. These strips accept micropreparative sample loads (1-2 mg). Notably, a given sample of cells yields a total of 8 protein samples. These samples include one protein sample composed of conditioned medium, one protein sample comprising of ECM proteins, three protein samples derived from plasma membrane lysates and three protein samples derived from total cell lysates, following application of a three-step protein extraction protocol to purified plasma membranes and total cells. Eight protein samples can thus translate into 24 large format (18 cm) gels corresponding to three overlapping 1st D gels; or 16 extra large format gels (24 cm) corresponding to two overlapping 1st D gels. Proteomics is no longer considered a single 2-D gel study. Taking advantage of the common spots in the 2nd D corresponding to overlapping regions, PDQUEST software can allow "stitching together" of the constituent gels, creating the so-called "cyber gel" providing a composite map for each protein sample. The data generated can be stored in an internet-accessible 2-D PAGE database in the form of 8 submaps. Three of these submaps correspond to plasma membrane proteins representing 3-step solubilization; one of them corresponds to secreted proteins; one of them corresponds to ECM proteins; and 3 of them correspond to total cell lysate proteins representing 3-step solubilization. These submaps can be linked to a master synthetic gel, a conglomerate of the submaps, representing the so-called "cyberproteome" of MPCs. Given the ability to run up to

12 IPG strips per 1st D gel (using IPGPhor) and 10 to 12 large or extra large SDS-PAGE gels per 2nd D gel run (using Hoefer DALI and Ettan DALI II, respectively), the resulting number of gels can be well within the manageable workload of one person (36). Although not easily accessible now, some innovative technological developments are on the horizon, e.g., development of fluorescence 2-D difference gel electrophoresis (DIGE), which could minimize the tedium. Unlike the current practice of running different protein samples on separate gels, and then staining and comparing the gels, DIGE technology uses matched, spectrally resolvable dyes (e.g., Cy2, Cy3 and Cy5) to label protein samples prior to 2-D separation. Differentially labeled protein samples are mixed and co-separated by 2-D electrophoresis, allowing analysis of at least three samples on a single gel. Gels are scanned and proteins are subjected to image analysis using appropriate software. Alternatively, one can use a highly sensitive silver stain to visualize the proteins after electrophoretic separation. Notably, the silver stain is compatible with subsequent mass spectrometry analysis.

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Follow-up strategy for 2-D PAGE using the so-called ultrazoom LPG gels with narrow-range pH gradients.

Commercially available narrow-range IPG strips include pH 3.54.5; 4.0-5.0; 4.5-5.5;5.0-6.0; 5.5-6.7. These are available as 18 cm and 24 cm-long strips, consequently allowing spanning of 1 pH unit over a distance of 18-24 cm and providing extraordinary resolution. By using narrow pH gradients (lpH unit) up to 10mg of protein would be loaded onto a single IPG gel strip, either by repeated sample cup application or by in-gel rehydration without incurring vertical or horizontal streaking. Employing a combination of such narrow-range overlapping IPG strips, one study utilized up to 40 2-D gels for analysis of a single protein sample. The preference is not to follow such extreme approach but rather to use these gradients as a backup in situations where a functionally relevant protein is first detected by the front-end strategy but could not be studied by mass spectrometry for lack of adequate resolution or due to overlapping spots. The 24-cm long narrow IPG strips can be subjected to 2nd D using correspondingly extra large slab gels (the required precast, plastic-backed gels can be purchased from Amersham Pharmacia Biotech). However, the "giant 2-DE" 30 X 40cm size gels are impractical to handle. The situations for the use of narrow range pH gradients include situations like detection

of proteins by Western blotting using anti-phosphotyrosine antibodies or Western ligand blotting using labeled IGF 1 or 2, which are probably more sensitive than silver staining. Consequently, these assays identify the functionally relevant proteins but without providing the actual identity of the individual proteins. Because the frontend strategy can at least provide the range of the phosphoprotein or the IGF-binding protein identified, on the basis of this information samples can be subjected 2-D PAGE using the appropriate ultrazoom IPG strip, which as indicated above can permit loading of several mg of protein sample. Extra large precast slab gels (26x20 cm) with plastic backing suitable for running the 24-cm long ultrazoom IPG strips and the appropriate electrophoretic system (Ettan DALI II 2 dimension electrophoresis system) that runs up to 12 of these gels are commercially available (Amersham Pharmacia Biotech).

Summary of subproteome strategy.

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The subproteome approach involves: 1) Cellular fractionation involving isolation of purified MPCs. 2) Subcellular fractionation involving preparation of functionally relevant protein sets. These include: 2a) secreted proteins such as colony stimulating factors (CSFs), cytokines, etc in the conditioned media; 2b) ECM proteins such as cell adhesion molecules (CAMs), etc; 2c) plasma membrane proteins such as various receptor molecules, CAMs and components of cell signaling systems, etc; 2d) finally, whole cell lysate proteins that include some of these proteins plus cytosolic and nuclear proteins. The cytosolic and nuclear proteins can be a rich source of target proteins for phosphorylation with a regulatory function.

2-D PAGE data capture and analysis

2-D PAGE data capture and analysis can be performed using standard equipment and protocols. Silver-stained gels can be scanned using an imaging densitometer and processed with QuantOne software (Bio-Rad) whereas gels stained with fluorescent Sypro Ruby (with 450 nm in the excitation range) can be scanned using a STORM 860 gel and blot imaging system and processed with ImageQuant Solutions software (Amersham Pharmacia Biotech). A number of factors, including differences in sample preparation and loading, staining and image acquisition can influence the reproducibility of 2-D gel protein separation. Quantitative data are reported as spot volumes (integrated spot densities). In

experiments comparing replicate 2-DE patterns of the same sample or 2-DE patterns of samples from different individuals, the spot volumes in each pattern are scaled to correct for differences in the total amount of protein loaded onto each gel. These variations are compensated by accurately comparing the quantity of any spot across multiple gels. These operations can be performed using a dedicated 2-D gel analysis software, Melanie 3. This program can analyze such variations by scatter analysis and can compensate for varying staining absorption across proteins by normalizing protein expression change. Varying stain intensities and sample sizes can be compensated for by relative spots quantification. The Melanie 3 software also has the capability to merge several gel electrophoretic patterns from the same sample into a composite gel, providing fine control over the included proteins. Finally, the software can compensate for gel distortions caused by variations in protein migration through alignment of the gels.

Mass spectrometric instrumentation.

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Examples of such mass spectrometers include, but are not limited to, Voyager DE Pro (Applied Biosystems, formerly Perceptive Biosystems, Inc.) and QSTAR (Applied Biosystems). Voyager DE Pro is a matrix-assisted laser desorption time-of-flight mass spectrometer (MALDI-IOF) that can be operated in a linear mode for the analysis of large biomolecules or in a reflector mode for high-resolution analysis of smaller molecules, i.e., peptides. The MALDI-TOF instrument also utilizes delayed extraction technology that results in greatly increased resolution, sensitivity and mass accuracy. This is the instrument of choice for high throughput analysis, with a capacity of up to 100 samples per sample plate. On the other hand, the QSTAR is a hybrid quadrupole-quadrupole-time-of-flight mass• spectrometer. Samples are introduced in solution and are ionized by electrospray. For samples requiring the highest sensitivity, Dr. Jackson utilizes a low flow rate (25 nl miff') electrospray called nanoelectrospray, typically requiring only 1-2 µl of a solution for sample analysis. The QSTAR instrument yields data quite similar to those obtained from the MALDI-TOF instrument, except that the QSTAR data analysis is somewhat more complex due to the multiple charging of peptides by the electrospray process compared to the single charging applied to peptides on the MALDI-TOF instrument. One important additional characteristic of the QSTAR is its ability to determine structural information from sample molecules by tandem MS/MS. This is achieved by

effectively "purifying" selected molecules within the mass spectrometer's first quadrupole section. For analysis of peptides produced by tryptic digestion, a single MS experiment is initially performed to determine the masses of components present in the mixture. Next, MS/MS experiments are carried out to select specific peptides for $de\ novo$ amino acid sequence determination. Typically 2 μ l of peptide mixture is sufficient for determining the sequences of ten to twelve peptides.

Mass spectrometric analysis by MALDI

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The scheme for mass spectrometral analysis of in-gel tryptic digests of proteins for the purpose of protein identification consists of several steps. First, the peptides extracted from the gel must be cleaned and concentrated. The cleanup is necessary to remove residual detergent and other non-peptide materials that can interfere with the analysis of the tryptic peptides. This step involves binding of the peptides to a Microcon-SCX adsorptive microconcentrator. This is a cation exchange membrane held within a microcentrifuge device. At low pH, the peptides bind to the negatively charged membrane, while uncharged or negatively charged molecules pass through. After a brief wash, the peptides are eluted from the membrane in two 25-μl steps of 1.5 N ammonium hydroxide in 1:1 methanol/water. The samples are then speed-vac dried for 10 minutes, and fresh solvent is added for additional treatment to concentrate the sample prior to MS analysis. Initially, all samples can be analyzed by MALDI-TOF MS. For this analysis, the sample from the Microcon-SCX elution can be dissolved in 0.1% trifluoroacetic acid (TFA) in water and loaded on a ZipTipC 18 Pipette tip. The tip is then washed with the same solution and the peptides are then eluted directly onto the MALDI-TOF sample plate with 2 μl matrix solution (cyano-4-hydroxy-cinnamic acid, 10 mg/mi in 0.1% TFA in 1:1 acetonitrile/water). The spotted sample is dried at room temperature for at least five minutes before the sample plate is loaded in the instrument. The instrument calibration is performed externally by the addition of a calibration mixture to the sample plate. Samples are calibrated internally if the known tryptic autodigestion peptides are observed in the sample. This can be used as long as the specific type of trypsin used in the proteolytic digestion step is known. After data collection, the data can be further processed in two ways. First, the data can be treated by noise reduction software and second, it can be deisotoped. Software for both operations of these programs are standard features of the Data Explorer system provided with the

Voyager DE Pro mass spectrometer. The obtained peptide mass data can be subjected to peptide fingerprint analysis utilizing one of the protein database search sites on the Internet, such as Mascot or MS-Fit. While each of these search sites has access to several databases, one can initially select either OWL or NCBInr. One can search the database with a standard set of criteria without using a species filter. The practice is to select three variable modifications to allow for conversion of peptide N-terminal glutamine to pyroglutamate, and oxidation of methionine residues: allowing for up to one missed cleavage. Neither the protein MW nor the PI can be used as a search parameter (these, however, can be used for subsequent validation of the matched protein). Also important is that expected peptide masses of known potential "contaminants" such as keratin and trypsin can be excluded from analysis. Finally, the peptide mass tolerance can be set to +1-0.15 Da relative to the monoisotopic MW of the singly charged peptide ion. Positive database hits are scored with a MOWSE number. The higher the number of hits the greater the confidence level. The database search algorithm relates the significance level for a given search. If a high MOWSE score is obtained indicating an unambiguous match, one can consider the protein positively identified, otherwise the sample can be subjected to analysis by use of the QSTAR mass spectrometer.

Mass spectrometric analysis by Nano ESI MS/MS.

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Samples that require analysis utilizing the QSTAR, following cleanup by Microcon-SCX adsorptive microconcentrator, can be concentrated by binding the peptide mix to a small amount of POROS R12 reversed-phase C18 chromatographic support packed into a nanopurification capillary. The packed capillary column volume is ~ 10-15 nl. The sample, dissolved in 10-p.l of 5% acetic acid in water, is applied to the capillary by use of a ten-µl gel loading pipette tip. A brief centrifugation forces the liquid down the capillary so that the peptides can bind to the support. The support is then washed with 10-15 p.1 of 0.5% acetic acid in 1:50 methanol/water. The peptides are eluted from the purification capillary into a nanospray capillary by the addition of 2 µ1 of 0.5% act id in 1:1 methanol/water followed by brief centrifugation with the nanospray capillary stacked just below the purification capillary in a micropurification holder (MDS Protana). Initially, data for a single MS run is collected. The peak masses are labeled and peptides are selected for potential MS/MS sequencing by locating those that appear to be doubly charged.

Most peptides resulting from a tryptic digest can have a significant doubly charged form, which is ideal for MS/MS sequencing. The first quadrupole of the QSTAR is tuned to pass a 2 Dalton window for the pre-selected doubly charged peptide ions, one at a time, for fragmentation by collision with low-pressure argon gas in the second quadrupole. Collision energy is adjusted for each peptide to obtain the best possible MS/MS spectra. Data are collected long enough to get good quality spectra. After MS/MS spectra are collected for all selected peptides, the data are manually interpreted. Internet protein database searches are performed similar to that for MALDI-TOF peptide fingerprint, except that the search is a partial amino acid sequence search with mass information (i.e., Mascot, employing Sequence Query format). The search criteria cannot screen for a species or a protein MW or PI (which, however, can be used for subsequent validation of the protein matched). Also important is that expected peptide masses of known potential "contaminants" such as keratin and trypsin can be excluded from MS/MS analysis. One missed cleavage can be allowed and two variable modifications can be selected, carbamidomethylation of cysteine and oxidation of methionine. The tolerance of the peptide monoisotopic mass can be set to +1- 0.3 and the MS/MS tolerance can be set at +1- 0.2. This type of search generally requires only two or three peptide sequences consisting of three of the amino acids per peptide to obtain a statistically significant match (a high MOWSE score). Once a match is identified, a list of the matched peptide's theoretical MS/MS fragments can be generated to compare with the observed fragments to further confirm the correctness of the match.

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Establishment of large-format 2-D PAGE protein maps for MPCs derived from normal BM.

The normal cell samples include, A) Untreated normal MPCs; B) Normal MPCs treated with TNF α ; C) Normal MPCs treated with TNF- α and IL-4. Each cell sample can generate a total of 8 protein samples, 1) culture supernatants/ secreted proteins (1 protein sample); 2) extracellular matrix (ECM) proteins (1 protein sample); 3) plasma membrane proteins solubilized using a three-step differential extraction protocol employing conditions of progressively increasing solubility (3 protein samples); 4) whole cell lysate proteins similarly solubilized using a 3-step differential extraction protocol (3 protein samples). Each protein sample can generate 3 large format 2 D gels (corresponding to 3 medium-range, overlapping

IPG gradient gels, pH 3-6; 5-8; 7-10). This means each cell sample can generate 24 large format 2 D gels, leading to generation of at least 72 large format gels for analysis of normal MPCs. To account for duplicate or triplicate samples, the gel number falls in the range of 200-300.

Establishment of large-format 2-D PAGE protein maps for MPCs derived from BM involved with representative pre-leukemic and leukemic conditions.

The disease-associated MPCs include those from MDS, CML, AML, CLL, ALL, and MM. As above, each MPC sample can generate 24 large-format 2 D gels. With 6 such diseases being studied, the gel number can reach 144. To account for duplicate or triplicate samples, the gel number falls within the range of 400-500. The use of IPGPhor, together with ready-made IPG strips, permits sample in-gel rehydration and performance of unattended IEF overnight by adding automation to the 2-D procedure.

Using high-resolution proteomics and with the added power of high-throughput robotics, identify on a larger (semi-comprehensive) scale the MPC proteins that are differentially expressed in conditions that simulate pre-leukemic bone marrow (following stimulation with different cytokines); and in actual pre-leukemic disorders (MDS) as well as in overt leukemias (CML, AML, CLL, ALL, MM).

A robotically guided system facilitates excision of protein spots (by a spot cutter or picker) from 2-D PAGE gels, transfer of protein samples to 96-well microplates, and automated protein digestion in the microwells. Such a system reduces the time and labor relative to manual procedures and provides high throughput while minimizing keratin contamination from human skin, a frequent problem in proteomics research. The preferred method is to excise all spots from a gel but to process only the spots of interest, storing the remaining excised proteins frozen at -70°C for a later use. The robotic components can include MALDI slide spotter in addition to an automated protein spot picker and digestion station.

Example 8

30 Methods

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The present study involved microarray analysis of 23 samples and a corresponding number of chips. The samples were obtained from 4 normal healthy adult human subjects, consisting of mixtures of unfractionated stromal cells

(collective USCs or cUSCs, 8 samples), Percoll gradient-purified MPCs (collective MPCs or cMPCs, 5 samples) and single-cell MPCs (sMPCs, 10 samples) obtained by laser-capture microdissection (LCM). The study design allowed for adequate controls and replicates appropriate for a comprehensive gene expression profiling of normal BM stromal cells. The isolated single stromal cells were selected on the basis of morphology. Wright-Giemsa stained cytospin preparation revealed characteristically large cells with a relatively irregular nucleus and cytoplasm compartmentalized into ectoplasm and endoplasm. Subsequently, applicant identified a hematoxylin stain as a substitute for Wright-Giemsa stain. The hematoxylin stain is simpler to use and provides morphologic detail sufficient to allow recognition and isolation of these cells by laser capture microdissection and does not interfere with the downstream microarray testing (see details under Materials & Methods). The photomicrographs of 10 stromal cells that have been subjected to microarray testing are shown in Figure 15. To serve as controls and facilitate comparison, applicant analyzed side-by-side 8 samples of unfractionated stromal cells that are "contaminated" by up to 35% macrophages and 5% hematopoietic cells (referred to collective USC, or cUSC), and 5 samples of Percollgradient purified stromal cells, up to 95% pure (referred to collective MPC, or cMPC to distinguish from sMPC). RNA isolated from sMPC samples was subjected to 2 rounds of amplification using RiboAmp kit (Arcturus, Inc) prior to in vitro transcription (IVT). In contrast, RNA samples isolated from cUSCs and cMPCs were used without amplification for IVT. The subsequent steps of microarray testing were standard for all 3 types of samples and are schematized as follows: Preparation of total RNA \rightarrow generation of cDNA \rightarrow preparation of ds cDNA \rightarrow in vitro transcription into cRNA \rightarrow fragmentation of cRNA → hybridization of target RNA to a microarray of known genes (Affymetrix U95Av2 oligonucleotide microarray, with 12,625 probe sets) → Signal quantification and first-tier analysis using the microarray quantification software, Microarray Suite (MAS v. 5, Affymetrix, Inc). The presence of a gene within a given a sample was determined at a detection p-value of <0.05, according to the statistical expression analysis algorithm employed by MAS v.5, and was graded absent (A), marginal (M) or present/ positive (P).

Assessment of RNA amplification method

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Since single-cell microarrays are relatively novel, applicant critically reviewed the

data with respect to two important statistics that would reflect on the reliability of RNA amplification assay procedure employed before analysis involving data-mining techniques. a) 3': 5' ratios of housekeeping control genes: As shown in Table 9, these ratios were close to 1 in the standard unamplified samples, whereas, they were increased in the amplified samples. Although this is to be expected due to preferential amplification toward 3' end, since amplification may not proceed all the way up to 5' end, applicant wanted to exclude possible sample degradation. For reasons unclear, in the case of ACTB (beta actin), the 3': 5' ratios were highly variable across single cell MPC samples. In any event, the 3': 5' ratios in case of GAPD (glyceraldehyde 3-phosphate dehydrogenase) were relatively tight, suggesting no evidence of sample degradation. Furthermore, both GAPD and ACTB gene probes that were employed as part of the standard gene probe set yielded relatively stable signals across replicates in each sample type, which is further evidence of intactness of RNA samples targeted for microarray analysis. b) Number of genes present or detected: As outlined in Table 9, the amplified single cell MPC RNA samples expectedly showed significantly lower number of genes compared to the standard RNA samples (on average 34% vs. 46% of the genes etched on the array). The fact that the number is relatively constant across single cell replicate samples is further indication of the reliability of the data. Notwithstanding the shortcomings of the amplification procedure, it is important to bear in mind that the conclusions are based only on those stromal cell genes that are detected commonly across unamplifed cMPCs and cUSCs as well as in amplified sMPCs (but do not include the genes undetected or the genes selectively detected in sMPCs).

Data mining and reproducibility of overall procedures

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The thrust of the present invention is to identify genes that are relatively uniformly expressed across normal untreated bone marrow stromal cell samples, regardless whether they are of single cell type or collective cell samples, purified or unpurified. As detailed under Materials & Methods, GeneSpring was used to achieve the following data-analysis objectives: a) Filtering for genes reliably detected in each sample group by eliminating the genes with weak expressions that are statistically close to the background estimate. b) Filtering for genes that are active or "present" across replicates in each sample group. c) Exclusion of genes

with weak expressions from genes "present" in each sample group. d) Preparation of master stromal cell gene list by intersecting gene lists from step (c) (as shown in Figure 16). These steps have led to identification of a list of 2755 genes that are detected in at least 7 of 8 cUSC samples AND 4 of 5 cMPC samples AND 9 of 10 sMPC samples, i.e., in at least 20 of 23 stromal cell samples investigated. The main conclusions of the present report are based on this "stromal cell gene list" that is broadly representative of all 3 types of stromal cell samples investigated, and not on a gene list that is selective to sMPCs. A hallmark of the quality of microarray data can be discerned from hierarchical cluster analysis of replicates, which involves the principles of vector algebra. An array of numbers representing expression levels of a particular gene in terms of normalized signal intensity in a group of samples is considered a gene expression vector. Likewise, an array of numbers showing expression levels of a group of genes by a particular tissue sample is considered a tissue expression vector. In the case, applicants have 2755 gene expression vectors and 23 tissue or sample expression vectors. These vectors are amenable to algebraic treatment, facilitating calculation of similarity between any two gene- or tissue-expression vectors on the basis of a correlative metric or a similarity-measure employed, e.g., Euclidean angle. Grouping together of two samples on the basis of these principles signifies that they are most closely related out of all the samples in terms of their overall pattern of gene expression. Construction of a bone marrow stromal cell hierarchical tree has enabled visualization of global gene expression patterns across replicates and conditions. As shown in Figure 17, stromal cell genes that are expressed at a relatively lower level in amplified samples (sMPCs) are clustered to the left of gene tree, genes that are more strongly expressed in sMPCs are prominently figured in the middle of gene tree, and genes that are expressed approximately at same level as in unamplified samples (cMPCs and cUSCs) are clustered to right of gene tree. Even more important as noticeable on the sample or experiment tree, hierarchical clustering segregated the members of each sample type into a separate group (cMPC, cUSC and sMPC). Note within each sample type, corresponding subject replicates clustered together with minor exceptions. This is a reflection on the reproducibility of the overall assay-procedures employed, which encompass a variety of stages and steps in addition to target RNA amplification prior to in vitro transcription (see Materials & Methods for details).

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Finally, it is important to keep in mind that the measured level of a transcript following amplification does not necessarily provide a quantitative estimate of gene expression, but only provides a qualitative indication that the gene is transcriptionally active, which by itself is sufficient grounds for the conclusions arrived at in the present report. As shown in Figure 18, the expression of genes within the stromal cell gene list ranges from 0.2 to 6 (on the log scale) in unamplified samples (cMPC and cUSC) and from 0.02 to 36 in amplified samples (sMPC), thus showing much greater variability in the amplified samples. For illustration purpose, the coloring of gene expression curves (following the linear color bar shown on the right) was based on the gene expression pattern of a particular single-cell sample, SCA1. Note that the genes that are detected at a low level in this sample (as indicated in blue) are not necessarily expressed at a low level in unamplified samples (as read by the log scale on Y-axis). In fact, a significant number of them are expressed at a high level in the unamplified samples. This finding together with the observation that amplified samples detected about 34% of genes as opposed to unamplified samples detecting about 46% of genes tested (Table 9), strikes a cautious note that some genes do not amplify at all by the method used, and other genes amplify to a sufficient degree to be detectable (shown in blue), while some other genes amplify to a degree equal to (in yellow) or surpassing (in red) the amounts in the collective samples. (The curve shown in white is the housekeeping gene, GAPD.) The statistical algorithm as implemented in the latest version of Microarray Analysis Suite (MAS v.5) determined that a gene within a given sample as positive, regardless of grading. To overcome the limitations of the amplification procedure employed, applicant focused only on genes that were positive in at least 20 of the 23 stromal cell samples investigated.

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A stromal cell gene list is expected to be representative of typical stromal cell gene expression profile. Such master gene list forms the basis for derivation of all other stromal cell gene lists, organized in accordance with lineage or functional categories. As depicted in Figure 19A & 19B, and listed in Tables 10 through Table 17, that were prepared according to lineage/ functional assignment, the findings show that isolated single cells simultaneously express genes associated with diverse mesenchymal cell lineages, namely osteoblasts, muscle cells, fibroblasts, adipocytes, epithelial cells, endothelial cells, nerve cells and glial cells,

providing confirmation of the existence of a pluridifferentiated progenitor cell type. By definition the stromal cell genes are present in at least 4 of 5 collective MPC samples AND 7 of 8 collective USC samples AND 9 of 10 single cell MPC samples; consequently, they are active in at least 20 of 23 samples tested, representing a typical genomic profile of stromal cells. The following gene lists are sub-lists of the master stromal cell gene list consisting of 2,755 genes. The stromal cell gene list contains a number of genes that are capable of causing endothelial differentiation and vasculogenesis within the marrow microenvironment; however, these genes themselves are not necessarily endothelial cell markers. In fact, stromal cells express a gene, EDF1, the expression of which inversely correlates with endothelial cell differentiation within the stromal cells. Of the 67AFFX control genes present on the U95A v2 chip, 22 genes are detected in at least 7 of 8 cUSC samples, 24 genes are detected in 4 of 5 cMPC samples and 19 genes are detected in at least in 9 of 10 sMPC samples. Thirteen of these genes are present in the stromal cell gene list, i.e., in 20 of the 23 samples investigated.

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As evident from these gene lists, note that an isolated single stromal cell simultaneously expresses transcripts for epithelial and neuroectodermal cell types as well. Departing even further from the initial thinking, the findings add to the evidence that the MPCs within the Dexter system might represent a form or stage of the progenitor cell that is common to nonhematopoietic and hematopoietic cells. As depicted in Figure 20, and listed in Table 18 through Table 21, the isolated single stromal cells express transcripts that are typical of hematopoietic cells, in particular precursor B cells. That BM stromal cells express CD10 (CALLA) is not novel since BM stromal cells as well as endometrial stromal cells and normal breast myoepithelial cells are known to express CD10. However, the expression of CD19, CD79A and immunoglobulin enhancer binding factors E12/E47 (proto-oncogene TCF3) by BM stromal cells is unforeseen, and forms the basis for postulating the existence of a common progenitor with B cell lineage. B-cell progenitors typically display the phenotype, (CD45 +/-, CD34 +/-, CD20 +/-), (CD10 +, CD19 +, CD79A +, HLA-Dr +), which as reported here is also displayed by isolated single stromal cells at least at the transcriptome level.

CD45 positivity by cMPC and cUSC samples is attributable to coexisting or contaminating hematopoietic cells in these samples as evidenced by

concurrent positivity for myelomonocytic markers CD13, CD33 and CD14 (Table 21). However, a similar explanation cannot hold true in case of isolated single stromal cells. The protein products or transcripts for CD45 and CD19 are most likely present in stromal cells at a basal level that is beyond the detection limits of conventional techniques, e.g., immunocytochemistry and Northern blotting, respectively. Conceivably, two rounds of amplification prior to IVT sufficiently increased their transcript levels to be detected by microarray analysis. In fact, the CD45 levels were several-fold lower in cMPC and cUSC compared to CD45 levels in sMPC, and CD19 was undetectable in unamplified samples. Finally, note that CD45 and CD19 are not isolated examples in this regard since applicant has identified at least 200 other genes that are uniquely present across sMPC samples but undetectable in cMPC and cUSC (Figure 16).

The issue of stromal cell – B cell connection

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Although no anlage of Bursa of Fabricius exists in mammals, bone marrow is generally regarded as the site of B-cell generation. While the Dexter type stromal cell culture system was devised for investigation of hematopoiesis, specifically myelopoiesis (see Introduction), Whitlock and Witte developed another system for the study of B-lymphopoiesis. Whitlock-Witte cultures, like Friedenstein cultures, are grown in the absence of hydrocortisone and horse serum. When stromal cell layers in W-W cultures are seeded with fresh bone marrow as a source of B cell precursors or with purified B cell precursors, the latter then differentiate into mature B cells. On the other hand, although Dexter cultures do not promote B cell maturation, Dexter cultures do contain B cell precursors, which upon switching of culture conditions from those of Dexter to Whitlock-Witte, differentiate into mature B cells. While BM stromal cells in one form or another are definitely known to support B-lymphopoiesis, it has not been so clear as to whether stromal cells actually give rise to B-cell precursors. Evidence for a progenitor cell common to stromal cells and hematopoietic cells has been coming to light piecemeal in the form of isolated reports. 1) Singer JW et al in 1984 in the course of investigating bone marrow cultures from human patients with clonal myeloproliferative disorders showed that the nonhematopoietic stromal cells were derived from the same clonal progenitors that were involved by the hematopoietic neoplasm, as revealed by G6PD marker analysis. 2) Huss R et al in 1995 in the course of investigating a canine BM stromal

cell line showed that the adherent stromal cells had "turned" into nonadherent hematopoietic cells, especially when the latter were cultured in presence of stem cell factor. 3) Pessina et al in 1997 showed that a particular murine stromal cell line upon stimulation with bFGF, expressed a B-cell phenotype, including CD45R and surface immunoglobulin. Although not by design, applicant shows for the first time that isolated single stromal cells express transcripts that are typically associated with hematopoietic lineage, namely, CD45 and CD19, as well as relevant protooncogenes and transcription factors. These results are strongly supportive of the existence of a progenitor cell common to bone marrow stromal cells and hematopoietic cells, particularly the bone marrow-derived (B) lymphocytes. Note that the study involves no feeder cells, no embryonic stem cells, no cell lines and no colonies of cells. Contrasting with the existing literature, the present study embarks on a new path of investigation entailing gene expression analysis of single, primary, normal human stromal cells that suggest a broad capacity for multilineage differentiation. On this model, progenitor cells express genes that are characteristic of any of the lineage fates that these cells are capable of adopting.

Perspective on pluripotentiality vs. pluridifferentiation

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The present investigation involves isolated single stromal cells, consisting of 10 cells from 4 different individuals (Figure 15). The cell culture system has been earlier characterized at light microscopic level, ultrastructural level and by karyotypic analysis, showing no evidence to suggest the artifacts discussed. Spontaneous cell fusion most likely involves monocytes/macrophages, forming multinucleated giant cells; however applicant observed no expression of myelomonocytic marker genes by isolated single stromal cells (Table 12). Keep in mind that the readout of in vivo transdifferentiation studies involves localization of different lineage cells in different tissues or organs; such a situation only requires fusion between two cell types (one donor cell and one recipient cell) for the investigators to believe the artifact as transdifferentiation. In contrast, applicant shows here presence of genes for a variety of cell-lineages simultaneously within the same cell. The probability of an array of different cell types fusing into one cell which then masquerading as a pluridifferentiated cell, and that too happening with 10 of 10 cells investigated, is in the opinion close to zero. There has never before been an opportunity to assess the extent of differentiation within these multipotential

progenitor cells in molecular terms at the single-cell level. Theoretically, a) A stem cell can directly become a terminally differentiated cell, or b) A stem cell can enter a phase of multilineage differentiation prior to becoming a single-lineage, mature cell. To the knowledge, this study is the first systematic attempt to answer these questions at the single cell level by using the marrow stromal cells as a model. Although numerous forward-looking reviews exist on the topic of single-cell genomics, only a rare report is available on the actual application of this technology. Applicant has applied this frontier technology to show that a phase of multilineage differentiation indeed exists at least in Dexter-type stromal cells. Pluripotentiality of the bone marrow mesenchymal stromal cells in terms of their ability to become muscle cells, bone cells, fat cells and fibroblasts under select culture conditions has been described by other investigators. Instead of documenting another example of the phenomenon per se, the results provide an independent validation of the studies on transdifferentiation by casting light at the molecular basis of cellular plasticity. Finally, to borrow a concept from the clinical practice setting, a morphologically "poorly" differentiated neoplasm expressing hematopoietic markers is classified as a lymphoma and treated as such. Similarly, a morphologically "undifferentiated" neoplasm marking for epithelial gene expression is diagnosed as a carcinoma and treated according to the protocols designed for a carcinoma. It is in this sense that applicant uses the term "pluridifferentiated" as opposed to "pluripotential" to characterize the BM stromal cells. Notwithstanding the semantics, applicant shows that the pluripotent stromal cells are pluridifferentiated, at least at the molecular level.

Conclusions

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The findings of the present study clarify the on-going controversy as to the co-existence of multiple stromal cell types vs. one stromal cell type with co-expression of multiple phenotypes within the Dexter system of BM stromal cell cultures. An isolated single stromal cell from these cultures simultaneously expresses an array of phenotypes, i.e., osteoblasts, fibroblasts, muscle cells, adipocytes, epithelial cells, endothelial cells, neural cells/glial cells and even hematopoietic cells, in particular, B-lymphoid progenitors, thus documenting its wide differentiation repertoire. The significance of the findings is three-fold, 1st) They validate the hypothesis that the BM stromal cells express a pluridifferentiated

progenitor cell phenotype, providing insight into the molecular basis of cellular plasticity as well as establishing the utility of single-cell genomics, 2nd) They provide evidence for a common progenitor for mesenchymal progenitors and BM-derived (B) lymphoid progenitors, 3rd) By establishing a comprehensive phenotype of cultured bone marrow stromal cells at single cell level for the first time, the findings pave the road for ultimate identification and investigation of these cells in fresh samples of marrow, normal as well as diseased, in which they occur at a low frequency.

Materials & Methods

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Second-tier data-analysis/ data mining

The microarray data outputted by MAS v.5 (in the form of tab delimited text files) were imported into GeneSpringTM software version 4.2.1 (Silicon Genetics, Redwood City, CA). Following instructions accompanying GeneSpring, each gene was normalized to itself (per-gene normalization) by using the median of the gene's expression values over all the samples of an experimental group (or groups) and dividing each measurement for that gene by the corresponding median value, assuming that it was at least 0.01. The ratios were then log transformed to base e. No per-sample normalization was performed in GeneSpring since it was already accomplished as part of MAS v.5 analysis. The purpose of the above data transformations, including scaling and normalization, was to remove systematic error within and across conditions or experimental groups prior to further analysis. GeneSpring was used to achieve the following data-analysis objectives. a) Filtering for reliably present genes by eliminating the genes with weak expressions that are statistically close to the background estimate. As per the instructions accompanying GeneSpring, random error was estimated from control strength or median measurement level using the two-component global error model of Rocke-Lorenzato that assumes variability between replicates as being similar for all genes showing similar measurement level. The formula for the error model of normalized expression levels can be written as follows:

 $S (norm)^2 = a^2/C^2 + b^2$

Where, S = standard error of normalized expression data, a & b are the two error components, a = an absolute or fixed error component impacting at lower measurement values, b = a relative or proportional error component impacting at higher measurement levels, and C = control strength. According to the

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manufacturer, a curve is fitted for each group of replicates, with standard error of normalized data on Y-axis vs. control strength on X-axis. At lower end of control strength, the normalized standard error would be high and as the control strength increases, the standard error would decrease reaching a point where the curve flattens and data become more reliable. Control strength for each condition or sample group at which the above-referred two error components contribute equally, was calculated as follows, for collective MPCs, C = 128.68; collective USCs, C = 253.52; single-cell MPCs, C = 348.32. Each condition was filtered for genes expressing signals greater than the respective control strength, thus eliminating the genes with weak expressions from each group. Note 7,196 genes (out of 12,625 gene probes tested) passed the restriction in case of cMPCs, 7,287 genes in case of cUSCs and 5.937 in case of sMPCs. Corresponding gene lists were created. b) Filtering for genes "present" across replicates in each sample group. GeneSpring's "Add data file restriction" feature was used to prepare the respective lists of genes that were present (or expressed or active) in a least 7 of 8 cUSC samples, 4 of 5 cMPC samples, and 9 of 10 sMPC samples. Note 5,204 genes (out of 12,625 gene probes tested) passed the restriction in case of cMPCs, 4,763 genes in case of cUSCs, and 3,124 genes in case of sMPCs. Corresponding gene lists were created. c) Exclusion of genes with weak expressions from genes "present" in each sample group. Respective gene-lists for each sample group from steps (a) and (b), were intersected via Venn diagrams. Note 5,204 genes passed the restriction in case of cMPCs, 4,761 genes in case of cUSCs, and 3,124 genes in case of sMPCs, which are almost identical to the numbers obtained as under step (b), except for a difference of 2 genes in case of cUSCs, thus providing no significant improvement in restricting the data beyond under step (b). This is a reflection of the high stringency of the criterion employed under step (b). The 2 genes in case of cUSCs that passed the restriction under step (b) but failed the combined restriction under step (c) did show weak expressions (raw signals ranging, 142-331). Corresponding gene lists were created. d) Preparation of master stromal cell gene list. Respective gene lists for the three sample groups from step (c) were intersected via Venn diagrams, resulting in identification of a list of 2,755 genes that are uniformly present or expressed in at least 20 of 23 stromal cell samples investigated. The stromal cell gene list thus arrived at contained genes that

are representative of diverse mesenchymal lineages. Parenthetically, intersecting of gene lists corresponding to the three sample groups from step (b) resulted in a stromal cell gene list consisting of 2,756 genes, thus differing by 1 gene from the "official" master stromal cell gene list. e) Two-way hierarchical clustering of 2755 stromal cell genes based on expression profiles in 23 stromal cell samples. Only the data that were "cleaned up" of genes with weak expressions as outlined under step (a) were used for hierarchical clustering. This necessitated further processing of data in Microsoft Access prior to analysis by GeneSpring. Note that the data for each individual sample as outputted by MAS v.5 contained probe IDs, quantitative and qualitative data, as well as other information such as annotations and are readily recognizable by GeneSpring. In contrast, the gene list, resulting from step (a), contained only probe IDs and could not contain the data associated with each individual sample and was not recognizable by GeneSpring for inputting as part of an Experiment. Therefore, the microarray data for each group of individual samples (in Excel format) as well as the corresponding gene list for that group from step (a) (also in Excel format) were imported into an Access database. The genes that did not pass the test under step (a) were deleted from the microarray data for each individual sample by querying and intersecting with the appropriate post-cleanup gene list. The resulting data files were saved first as Excel files, then re-saved as tab delimited text files and then imported into GeneSpring. Per-gene normalization and log transformation were applied as described above. "Gene Tree" and "Experiment Tree" were constructed by applying a method similar to that of Eisen et al as implemented in GeneSpring and by using the stromal cell gene list and the following parameters: standard correlation as similarity measure; a minimum distance of 0.001; and a separation ratio of 0.5 in case of Gene Tree and 1.0 in case of Experiment Tree. f) Preparation of stromal cell gene lists as relevant to different cellular phenotypes and/ or functions. The gene lists associated with distinct mesenchymal cell lineages or phenotypes, i.e., osteoblasts, fibroblasts, muscle cells and adipocytes, etc, were prepared using a combination of methods. These include 1) Visually inspecting the entire stromal-cell gene list for relevant key words. 2) Directly searching the stromal cell gene list by using key words of interest via "Advanced Find Genes" feature under Edit menu in GeneSpring and by selecting "Search Only Current Gene List". 3) Intersecting the stromal cell gene list with gene

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lists of interest from Gene Ontology lists, e.g., list of oncogenes, via Venn diagrams. g) Visualization of gene-expression plots. The expression pattern of a gene across a given group (or groups) of samples of interest was pictured via Gene Inspector window, utilizing desired display options.

Throughout this application, various publications, are referenced by author and year. Full citations for the publications are listed below. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

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The invention has been described in an illustrative manner, and it is to be understood that the terminology which has been used is intended to be in the nature of words of description rather than of limitation.

The preceding descriptions of the invention are merely illustrative and should not be considered as limiting the scope of the invention in any way. From the foregoing description, one of ordinary skill in the art can easily ascertain the essential characteristics of the instant invention, and without departing from the spirit and scope thereof, can make various changes and/or modifications of the inventions to adapt it to various usages and conditions. As such, these changes and/or modifications are properly, equitably, and intended to be, within the full range of equivalence of the following claims.

Tables

Table 5

Summary of bone marrow stromal cell samples targeted for microarray analysis with an outline of the corresponding indicators of assay quality performance

	Unfractionated stromal	Percoll gradient-	LCM-dissected single
	cells	purified stromal	cell samples
•	(Collective USC, 8	cells (Collective	(Single Cell MPC, 10
	replicates)	MPC, 5 replicates)	replicates)
	reprieates)	ivii C, 5 reprieates)	tophicates)
Subject A	UNFR A	MPC A	SCA1, SCA2,
Subject A	ONIKA	I WIN CON	SCA3
Subject B	UNFR B, UNFR B	MPC B R2	SCB1,
	R1, UNFR B R2		SCB3
Subject C	UNFR C R1,	MPC C R2	SCC1,
•	UNFR C R2		SCC3
Subject D	UNFR D RI,	MPC D R1,	SCD1, SCD2,
	UNFR D R2	MPC D R2	SCD3
Amplification of RNA			
before IVT	No	No	Two rounds
Number of genes	Mean: 46.63	Mean: 46.54	Mean: 33.93
present (% of 12,625)	SD: 5.95	SD:3.66	SD: 3.94
3':5' ratio, GAPD	Mean: 0.89	Mean: 1.23	Mean: 6.76
M33197 (Probe used as	SD: 0.33	SD:0.53	SD: 2.97
part of housekeeping			
control gene probe set)			
GAPD signal	Mean: 130,723	Mean: 164,593	Mean: 43,235
35905_s_at (Probe	SD: 36,990	SD: 40,204	SD: 14,413
used as part of standard		(See Figure 5B.)	(See Figure 5B.)
gene probe set)			
3':5' ratio, ACTB	Mean: 1.44	Mean: 2.29	Mean: 57.92
X00351 (Probe used as	SD: 0.60	SD: 1.57	SD: 67.82
part of housekeeping			·
control gene probe set)			
ACTB signal	Mean: 86,104	Mean: 100,383	◆ Mean: 4,445
32318_s_at (Probe	SD: 18,458	SD: 28,427	◆SD: 884
used as part of standard	•	(See Figure 5B.)	(See Figure 5B.)
gene probe set)			

Footnote to Table 5

Replicate samples shown under each sample type as indicated correspond to each subject. The replicates of collective USC and collective MPC represent cell-culture or biological replicates of stromal cells grown in parallel flasks (instead of technical replicates). We started with 27 samples of which 2 collective MPC samples and 2 single cell MPC samples failed either at the test chip stage or produced unusual results in terms of the number of genes present and/ or 3':5' ratios and were therefore excluded as outliers. Only those samples that were targeted for the data mining analysis are represented in this table. The statistics shown (means and SDs) were based on the number of sample replicates indicated in the top row of the table except for ACTB-signal for single cell MPCs (noted in the table by \spadesuit), which were based on 9 replicates instead of 10.

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Table 6: Osteoblast/ bone cell/ bone disorders (Seshi, B)

Systematic	Common	Genbank	Description	Phenotype/ Function
38112_g_at	CSPG2	X15998	chondroitin sulfate proteoglycan 2 (versican)	
38111_at	CSPG2	X15998	chondroitin sulfate proteoglycan 2 (versican)	•
38126_at	BGN	J04599	biglycan	
36976_at	CDH11	D21255	cadherin 11, type 2, OB-cadherin (osteoblast)	
37315_f_at	BM036	Al057607	uncharacterized bone marrow protein BM036	
36996_at	OS-9	U41635	amplified in osteosarcoma	
41202_s_at	OS4	AF000152	conserved gene amplified in osteosarcoma	
671_at	SPARC	J03040	secreted protein, acidic, cysteine-rich (osteonectin)	
2087_s_at	CDH11	D21254	cadherin 11, type 2, OB-cadherin (osteoblast)	
1916_s_at	c-fos	V01512	Human cellular oncogene c-fos (complete sequence).	OMIM Notes: c-fos restricted to perichondrial growth regions of the
		c .		cartilaginous skeleton.
1915_s_at	c-fos	V01512 _.	Human cellular oncogene c-los - (complete sequence).	
1388_g_at	VDR	J03258	vitamin D (1,25- dihydroxyvitamin D3) receptor	?Osteoporosis, involutional; Rickets, vitamin D-resistant
1451_s_at	OSF-2	D13666	osteoblast specific factor 2 (fasciclin I-like)	•
32094_at	CHST3	AB017915	carbohydrate (chondroitin 6) sulfotransferase 3	
32307_s_at	COL1A2	V00503	collagen, type I, alpha 2	Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic
32306_g_at	COL1A2	J03464	collagen, type I, alpha 2	Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic

32305_at	COL1A2	J03464	collagen, type I, alpha 2	Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic
34321_i_at	GS3786	D87120	predicted osteoblast protein	
34342_s_at	SPP1	AF052124	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	
34763_at	CSPG6	AF020043	chondroitin sulfate proteoglycan 6 (bamacan)	
222_at	EXT1	S79639	exostoses (multiple) 1	Chondrosarcoma; Exostoses, multiple, type 1
36822_at	WAC	U51334	WW domain-containing adapter with a coiled-coil region	Chondrosarcoma, extraskeletal myxoid
41202_s_at	OS4	AF000152	conserved gene amplified in osteosarcoma	, , , , , , , , , , , , , , , , , , ,
40790_at	BHLHB2	AB004066	basic helix-loop-helix domain containing, class B, 2; OMIM Notes: Alternative title, DEC1, expressed primarily in differentiated chondrocytes.	/ transcription factor

Table 7: Muscle/ muscle disorders (Seshi, B)

Systematic	Common 1	Genbank	Description	Phenotype/ Function
38251_at 38923_at	MLC1SA FRG1	Al127424 L76159	myosin light chain 1 slow a FSHD (Facioscapulohumoral muscular dystrophy) region gene 1	
37012_at	CAPZB	U03271	capping protein (actin filament) muscle Z-line, beta	
37279_at	GEM	U10550	GTP binding protein overexpressed in skeletal muscle	/ GTPase
36791_g_at	TPM1	M19267	tropomyosin 1 (alpha)	Cardiomyopathy, familial hypertrophic, 3
36790_at	TPM1	M19267	tropomyosin 1 (alpha)	Cardiomyopathy, familial hypertrophic, 3
36792_at	TPM1	Z24727	tropomyosin 1 (alpha)	
36678_at	TAGLN2	D21261	transgelin 2	
36641_at	CAPZA2	U03851	capping protein (actin filament) muscle Z-line, alpha 2	•
36931_at	TAGLN	M95787	transgelin	·
37631_at	MYO1E	U14391	myosin IE	
41439_at	MYO1B	AJ001381	myosin IB	
40910_at	CAPZA1	U56637	capping protein (actin filament) muscle Z-line, alpha 1 -	/ binds barbed ends of actin filaments
41187_at	MLC-B	U26162	myosin regulatory light chain	
41747_s_at	MEF2A	U49020	Human myocyte-specific enhancer	• .
			factor 2A (MEF2A) gene, last coding	
	. •		exon, and complete cds.	
41738_at	CALD1	M64110	caldesmon 1	
41739_s_at	CALD1	M83216	caldesmon 1	
39791_at	ATP2A2	M23114	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	
39790_at	ATP2A2	M23115	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Darier disease
39378_at	BECN1	U17999	beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)	
40488_at	DMD ·	M18533	dystrophin (muscular dystrophy, Duchenne and Becker types)	Becker muscular dystrophy; Cardiomyopathy, dilated, X-linked; Duchenne muscular dystrophy
40438_at	PPP1R12A	D87930	protein (myosin) phosphatase 1, regulatory (inhibitor) subunit 12A	OMIM Notes: Regulates the interaction of actin and myosin downstream of the guanosine triphosphatase Rho.

			• •	
32838_at	smooth muscle myosin heavy chain isoform SMemb		Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly similar to HUMMYOHCB Human nonmuscle myosin heavy chain-B (MYH10) mRNA	
32755_at	ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	
33994 <u>g</u> _at	MLC	M22919	Human nonmuscle/smooth muscle alkali myosin light chain gene, complete cds.	
33447_at	MLCB	X54304	myosin, light polypeptide, regulatory, non-sarcomeric (20kD)	
32313_at	TPM2	M12125	tropomyosin 2 (beta)	OMIM Notes: Fibroblast and muscle isoforms result from alternative splicing on exons 6 and
35362_at	MYO10	ADO10040		9.
34306_at	MBNL	AB018342 AB007888	myosin X	•
36989_at	DAG1	L19711	muscleblind-like (Drosophila)	
30303_at	DAGI	L19/11	dystroglycan 1 (dystrophin-	
40022_at	FCMD	AB008226	associated glycoprotein 1)	0141-11 141
,40022_at	FCIVID	AB008228	Fukuyama type congenital muscular	-
	. •		dystrophy (fukutin)	syndrome; Muscular dystrophy, Fukuyama congenital
39031_at	COX7A1	AA152406	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	oongoma.
35729_at	MYO1D	AB018270	myosin ID	
32378_at	PKM2	M26252	pyruvate kinase, muscle	
40375_at	EGR3	X63741	early growth response 3; OMIM	
			Notes: Expressed in developing	•
			muscle spindles.	
1637_at	MAPKAPK3	U09578	mitogen-activated protein kinase-	
		•	activated protein kinase 3; OMIM	
			Notes: Expressed especially high in	
40000			heart and skeletal muscle.	
40399_r_at	MEOX2	A1743406	mesenchyme homeobox 2 (growth	
			arrest-specific homeobox).OMIM	
			Notes: Important regulator of myogenesis.	
39565_at	BMPR1A.	Z22535	bone morphogenetic protein receptor, type IA. OMIM Notes: Alternative title, activin receptor-like kinase 3; ALK3. Expressed almost exclusively in skeletal muscle with weak expression in heart and	Polyposis, juvenile intestinal
41449_at	SGCE	A 1000534	placenta.	Ductorio mussissis
	JGOE	AJ000534	sarcoglycan, epsilon	Dystonia, myoclonic

Table 8: Fibroblast (Seshi, B)

	Systematic	Common	Genbank	Description	Phenotype/ Function
	39333_at	COL4A1	M26576	Human alpha-1 collagen type IV gene, exon 52.	·
	37037_at	P4HA1	M24486	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase),	
	36666_at	P4H8	M22806	alpha polypeptide I precursor; Human prolyl 4- hydroxylase beta-subunit and disulfide isomerase (P4HB) gene, exon 11, clones 6B-(1,3,5,6).	
	41504_s_at	MAF	AF055376	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	
	39757_at	SDC2	J04621	syndecan 2 (heparan sulfate proteoglycan 1, cell surface- associated, fibroglycan)	
,	39945_at	FAP	U09278	fibroblast activation protein, alpha	OMIM Notes: Expressed in fetal normal mesenchymal tissues and stromal fibroblasts within common types of epithelial tumors.
	32835_at	MAFF	AA725102	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	
	32535_at	FBN1	X63556	fibrillin 1 (Marfan syndrome)	Ectopia lentis, familial; Marfan syndrome; MASS syndrome; Shprintzen- Goldberg syndrome
	2057_g_at	FGFR1	M34641	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	Jackson-Weiss sydnrome; Pfeiffer syndrome
	1380_at	FGF7	M60828	fibroblast growth factor 7 (keratinocyte growth factor)	OMIM Notes: May play a role in mesenchymal stimulation of epithelial cell proliferation.
	32313_at	ТРМ2	M12125	tropomyosin 2 (beta)	OMIM Notes: Fibroblast and muscle isoforms result from alternative splicing on exons 6 and 9.
	31720_s_at	FN1	M10905	fibronectin 1	•
	31719_at	FN1	X02761	fibronectin 1	
	35835_at	PDL-108	AB019409	periodontal ligament fibroblast protein	
	34390_at	P4HA2	U90441	procollagen-proline, 2-oxoglutarate 4 dioxygenase (proline 4-hydroxylase) alpha polypeptide II	

Table 9: Adipocyte (Seshi, B, et al)

Probe ID	Gene Name	Genbank ID	Description	OMIM Notes
34378_at	ADRP	X97324	adipose differentiation-related protein (adipophilin) / lipid-droplet binding/ adipocyte-specific	mRNA levels are induced rapidly and maximally after triggering adipocyte differentiation.
40282_s_at	DF	M84526	D component of complement (adipsin)	High level of expression in fat.
33337_at	DEGS	AF002668	degenerative spermatocyte homolog, lipid desaturase (Drosophila)	
39673_i_at	ECM2	AB011792	extracellular matrix protein 2, female organ and adipocyte specific	• • • • • • • • • • • • • • • • • • • •
39674_r_at	ECM2	AB011792	extracellular matrix protein 2, female organ and adipocyte specific	
31504_at	HDLBP	M64098	high density lipoprotein binding protein (vigilin)	
37542_at	LHFPL2	D86961	lipoma HMGIC fusion partner-like	
36073_at	NDN	U35139	nėcdin homolog (mouse)/ Prader- Willi syndrome	
37122_at	PLIN	AB005293	Perilipin (Did not meet the criteria to be included in stromal cell gene list because it was positive in 5 of	Plays an important role in adipocyte metaboloism. Has significant sequence
			5 cMPC and 9 of 10 sMPCs, but only 6 of 8 cUSc instead of 7 of 8 cUSC samples).	relationship with ADRP.

Table 10: Epithelial cell/ carcinoma (Seshi, B)

Systematic	Common	Genbank	Description	Phenotype/ Function
38590_r_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	
38589_i_at	РТМА	M14630	prothymosin, alpha (gene sequence 28)	. •
38610_s_at	KRT10; KPP	X14487	unnamed protein product; Human gene for acidic (type I) cytokeratin 10.	Epidermolytic hyperkeratosis
37326_at	A4	U93305	integral membrane protein; swiss-prot accession: O04901; may play role in cell differentiation in intestinal epithelium	
36812_at	BCAR3	U92715	breast cancer anti-estrogen resistance	
36953_at	MADH4	U44378	MAD, mothers against decapentaplegic homolog 4 (Drosophila)	Pancreatic cancer; Polyposis, juvenile intestinal
36852_at	N33	U42349	Putative prostate cancer tumor suppressor	
36851 <u>g</u> at	N33 [*]	U42360	39 kDa protein; Human N33 protein form 2 (N33) gene, exon 11 and complete cds.	?Prostate cancer, susceptibility to
37762_at	EMP1	Y07909	epithelial membrane protein 1	/ receptor
37731_at	EPS15	Z29064	epidermal growth factor receptor pathway substrate 15	
40856_at	SERPINF1; PEDF; EPC		PEDF; Human pigment epithelium- derived factor gene, complete cds.	
41431_at	ICK	AB023153	intestinal cell kinase	
39363_at	BC-2	AF042384	putative breast adenocarcinoma marker (32kD)	
39631_at	EMP2	U52100	epithelial membrane protein 2	
39542_at	ENC1	AF059611	ectodermal-neural cortex (with BTB-like domain)	e / associates with p110(RB)
40454_at	FAT	X87241	FAT tumor suppressor homolog 1 (Drosophila)	
32781_f_at	BPAG1	AA058762	bullous pemphigoid antigen 1 (230/240kD)	-
32780_at	BPAG1	AB018271	bullous pemphigoid antigen 1 (230/240kD)	•
32329_at 34005_at	KRTHB6 PIGR	X99142 X73079	keratin, hair, basic, 6 (monilethrix) polymeric immunoglobulin receptor, expressed in glomerular epithelial cells	Monilethrix / Binds and transports polymeric immunoglobulin
1846_at	LGALS8	L78132	lectin, galactoside-binding, soluble, 8 (galectin 8); OMIM Notes: Expressed in prostate carcinoma cells but only rarely in prostatic hypertrophy.	i .

Table 11: Endothelial cell (Seshi, B)

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Systematic	Common	Genbank	Description	Phenotype/ Function
32755_at	ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	
39315_at	ANGPT1	D13628	angiopoietin 1	
1929_at	ANGPT1	U83508	angiopoietin 1	/ ligand for the TIE2 receptor
40387_at	EDG2	U80811	endothelial differentiation, lysophosphatidic acid (LPA) G-	
		•	protein-coupled receptor, 2	
40874_at	EDF1	AJ005259	endothelial differentiation-related factor 1; OMIM Notes: EDF1 level	· .
		•	inversely correlates with the level of	
			endothelial differentiation. Inhibition	
			of EDF1 expression promotes	
	•		endothelial cell differentiation. It is postulated that EDF1 may function	
			as a bridging molecule that	•
	•		interconnects regulatory proteins and	
	:		the basal transcriptional machinery,	
	•	• •	thus modulating the transcription of the genes involved in endothelial	•
•			differentiation.	
37907_at	F8A; DXS522E	M34677	Factor VIII-associated gene 1; CpG	
			island protein; Human nested gene	•
41433_at	VCAM1	M73255	protein gene, complete cds. Human vascular cell adhesion	·
41455_at	VOAIVII	1017 3233	molecule-1 (VCAM1) gene,	•
		•	complete CDS.	• •
36988_at	TNFAIP1	M80783	tumor necrosis factor, alpha-induced	
			protein 1 (endothelial); OMIM Notes: Involved in the promary response of	
•	• ,		the endothelium to TNF.	· .
583_s_at	VCAM1	M30257	vascular cell adhesion molecule 1	•
1953_at	VEGF	AF024710	vascular endothelial growth factor	
36100_at 37268_at	VEGE	AF022375 U43368	vascular endothelial growth factor vascular endothelial growth factor B	
31200_al	VEGFB	U43368	vascular endotnellar growth factor B	•
159_at	VEGFC	U43142	vascular endothelial growth factor C	/ ligand and activator of the receptor tyrosine kinase Flt4

Table 12: Nerve cell/ neuroendocrine/ neurologic disorders (Seshi, B)

			• • • • • • • • • • • • • • • • • • • •	
Systematic	Common	Genbank	Description	Phenotype/ Function
37298_at	GABARAP	AF044671	GABA(A) receptor-associated protein diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme	
37692_at	DBI GABARAPL	Al557240	A binding protein) GABA(A) receptor-associated	
35767_at	2 GABARAPL	Al565760	protein-like 2 GABA(A) receptor-associated	
35785_at	1	W28281	protein like 1	
38406_f_at	PTGDS	Al207842	prostaglandin D2 synthase (21kD, brain)	
38657_s_a	t CLTA	M20471	clathrin, light polypeptide (Lca), brain specific insertion sequences	
38653_at	PMP22	D11428	peripheral myelin protein 22.	Charcot-Marie-Tooth disease with deafness; Charcot-Marie-Tooth neuropathy-1A; Dejerine-
				Sottas disease; Neuropathy, recurrent, with pressure palsies
38291_at	PENK	J00123	preproenkephalin (; Human enkephalin gene: exon 3 and 3 flank	
39072_at	MXI1	L07648	MAX interacting protein 1	Neurofibrosarcoma; Prostate cancer, susceptibility to/ transcription factor; forms heterodimers with Max protein
38841_at	GDBR1	AF068195	putative glialblastoma cell differentiation-related	
38818_at	SPTLC1	Y08685	serine palmitoyltransferase, long chain base subunit 1	Neuropathy, hereditary sensory and autonomic, type 1
36990_at	UCHL1	X04741	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase), neuron-specific. OMIM Notes: Highly specific to neurons and to cells of the diffuse neuroendocrine system and their tumors.	Parkinson disease, familial
37005_at	NBL1	D28124	neuroblastoma, suppression of tumorigenicity 1	
37286_at	NRCAM	AB002341	neuronal cell adhesion molecule	
36667_at	PYGB	U47025	phosphorylase, glycogen; brain	
36965_at	ANK3	U13616	ankyrin 3, node of Ranvier (ankyrin	/ peripheral proteins
			G)	believed to act as membrane-cytoskeleton
				linker molecules

			· ·	•
38040_at	SPF30	AF107463	splicing factor 30, survival of motor neuron-related	
37958_at	BCMP1	AL049257	brain cell membrane protein 1	
41221_at	PGAM1	J04173	phosphoglycerate mutase 1 (brain)	
40936_at 41091_at	CRIM1 FALZ	Al651806 U05237	cysteine-rich motor neuron 1 fetal Alzheimer antigen. OMIM Notes: Abnormally expressed in fetal brain. The corresponding antibody ALZ50 recognizes neurofibrillary pathology associated with Alzheimer's disease.	
41136_s_at	APP .	Y00264	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	Alzheimer disease-1, APP- related; Amyloidosis, cerebroarterial, Dutch type; Schizophrenia, chronic
763_at	GMFB	AB001106	glia maturation factor, beta	
641_at	PSEN1	L76517	presenilin 1 (Alzheimer disease 3)	Alzheimer disease, familial, with spastic paraparesis and unusual plaques; Alzheimer disease-3
39793_at 40023_at	GBAS BDNF	AF029786 X60201	glioblastoma amplified sequence brain-derived neurotrophic factor	
39687_at	E46L	AI524873	like mouse brain protein E46	·
39686_g_at 39542_at	E46L ENC1	AL050282 AF059611	like mouse brain protein E46 ectodermal-neural cortex (with BTB-	/ associates with p110(RB).
	•	:	like domain)	OMIM Notes: Expressed highest in brain.
40193_at	ENO2	X51956	Human ENO2 gene for neuron specific (gamma) enolase.	
40121_at	HIP2	U58522	huntingtin interacting protein 2	
40467_at	SDHD	AB006202	succinate dehydrogenase complex, subunit D, integral membrane protein	Paragangliomas, familial central nervous system; Paragangliomas, familial nonchromaffin, 1, with and without deafness; Pheochromocytoma
40281_at	NEDD5	D63878	neural precursor cell expressed, developmentally down-regulated 5	, <u>,</u>
32824_at	CLN2	AF039704	deficient in late-infantile neuronal ceroid lipofuscinosis; Homo sapiens lysosomal pepstatin insensitive protease (CLN2) gene, complete cds.	Ceroid-lipofuscinosis, neuronal 2, classic late infantile
32607_at	BASP1	AF039656	brain abundant, membrane attached signal protein 1	
			÷ •	

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33817_at	D10S102	S63912	FBRNP; heterogeneous ribonucleoprotein homolog; This sequence comes from Fig. 3; D10S102=FBRNP [human, fetal brain, mRNA, 3043 nt].	. ·
33942_s_at	STXBP1	AF004563	syntaxin binding protein 1	/ implicated in vesicle trafficking and neurotransmitter release
1659_s_at 1695_at	RHEB2 NEDD8	D78132 D23662	Ras homolog enriched in brain 2 neural precursor cell expressed, developmentally down-regulated 8	
2053_at	CDH2	M34064 ·	cadherin 2, type 1, N-cadherin (neuronal)	
216_at	PTGDS	M98539	Human prostaglandin D2 synthase gene, exon 7, brain	
32102_at	SACS	AB018273	spastic ataxia of Charlevoix- Saguenay (sacsin)	Spastic ataxia, Charlevoix- Saguenay type
31896_at 35681_r_at	NAG ZFHX1B	AL050281 AB011141	neuroblastoma-amplified protein zinc finger homeobox 1b. OMIM Notes: SMAD-interacting protein 1 (SMADIP1) appears to be essential to embryonic neural and neural crest development.	Hirschsprung disease- mental retardation syndrome; Hirschsprung disease-mental retardation syndrome without
				Hirschsprung disease
35268_at 36190_at	AXOT CDR2	AL050171 M63256	axotrophin cerebellar degeneration-related protein (62kD)	
36609_at	SLC1A3	D26443	solute carrier family 1 (glial high affinity glutamate transporter), member 3	
35973_at 36142_at	HYPH SCA1	AB023163 X79204	Huntingtin interacting protein H spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	Spinocerebellar ataxia-1
34817_s_at 34777_at	A2LP ADM	U70671 D14874	ataxin 2 related protein adrenomedullin	
-			activity-dependent neuroprotector	
34394_at 32606_at	ADNP BASP1	AB018327 AA135683	brain abundant, membrane attached signal protein 1	
38233_at	HOMER-3	AF093265	Homer, neuronal immediate early gene, 3	
36998_s_at	SCA2	Y08262	spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2)	Spinocerebellar ataxia-2
35150_at	TNFRSF5	X60592	tumor necrosis factor receptor superfamily, member 5	Immunodeficiency with hyper-IgM, type 3
34166_at	SLC6A7	S80071	solute carrier family 6 (neurotransmitter transporter, L- proline), member 7	
•			F. C. (10)	

34265_at	SGNE1	Y00757	secretory granule, neuroendocrine protein 1 (7B2 protein)	· .
654_at	MXI1	L07648	MAX interacting protein 1	Neurofibrosarcoma; Prostate cancer, susceptibility to/ transcription factor; forms heterodimers with Max protein
37945_at 39685_at 33769_at 39356_at	BACH E46L MPZL1 NEDD4L	U91316 AL050282 AF087020 AB007899	brain acyl-CoA hydrolase like mouse brain protein E46 myelin protein zero-like 1 neural precursor cell expressed, developmentally down-regulated 4- like	
38800_at	STMN2	D45352	stathmin-like 2; OMIM Notes: Neuronal growth-associated protein SCG10.	
36933_at	NDRG1	D87953	N-myc downstream regulated gene	Neuropathy, hereditary motor and sensory, Lom type
40140_at	ZFP103	D76444	zinc finger protein 103 homolog (mouse); OMIM Notes: Alternative title, KF1, expressed in normal cerebellum and Alzheimer disease cerebral cortex, but not in normal cerebral cortex.	,
1452_at	LMO4	U24576	LIM domain only 4	OMIM Notes: is highly expressed in the cranial neural crest cells, somite, dorsal limb bud mesenchyme, motor neurons, Schwann cell progenitors, and T-lymphocyte lineage.
1058_at	WASF3	S69790	WAS protein family, member 3	iyinphocyte inteage.

Table 13: Drosophila and/ or homeotic genes (Seshi, B)

			•	
Systematic	Common	Genbank	Description	Phenotype/ Function
38288_at	SNAI2	U69196	snail homolog 2 (Drosophila). OMIM Notes: Neural crest transcription factor SLUG. A zinc fanger protein that plays an important role in the transition of epithelial to mesenchymal characteristics within the neural crest.	
39037_at	MLLT2	L13773	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2	
39070_at	SNL	U03057	singed-like (fascin homolog, sea urchin) (Drosophila). OMIM Notes: Positive in dendritic cells of lymph nodes and Reed-Sternberg cells.	
39164_at	ARIH2	AF099149	ariadne homolog 2 (Drosophila). OMIM Notes: Upregulated during retinoic acid-induced granulocytic differentiation of APL cells.	
38750_at	NOTCH3	U97669	Notch homolog 3 (Drosophila). OMIM Notes: Promotes the differentiation of astroglia from multipotent progenitors.	Cerebral (autosomal dominant) arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL)
38944_at	марнз	U68019	MAD, mothers against decapentaplegic homolog 3 (Drosophila)	OMIM Notes: SMAD3 signal transduction important in the regulation of muscle-specific genes.
37693_at	NUMB	L40393	numb homolog (Drosophila)	OMIM Notes: Numb directs neuronal cell fate decisions.
40004_at	SIX1	X91868	sine oculis homeobox homolog 1 (Drosophila)	OMIM Notes: Expressed in adult skeletal muscle, and in multiple tumors including mammary carcinoma.
39610_at	HOXB2	X16665	homeo box B2	OMIM Notes: Essential for motor neuron development. Within the hematopoietic compartment, expressed specifically in erythromegakaryocytic cell lines.

40575_at	DLG5	AB011155	discs, large (Drosophila) hornolog 5	OMIM Notes: Expressed in prostate gland epithelial cells.
40570_at	FOXO1A	AF032885	forkhead box O1A (rhabdomyosarcoma)	Rhabdomyosarcoma, alveolar. OMIM Notes: Activates myogenic transcription program.
40127_at	PMX1	M95929	paired mesoderm homeo box 1	OMIM Notes: Expressed in cardiac, skeletal and smooth muscle tissues.
40454_at	FAT	X87241	FAT tumor suppressor homolog 1 (Drosophila)	OMIM Notes: Expressed in many epithelial, some endothelial and smooth muscle cells.
40328_at	TWIST	X99268 .	twist homolog (acrocephalosyndactyly 3; Saethre- Chotzen syndrome) (Drosophila)	Saethre-Chotzen syndrome. OMIM Notes: Required for cranial neural tube morphogenesis.
33222_at	FZD7	AB017365	frizzled homolog 7 (Drosophila)	OMIM Notes: Highest expression adult skeletal muscle and fetal kidney. FZD7 dependent PKC signaling controls cell sorting behaviour in the mesoderm.
32696_at	PBX3	X59841	pre-B-cell leukemia transcription	mesocenn.
33337_at	DEGS	AF002668	factor 3 degenerative spermatocyte homolog, lipid desaturase (Drosophila); adipocyte associated.	
1857_at	MADH7	AF010193	MAD, mothers against decapentaplegic homólog 7 (Drosophila)	OMIM Notes: MAD proteins were originally defined in Drosophila as essential components of the signaling pathways of the TGF-beta receptor family (e.g., TGFBR1). MADH7 and MADH6 as shown by IHC and ISH are predominantly expressed in vascular endothelium.
1955_s_at	MADH6	AF035528	MAD, mothers against decapentaplegic homolog 6 (Drosophila)	/ inhibitor of BMP signaling

1013_at	MADH5	U59913	MAD, mothers against decapentaplegic homolog 5 (Drosophila)	OMIM Notes: SMAD5 plays a critical role in the signaling pathway by which TGF-beta inhibits the proliferation of human hematopoietic progenitor cells.
1453_at .	MADH2	U68018	MAD, mothers against decapentaplegic homolog 2 (Drosophila)	•
1433 <u>g</u> _at	MADH3	U68019	MAD, mothers against decapentaplegic homolog 3 (Drosophila)	OMIM Notes: SMAD2/ SMAD3 signal transduction appears to be important in the regulation of muscle-specific genes.
35681_r_at	ZFHX1B	AB011141	zinc finger homeobox 1b. OMIM Notes: SMAD-interacting protein 1 (SMADIP1) appears to be essential to embryonic neural and neural crest development.	Hirschsprung disease- mental retardation syndrome; Hirschsprung disease-mental retardation syndrome without Hirschsprung disease
35226_at	EYA2	U71207	eyes absent homolog 2 (Drosophila)	OMIM Notes: Expressed in extensor tendons, and in lens fibers and participates inconnective tissue patterning.
36308_at	ZIC1	D76435	Zic family member 1 (odd-paired homolog, Drosophila)	OMIM Notes: Specifically expressed in nervous tissue and in particular cerebellar granule cells, potential biomarker for cerebellar granule cell lineage and medulloblastoma.
34306_at	MBNL	AB007888	muscleblind-like (Drosophila)	OMIM Notes: Expressed in skeletal muscle myoblasts, also in lymphoblastoid cell lines.
33710_at	C3F	U72515	putative protein similar to nessy (Drosophila)	OMIM Notes: Expressed in fibroblasts and hepatocytes.

Table 14:	B-cell/ B-cell neoplasms (Seshi, B)				
Systematic	Common	Genbank	Description	Phenotype/ Function	
41562_at	BMI1	L13689	B lymphoma Mo-MLV insertion region (mouse)	/ proto-oncogene	
37294_at	BTG1	X61123	B-cell translocation gene 1, anti-proliferative		
38418_at	CCND1	X59798	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Centrocytic lymphoma; Leukemia/lymphoma, B- cell, 1; Multiple myeloma; Parathyroid adenomatosis 1	
37730_at	p100	U22055	EBNA-2 co-activator (100kD); OMIM Notes: EBNA-2 activates transcription of specific genes and is essential for EBV-mediated B-lymphocyte transformation.	nuclear protein 2 acidic	
466_at	GTF2I	U77948	general transcription factor II, I; OMIM Notes: Alternative title, BTK-associated protein, 135kD (BAP135). Bruton's tyrosine kinase (BTK) is essential for B-cell activation and phosphorylates BAP135 in B cells.		
36875_at 38438_at	IBTK NFKB1	AL050018 M58603	inhibitor of Bruton's tyrsoine kinase nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)		
39730_at	ABL1	X16416	v-abl Abelson murine leukemia viral oncogene homolog 1	Leukemia, chronic myeloid	
38743_f_at	RAF1	X06409	v-raf-1 murine leukemia viral oncogene homolog 1	•	
36645_at	RELA	L19067	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)		
41436_at	ZNF198	AJ224901	zinc finger protein 198; OMIM Notes: ZNF198 involves T- or B-cell lymphoblastic lymphoma, myeloid hyperplasia, and eosinophilia and evolves toward AML. This multilineage involvement suggests the malignant transformation of primitive hematopoietic stem cell.	Stem-cell leukemia/lymphoma syndrome	
40091_at	BCL6	U00115	B-cell CLL/lymphoma 6 (zinc finger protein 51); OMIM Notes: BCL6 is predominantly expressed in the B-cell lineage, especially mature B cells (centrocytes and centroblasts).	Lymphoma, B-cell, Diffuse Large	
32776_at	RALB	M35416	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	· :	
32696_at 33791_at	PBX3 DLEU1	X59841 Y15227	pre-B-cell leukemia transcription factor 3 deleted in lymphocytic leukemia, 1		

34005_at	PIGR	X73079	polymeric immunoglobulin receptor	/ Binds and transports polymeric immunoglobulin
1636_g_at	ABL	U07563	ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t9:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia.	Leukemia, chronic myeloid
1728_at	BMI1	L13689	B lymphoma Mo-MLV insertion region (mouse)	/ proto-oncogene
2020_at	CCND1	M73554	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Centrocytic lymphoma; Leukemia/lymphoma, B- cell, 1; Multiple myeloma; Parathyroid adenomatosis
1295_at	RELA	L19067	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	
1377_at	NFKB1	M58603	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	
1461_at	NFKBIA	M69043	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	/ IkB-like activity
1389_at	MME	J03779	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	
35350_at	GALNAC4 S-6ST	AB011170	B cell RAG associated protein	
35992_at	MSC	AF087036	musculin (activated B-cell factor-1, ABF1); OMIM Notes: Downstream target of B-cell receptor signal transduction pathway. Also expressed in proliferating undifferentiated myeloblasts.	/ basic helix-loop-helix transcription factor
34344_at	IKBKAP	AF044195	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex- associated protein	Dysautonomia, familial
34350_at	RSN	X64838	restin (Reed-Sternberg cell-expressed intermediate filament-associated protein); Note R-S cell is a form of B-cell.	
36204_at	PTPRF	Y00815	protein tyrosine phosphatase, receptor type F: OMIM Notes: Alternative title, Leukocyte antigen-related tyrosine phosphatase (LAR) Both LAR and LCA (CD45) map to chromosome 1. LCA is protein-tyrosine phosphatase, receptor-type C, PTPRC, whereas LAR is PTPRF.	
34391_at	IGBP1	Y08915	immunoglobulin (CD79A) binding protein 1.	IGBP1, a marker for early B-cells

1373_at	TCF3	M31523	proto-oncogene or transcription factor 3 TCF3 (E2A immunoglobulin enhancer binding factors E12/E47); OMIM Notes: E2A mutant mice will have selective failure to develop B cells, all other hematopoietic cell lineages being intact. The block to B cell development occurs before immunoglobulin D(H)-J(H) rearrangement.	contributing the DNA binding domain of the t(1:19) translocation
35150_at	TNFRSF5	X60592	tumor necrosis factor receptor superfamily, member 5; OMIM notes: Alternative title, B-cell associated molecule CD40; expressed on the surface of all mature B cels, most mature B-cell malignancies and some early B-cell ALL.	Immunodeficiency with hyper-IgM, type 3
38740_at	ZFP36L1	X79067	zinc finger protein 36, C3H type-like 1; OMIM Notes: Alternative title, BERG36 (B-cell early response gene encoding a 36 kD protein).	
37026_at	COPEB	AF001461	core promoter element binding protein; OMIM Notes: Alternative title, B-cell-derived 1, BCD1. The expression of BCD1 was limited to two tissues, CD19+ B-cells and testis of normal individuals. B-cell maturation is associated with BCD1- expression.	/ transcription factor involved in hepatic wound healing
38050_at 32696_at	BTF PBX3	D79986 X59841	Bcl-2-associated transcription factor pre-B-cell leukemia transcription factor 3	

Table 15: Myeloid cell/ myeloid leukemia (Seshi, B) Description Phenotype/ Function **Systematic** Common Genbank myeloid/lymphoid or mixed-lineage 39037_at MLLT2 L13773 leukemia (trithorax homolog, Drosophila); translocated to, 2 MEIS3 U68385 Meist, myeloid ecotropic viral 37486_f_at integration site 1 homolog 3 (mouse) phosphatidylinositol binding clathrin Leukemia, acute U45976 37685_at PICALM myeloid; Leukemia, assembly protein acute T-cell lymphoblastic MLL septin-like fusion; a fusion partner Leukemia, acute AB023208 41220_at MSF gene of MLL myeloid, therapyrelated; Ovarian carcinoma Myeloid leukemia, core-binding factor, beta subunit 41175_at **CBFB** L20298 acute, M4Eo subtype Leukemia, acute runt-related transcription factor 1 943_at **RUNX1** D43968 myeloid; Platelet (acute myeloid leukemia 1; aml1 disorder, familial, with oncogene) associated myeloid malignancy Leukemia, chronic v-abl Abelson murine leukemia viral : 39730_at ABL1 X16416 myeloid oncogene homolog 1 myeloid cell leukemia sequence 1 33146_at MCL1 L08246 (BCL2-related) Leukemia, chronic ABL is the cellular homolog proto-1636_g_at ABL U07563 oncogene of Abelson's murine myeloid leukemia virus and is associated with the t9:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia. myeloid cell leukemia sequence 1 277_at MCL₁ L08246 (BCL2-related) Meis1, myeloid ecotropic viral 41388 at MEIS2 AF017418 integration site 1 homolog 2 (mouse) SET translocation (myeloid leukemia-40189_at SET M93651 associated, M2/M4 AML); SET stands for suppressor of variegation, enhancer of zeste and trithorax. Leukemia, acute DEK oncogene (DNA binding) 38992_at DEK X64229 nonlymphocytic 36941_at AF1Q U16954 ALL1-fused gene from chromosome Leukemia, acute myelomonocytic

	Table 16:	T cell/ NK ce	ell (Seshi, B)		
	Systematic	Common	Genbank	Description	Phenotype/ Function
	37685_at	PICALM	U45976	phosphatidylinositol binding clathrin assembly protein	Leukemia, acute myeloid; Leukemia, acute T-cell lymphoblastic
	498_at	TAX1BP1	U33821	Tax1 (human T-cell leukemia virus type I) binding protein 1	
	40822_at	NFATC3	L41067	nuclear factor of activated T- cells, cytoplasmic, calcineurin- dependent 3	
	34003_at	CD4	U47924	major receptor for HIV-1; member of immunoglobulin supergene family; T cell surface glycoprotein T4	/ T-cell coreceptor; involved in antigen recognition; participant in signal transduction pathway
	32602_at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1	Lymphocytic leukemia, acute T-cell (T-ALL)
	35279_at	TAX1BP1	U33821	Tax1 (human T-cell leukemia virus type I) binding protein 1	,
•	34234_f_at	NKTR	Al688640	natural killer-tumor recognition sequence; OMIM Notes: The protein product of the NKTR gene is present on the surface of LGLs and facilitates their binding to tumor targets.	
	39426_at	TCERG1	AF017789	transcription elongation regulator 1 (CA150)	/ HIV-1 Tat transcriptional coactivator
	32602_at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1	Lymphocytic leukemia, acute T-cell

Table 17
Stromal cells showing expression of genes that are typically affiliated with B-cell progenitors

Gene	Probe ID	GenBank ID	cMPC	cUSC	sMPC
CD45	40518_at		Positive in	Positive in	Positive in
			4/5 samples	8/8 samples	6/10 samples
CD34	538_at		4/5	5/8	4/10
CD19	1116_at		0/5	0/8	10/10
CD20	619_at		1/5	0/8	3/10
CD22	38521_at		0/5	2/8	1/10
*CD10 (CALLA)	1389_at		5/5	8/8	10/10
Common acute					
lymphoblastic				,	
leukemia antigen.					
*Transcription	1373_at		5/5	8/8	9/10
factor 3 (E2A)					
Immunoglobulin	-				
enhancer binding					
factors E12/E47					
*CD79A (IGBP1)	34391_at		5/5	8/8	9/10
Immunoglobulin					
binding protein 1, a					
marker for early B-					
cells			,		
*HLA class II,	37039_at		5/5	8/8	9/10 .
Dr alpha					

*HLA class II,	33261_at	5/5	8/8	10/10
Dr beta l				
*B2M	34644_at	5/5	8/8	10/10
Beta-2				
microglobulin				
CD2	40738_at	1/5	2/8	2/10
CD5	32953_at	0/5	0/8	0/10
CD7	771_s_at	0/5	0/8	-0/10
CD13	39385_at	5/5	8/8	0/10
CD33	36802_at	2/5	4/8	0/10
CD14	36661_at	3/5	8/8	0/10

Footnote to Table 17

Genes marked with asterisk (*) have met the criteria for inclusion in stromal cell gene list.

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CLAIMS

What is claimed is:

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1. Isolated mesenchymal progenitor cells that are pluri-differentiated.

- 2. A therapeutic composition comprising an isolated pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier, wherein said isolated pluri-differentiated mesenchymal progenitor cells are present in an amount effective for treating a disease state in a mammal in need thereof.
- 3. A therapeutic composition comprising isolated pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier, wherein said isolated pluri-differentiated mesenchymal progenitor cells are present in an amount effective to enhance hematopoietic progenitor cell engraftment in a mammal in need thereof.
- 4. A therapeutic composition comprising isolated pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier, wherein said pluri-differentiated mesenchymal progenitor cells are present in an amount effective to treat GvHD in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation.
- 5. A method for purifying pluri-differentiated mesenchymal progenitor cells comprising the steps of:
 - a) providing a cell culture preparation by the Dexter method;
 - b) treating the cells to obtain a cell suspension;
 - c) removing macrophages;
 - d) fractionating the cells; and
 - e) collecting the fraction of pluri-differentiated mesenchymal progenitor cells.
- 6. A method for enhancing bone marrow engraftment in a mammal in need thereof which comprises administering to the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) a bone marrow graft, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the bone marrow in the mammal.

7. The method according to claim 6, wherein said administrating step includes intravenously injecting or directly injecting the isolated pluri-differentiated mesenchymal progenitor cells to the site of intended activity.

- 8. A gene in an MPC for detecting the presence of cancer or pre-cancer in a cell population.
 - 9. A pharmaceutical for modulating the gene of claim 10.

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- 10. A method for enhancing engraftment of cells in a mammal in need thereof which comprises administering to the mammal isolated pluri-differentiated mesenchymal progenitor cells wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the cells in the mammal.
- 11. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered by intravenous injection or by injecting directly to the site of intended activity.
- 12. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered prior to administration of the hematopoietic progenitor cells.
- 13. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are introduced in a cell suspension also containing hematopoietic progenitor cells.
 - A SCID mouse model for investigating MPC function.
- 15. Phenotypic cultured bone marrow stromal cells capable of being analyzed at single cell level.
- 16. A diagnostic test for screening for abnormalities of bone marrow stromal cells.
 - 17. The diagnostic test according to claim 16, wherein said test can be used for screening for various hematologic diseases and other diseases effecting stromal cells
- 18. The diagnostic test according to claim 16, wherein said abnormalities30 are phenotypic abnormalities that can be discerned at a single cell level.
 - 19. Stromal cells for use in combination with engraftment or other similar procedures for enhancing the effectiveness of the treatment.

20. A method for treating graft-versus-host disease (GvHD) in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation, by administering to the mammal an effective amount of isolated pluri-differentiated mesenchymal progenitor cells.

21. A method for diagnosing a disease state comprising the steps of:

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- a) establishing gene expression patterns of normal state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells;
- b) establishing gene expression patterns of various leukemic state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells;
- c) identifying gene sets that are unique to a given state; and
- d) comparing a profile of bone marrow derived isolated mesenchymal progenitor cell of unknown state to said gene sets.
- 22. A method for identifying therapeutic targets for treatment of hematopoietic function comprising the steps of:
 - a) determining the median gene expression profile of bone marrow isolated pluri-differentiated mesenchymal progenitor cells associated with each disease state of interest;
 - b) identifying gene groups that are up-regulated, down regulated, and common to each disease state; and
 - c) identifying gene sets that are unique to a given state.

Figure - 1

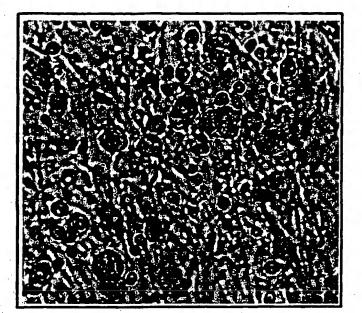
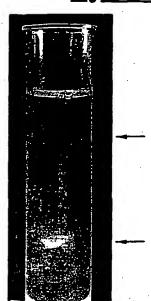


Figure - 2



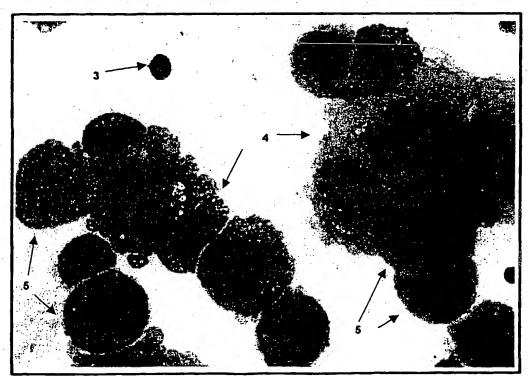
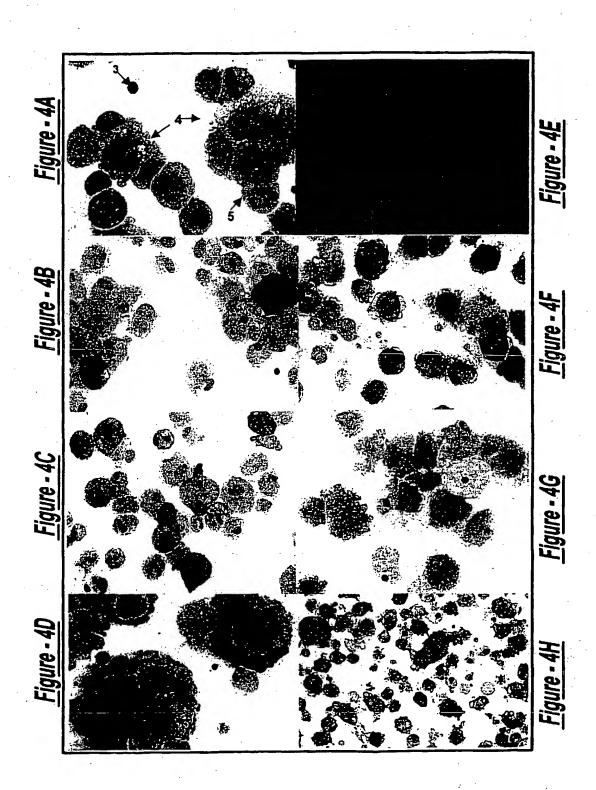
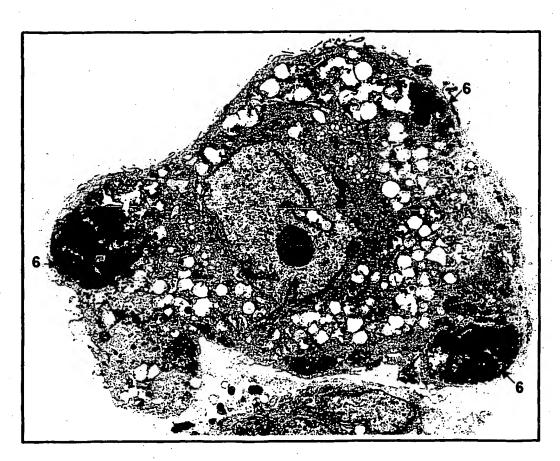
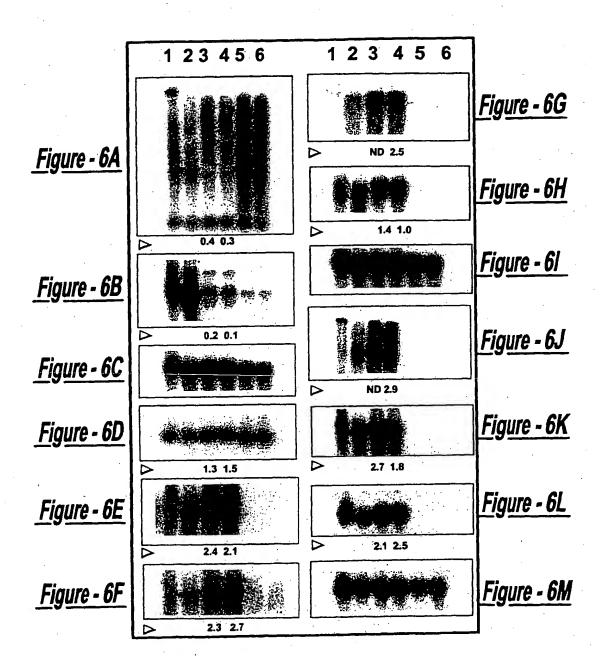


Figure - 3





<u>Figure - 5</u>



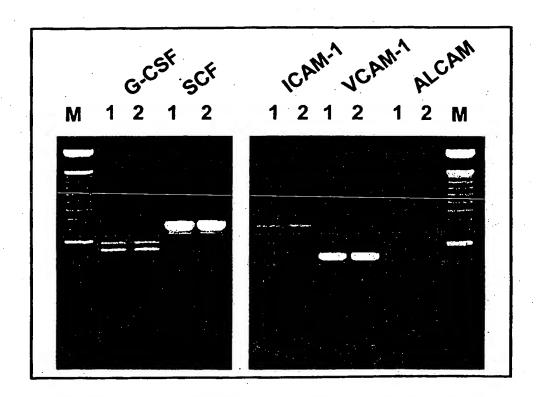


Figure - 7

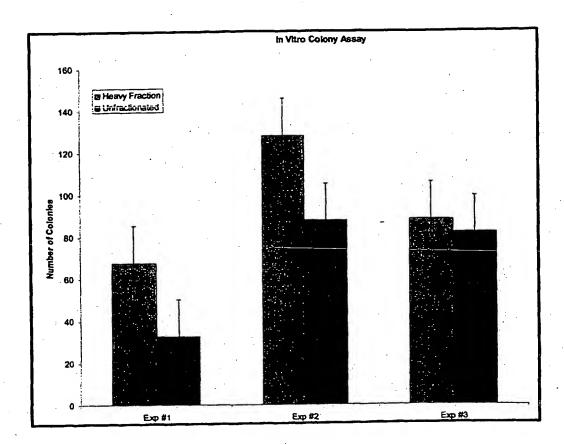


Figure - 8

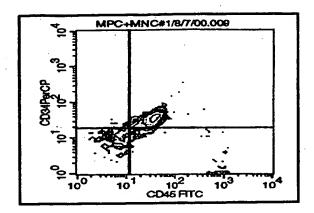


Figure - 9A

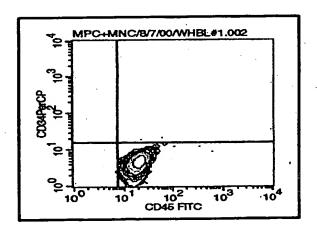


Figure - 9B

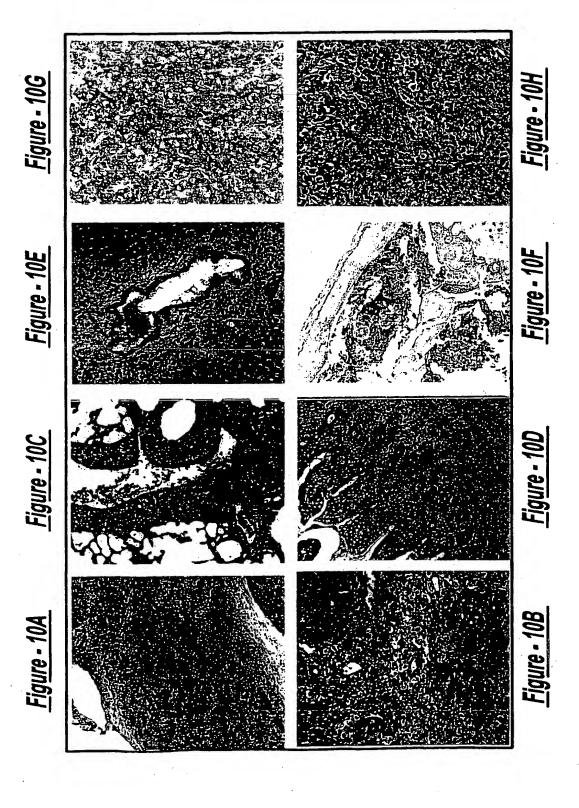


Figure - 11A

Figure - 11B

Figure - 11C

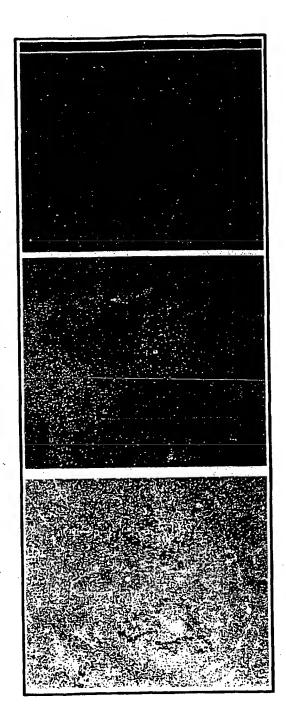


Figure - 13A

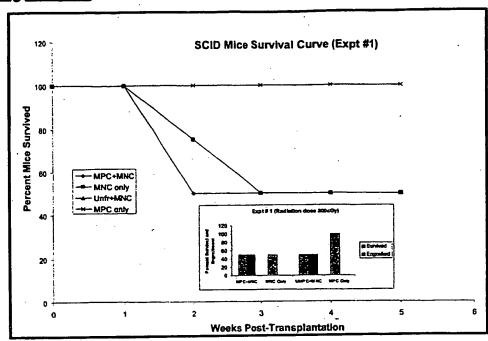
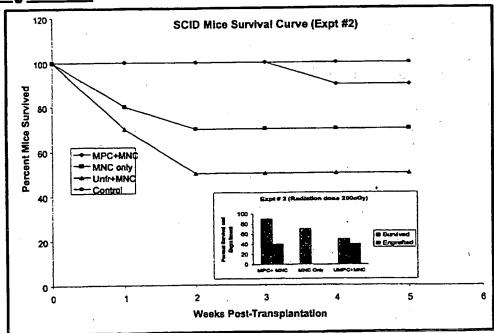
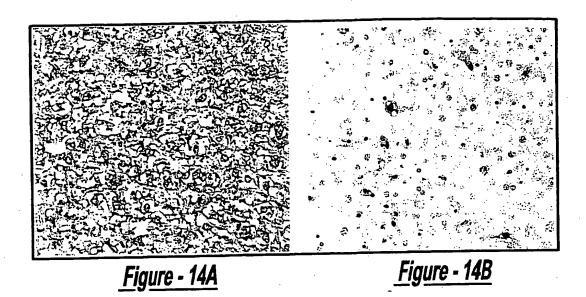


Figure - 13B





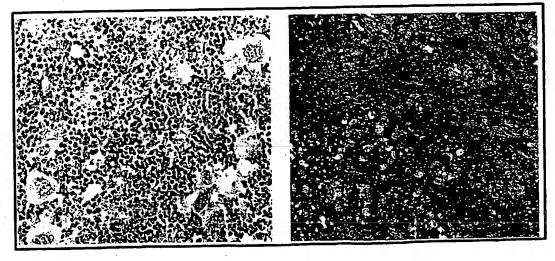
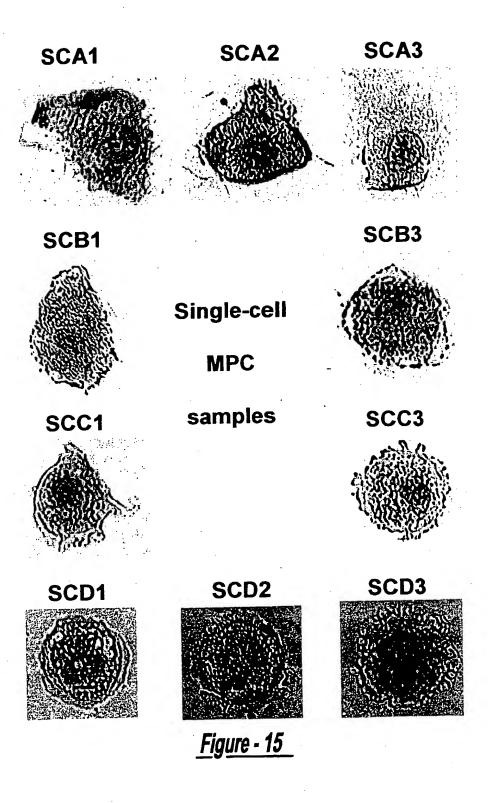


Figure - 14C

Figure - 14D



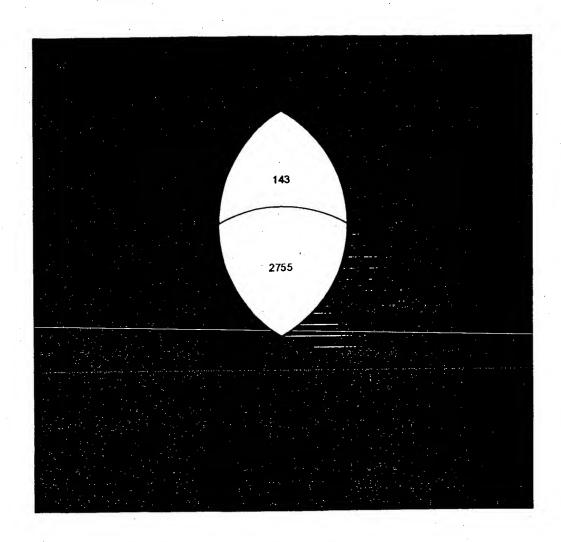


Figure - 16

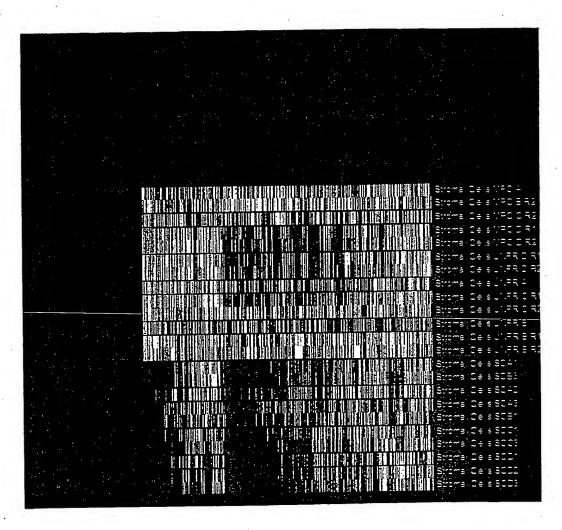


Figure - 17

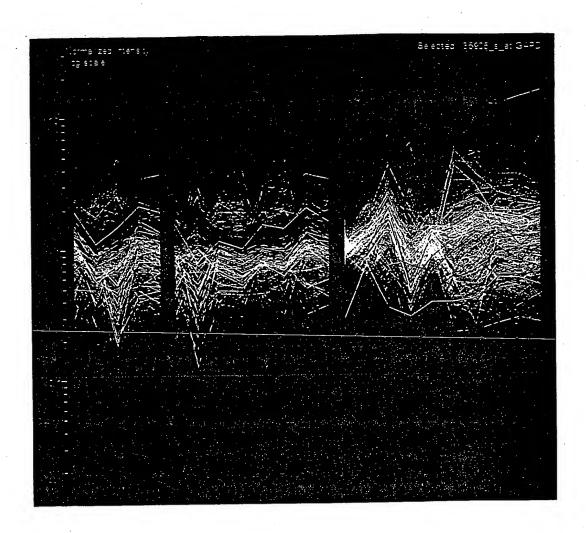
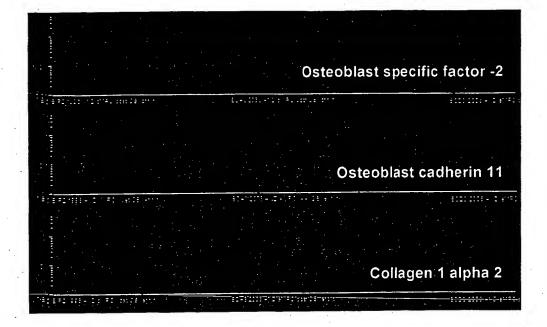


Figure - 18

Collective MPCs (Samples 1-5)

Single cell MPCs (Samples 6-15)



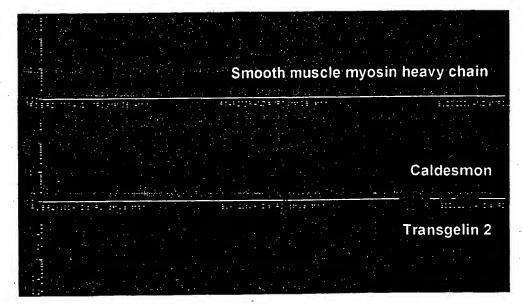
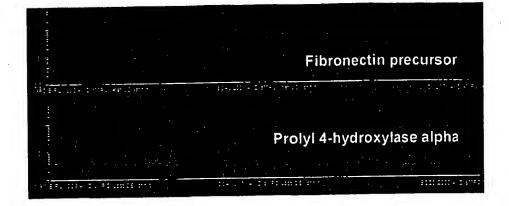
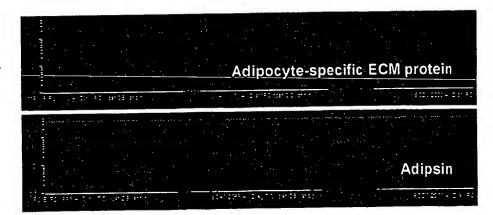


Figure - 19

Collective MPCs (Samples 1-5)

Single cell MPCs (Samples 6-15)





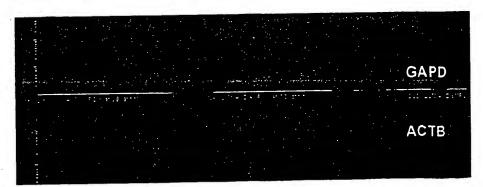


Figure - 20

Collective MPCs (Samples 1-5)

Single cell MPCs (Samples 6-15)

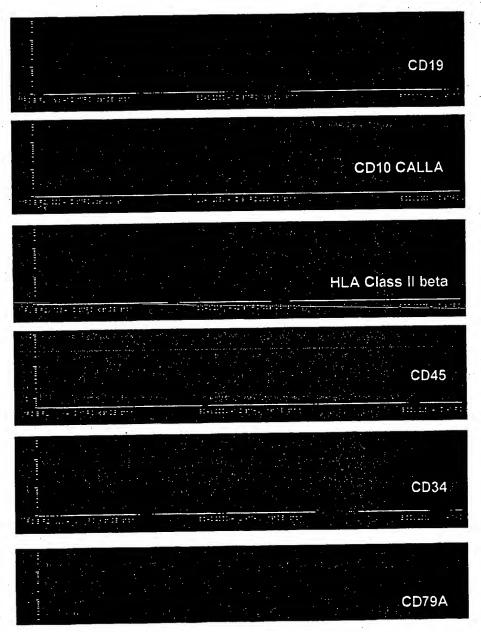


Figure - 21

	A	8	၁	Q	ш
-	Systematic	Common	Genbank	Description	Product
				***ALU WARNING: Human Alu-Sq	
7	AFFX-hum_alu_at	at	U14573	subfamily consensus sequence.	
3	38820_at	15-Sep	15-Sep AF051894	15 kDa selenoprotein	15 kDa selenoprotein
				26S proteasome-associated pad1	5.
4	33247_at	POH1	U86782	homolog	26S proteasome-associated pad1 homolog
				35 kDa protein; Homo sapiens splicing	
		•		factor, arginine/serine-rich 7 (SFRS7)	
2	32165_at	SFRS7	L41887	gene, complete cds.	splicing factor, arginine/serine-rich 7
				39 kDa protein; Human N33 protein form	
9	36851_g_at	N33	U42360	2 (N33) gene, exon 11 and complete cds.	N33 protein form 2
				3-hydroxy-3-methylglutaryl-Coenzyme A	3-hydroxy-3-methylglutaryl-Coenzyme A
7	39328_at	HMGCR	M11058	reductase	reductase
ï					succinyl CoA:3-oxoacid CoA transferase
æ	41142_at	охст	U62961	3-oxoacid CoA transferase	precursor
				3'-phosphoadenosine 5'-phosphosulfate	
6	34411_at	PAPSS1	Y10387	synthase 1	PAPS sunthetase
9	j	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase
Ξ	31794_at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase
				5-aminoimidazole-4-carboxamide	
				ribonucleotide formyttransferase/IMP	5-aminoimidazole-4-carboxamide-1-beta-D-
12	38811_at	ATIC	D82348	cyclohydrolase	ribonucl eotide transformylase/inosinicase
				5-methyltetrahydrofolate-homocysteine	
1 3	38383_at	MTR	U73338	methyltransferase	methionine synthase
14	39025_at	LOC54543	AI557912	6.2 kd protein	

							_		_
ш		divalent cation tolerant protein COTA	ADAM10		metalloprotease/disintegrin/cysteine-rich protein precursor	gravin		KIAA0629 protein	ווויאטפט אייוויו
Q	60S Ribosomal Protein L35A LIKE pseudogene match: proteins P04646 P02434 P18077 P05744 P41056 CE04362 match: cDNAs Y16430 X52966 X03475 V01440 X55030 J00995 match: ESTs AA554649 AA747384 AA572868 AA329139 AA745138 AA330809 AA483371 AA507788 AA483213 D55111 N90267 N91909 AA662153 AA720551 AA836920 AA501529 AA526745 AA608598 AA649846 AA654164 match: genomic DNAs Z32550 X05705 X05706	X05/04 (23465 145/58 7. dehydrocholesterol reductese	a disintegrin and metalloproteinase domain 10	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	a disintegrin and metalloproteinase domain 9 (mettrin gamma)	A kinase (PRKA) anchor protein (gravin)	A kinase (PRKA) anchor protein 10	A kinge (PBKA) anchor protein 11	A KIII ISSO (FINA) BIICIINI PINIOII E
O		AL021366	AF009615	AA142964	U41766	U81607	AA114830	AB014529	ABUZ3137
В		cICK0721Q.1	ADAM10	ADAM17	ADAM9	AKAP12	AKAP10	AKAP11	ANAPZ
A		40446_at		41601_at	34761_r_at	37680_at	36633_at		32982_#I
Γ		15		8	5	ຊ	2		3



								_	_		_	_
ш	proto-oncogene tyrosine-protein kinase	accessory proteins BAP31/BAP29	mitochondrial 3-oxoacyl-CoA thiolase	acetyl-coenzyme A transporter		acidic nuclear phosphoprotein pp32	APRIL	okadaic acid-inducible phosphoprotein	KIAA0785 protein	iron regulatory factor	actin filament associated protein	actin related protein 2/3 complex, subunit 2 (34 kD)
Q	ABL is the cellular homolog proto- oncogene of Abelson's murine leukemia virus and is associated with the 19:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; atternative splicing using atternative first exon 1b; ABL is the cellular homolog proto- oncogene of Abelson's murine leukemia virus and is associated with the 19:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; atternative splicing using exon 1a; Human proto- oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete	accessory proteins BAP31/BAP29	acetyl-Coenzyme A acytransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	acetyl-Coenzyme A transporter	acetylserotonin O-methyltransferase-like	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	acid-inducible phosphoprotein	Ac-like transposable element	aconitase 1, soluble	actin filament associated protein	actin related protein 2/3 complex, subunit 2 (34 kD)
0		X81817	D16294	D88152	AA669799	U73477	Y07969	AF069250	AB018328	Z11559	D25248	U50523
8	ABI	DXS1357E	ACAA2	ACATN	ASMTL	ANP32A	ANP32B	OA48-18	ALTE	ACO1	AFAP	ARPC2
V		41724 at	41530_at			37034_at	38479_at	34397_at	39168_at	40077_at	37578_at	1718_at
		52	26	27	28	29	30	31	32	33	34	35

	•	ď	C	Q	ш
				actin related protein 2/3 complex, subunit	
36	34692_r_at	ARPC4	AF006087	\neg	p20-Arc
_				actin related protein 2/3 complex, subunit	
37	38392_at	ARPC5	AF006088	5 (16 kD)	p16-Arc
88	32755_at	ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	alpha 2 actin
33	AFFX-HSAC07/AACTB	ACTB	X00351	actin, beta	beta actin
6	AFFX-HSAC07/AACTB	ACTB	X00351	actin, beta	beta actin
41	32318_s_at	ACTB	X63432	actin, beta	mutant beta-actin (beta'-actin)
42	at	ACTG1	X04098	actin, gamma 1	gamma-actin
	at	ACTN1	X15804	actinin, alpha 1	actinin, alpha 1
1	at	ACTN4	U48734	actinin, alpha 4	alpha actinin
45	18 C198E	AI CAM	710183	activated leucocyte cell adhesion molecule MEMD protein	MEMD protein
	-			activated RNA polymerase II transcription	
46	36171_at	PC4	AI521453		
47	39764_at	ACVR1	Z22534	activin A receptor, type I	ALK-2
48	35162 s at	ACVR2	D31770	activin A receptor, type II	activin typell A receptor precursor
8	34394 at	ADNP	AB018327	activity-dependent neuroprotector	KIAA0784 protein
				acyl-Coenzyme A dehydrogenase,	
22	40673_at	ACADSB	U12778	short/branched chain	acyl-CoA dehydrogenase
51	40459_at	ACOX1	S69189	acyl-Coenzyme A oxidase 1, palmitoyl	peroxisomal acyl-coenzyme A oxidase
				adaptor-related protein complex 1, beta 1	
52	40745_at	AP1B1	L13939	subunit	beta-prime-adaptin
				adaptor-related protein complex 1,	
23	35275_at	AP1G1	AL050025	gamma 1 subunit	hypothetical protein
				adaptor-related protein complex 2, mu 1	adaptor-related protein complex 2, mu 1
54	39795_at	APZM1	U63475	Subunit	Subusin
		!		adaptor-related protein complex 2, sigma	
55	39347_at	AP2S1	X97074	1 subunit	clathrin-associated protein
				adaptor-related protein complex 3, beta 1	
26	32039_at	AP3B1	U81504	subunit	beta-3A-adaptin subunit of the AP-3 complex
				adaptor-related protein complex 3, delta 1	
27	36172_s_at	AP3U1	AF002163	Subunit	delia-adapilii
				adaptor-related protein complex 3, sigma	
28		AP3S1	U91932	1 subunit	AP-3 complex sigma3A subunit
29	33102_at	ADD3	D67031	adducin 3 (gamma)	adducin-like protein

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	٨	В	ပ	Ο	П
					adenosine deaminase, RNA-specific, isoform ADAR-a; adenosine deaminase,
9	38014 at	ADAR	X79448	adenosine deaminase, RNA-specific	RNA-specific, isoform ADAR-b; adenosine deaminase, RNA-specific, isoform ADAR-c
†				adenosine deaminase, RNA-specific, B1	
61	38748_at	ADARB1	U76421	(RED1 homolog rat)	dsRNA adenosine deaminase DHADAZD
62	168_at	ADK	U50196	adenosine kinase	adenosine kinase
63	33865_at	BS69	AA127624	adenovirus 5 E1A binding protein	
	33134_at	ADCY3	AB011083	adenylate cyclase 3	KIAA0511 protein
•	40585_at	ADCY7	D25538	adenylate cyclase 7	adenylate cyclase 7
99		ADCY9	AF036927	adenylate cyclase 9	adenylyl cyclase type IX
		AK2	U84371	adenylate kinase 2	adenylate kinase 2A
	at	ADSL	AF067853	adenylosuccinate lyase	adenylosuccinate lyase
	. !	CAP	L12168	adenylyl cyclase-associated protein	adenylyl cyclase-associated protein
1	at	CAP2	N90755	adenylyl cyclase-associated protein 2	
7.1	34378_at	ADFP	X97324	adipose differentiation-related protein	adipophilin
72	36861_at	DKFZp56411922	AL049946	adlican	hypothetical protein
73	33987_at	ARF1	M36340	ADP-ribosylation factor 1	ADP-ribosylation factor 1
74	39336_at	ARF3	M74491	ADP-ribosylation factor 3	ADP-ribosylation factor 3
75	36585_at	ARF4	M36341	ADP-ribosylation factor 4	ADP-ribosylation factor 4
				ADP-ribosylation factor domain protein 1,	
76	37537_at	ARFD1	L04510	64kD	nucleotide binding protein
				ADP-ribosylation factor GTPase activating	-
11	39905_i_at	ARFGAP1	AA402332	protein 1	
78	37296_at	ARL1	L28997	ADP-ribosylation factor-like 1	ADP-ribosylation factor-like 1
				ADP-ribosylation factor-like 6 interacting	
29	36572_r_at	ARLGIP	D31885	protein	
				ADP-ribosyltransferase (NAD+; poly (ADP	-
8	41146_at	ADPRT	J03473	ribose) polymerase)	poly(ADP-ribosyl)transferase
				ADP-ribosytransferase (NAD+; poly (ADP	_
81	1287_at	ADPRT	J03473	ribose) polymerase)	poly(ADP-ribosyl)transferase
82	34777_at	ADM	D14874	adrenomedullin	adrenomedullin precursor
				AF034176 Human mRNA (Tripodis and	
8	32218 at		AF034176	hagoussis) nomo sapiens cuiva cione integnis contidi.	
3			2:::22:::2		

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8	34315_at	AFG3L2	Y18314	AFG3 ATPase family gene 3-like 2 (yeast) paraplegin-like protein	paraplegin-like protein
		AGRN	AF016903	agrin	agrin precursor
88	37027_at	AHNAK	M80899	AHNAK nucleoprotein (desmoyokin)	
		AARS	D32050	alanyl-tRNA synthetase	alanyl-tRNA synthetase
				aldehyde dehydrogenase 1 family,	
88	36686_at	ALDH1A3	U07919		aldehyde dehydrogenase 6
				aldehyde dehydrogenase 2 family	aldehyde dehydrogenase 2 family
83	32747_at	ALDH2	X05409	(mitochondrial)	(mitochondrial)
				aldehyde dehydrogenase 3 family,	
90	40409_at	ALDH3A2	U46689	member A2	aldehyde dehydrogenase
				aldehyde dehydrogenase 4 family,	
91	37331_g_at	ALDH4A1	U24266	member A1	pyrroline-5-carboxylate dehydrogenase
				aldehyde dehydrogenase 7 family,	
92	36132_at	ALDH7A1	S74728	member A1	antiquitin
				aldehyde dehydrogenase 9 family,	
93	33899_at	ALDH9A1	U34252	member A1	gamma-aminobutyraldehyde dehydrogenase
		,		aldo-keto reductase family 1, member A1	aldo-keto reductase family 1, member A1
94	38780_at	AKR1A1	J04794	(aldehyde reductase)	(aldehyde reductase)
				aldo-keto reductase family 1, member B1	aldo-keto reductase family 1, member B1
92	36589_at	AKR1B1	X15414	(aldose reductase)	(aldose reductase)
L				aldo-keto reductase family 1, member C3	
				(3-alpha hydroxysteroid dehydrogenase,	aldo-keto reductase family 1, member C3 (3-
96	37399_at	AKR1C3	D17793	type II)	alpha hydroxysteroid dehydrogenase, type II)
L				aldo-keto reductase family 7, member A2	
97	32510_at	AKR7A2	AF026947	(aflatoxin aldehyde reductase)	aflatoxin aldehyde reductase AFAR
					alkyi-dihydroxyacetonephosphate synthase
86	39225_at	AGPS	Y09443	alkylglycerone phosphate synthase	precursor
66	36941_at	AF1Q	U16954	ALL1-fused gene from chromosome 1q	AF1Q protein
8		GZAN	D42041	alpha glucosidase II alpha subunit	alpha glucosidase II alpha subunit
101	35223_at	KIAA1017	AB023234	alpha integrin binding protein 63	KIAA1017 protein
L				alpha thalassemia/mental retardation	
-	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	7074	170000	syndrome X-linked (RAD54 homolog, S.	putative DNA dependent A l Pase and
20	102 3914/_g_al	WI W	0/2330	Colovisias	0.000000

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103	818 s at	ATBX	U72936	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	putative DNA dependent ATPase and helicase
	 			atternative translation initiation; H.sapiens HI TF gene for helicase-like transcription	
104	34327_at	HLTF	246606	factor.	helicase-like transcription factor
				aminoadipate-semialdehyde	
105	35761 at	AASDHPPT	A1 050073	dehydrogenase-phosphopantetheinyl Iransferase	hypothetical protein
		NPEPPS	AJ132583	aminopeptidase puromycin sensitive	puromycin sensitive aminopeptidase
107	41338_at	AES	Al951946	amino-terminal enhancer of split	
108	36996_at	6-80	U41635	amplified in osteosarcoma	OS-9 precurosor
				amylo-1, 6-glucosidase, 4-alpha-	
				glucanotransferase (glycogen	
		,		debranching enzyme, glycogen storage	
109	38253_at	AGL	U84011	disease type III)	glycogen debranching enzyme isoform 6
				amyloid beta (A4) precursor protein	amyloid beta (A4) precursor protein
110	41136_s_at	APP	Y00264	(protease nexin-II, Alzheimer disease)	(protease nexin-II, Alzheimer disease)
111	4014B at	APBB3	1169395	amyloid beta (A4) precursor protein-	ECRE-like protein
	10110	200 10	005050	Diriging, Idining D, Molinol E (1 000-1100)	- EOG-IIVO PIOCOIII
,	7			amyloid beta precursor protein	
717	38471_r_at	APPBP2	U86981	(cytoplasmic tail) binding protein 2	KIAAU228 protein
		1		amyloid beta precursor protein	
113	38470_i_at	APPBP2	D86981	(cytoplasmic tail) binding protein 2	KIAA0228 protein
117	3536A at	A DODGO	1150030	amyloid beta precursor protein binding	t distant projection of the control
	2000		60000	, 2000	אוואוסים ליישווים וויפיסים ליישומיים איים איים איים איים איים איים איים
				amyotrophic lateral sclerosis 2 (juvenile)	
115	40064_at	ALS2CR3	AB011121	chromosome region, candidate 3	KIAA0549 protein
				androgen receptor (dihydrotestosterone	
				receptor; testicular teminization; spinal	
			;	and bulbar muscular atrophy; Kennedy	
116		AR	M23263	disease)	androgen receptor
=	38842_at	AMOTL2	AB023206	angiomotin like 2	angiomotin like 2
2 8		ANGPT1	D13628	angiopoietin 1	angiopoietin 1
119	1929_at	ANGPT1	U83508	angiopoietin 1	angiopoietin-1

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	A	8	ပ		Ш
120	36965_at	ANK3	U13616	ankyrin 3, node of Ranvier (ankyrin G)	ankyrin G
121	37403_at	ANXA1	X05908		annexin I
r	36637_at	ANXA11	L19605	annexin A11	56K autoantigen
123	123 769_s_at	ANXA2	D00017	annexin A2	lipocortin II
124	124 31684_at	ANXA2P1	M62896	annexin A2 pseudogene 1	
125	125 31444_s_at	ANXA2P3	M62895	annexin A2 pseudogene 3	
5	1- 1-0-0-0	747	Modeo	**************************************	annexin IV (placental anticoagulant protein
g	3/3/4_ai	AIVAN	NIOCOUS	allidalii At	
127	37670_at	ANXA7	J04543	annexin A7	annexin VII isoform 1; annexin VII isoform 2
128	128 41138_at	MIC2	M16279	antigen identified by monoclonal antibodies 12E7, F21 and O13	antigen
129	40506 s at	PABPC4: APP1: A	P1: AU75686	APP-1; Homo sapiens polyadenylate binding protein mRNA, complete cds.	polyadenylate binding protein
	34370_at		X81198	archain 1	archain
131	32253 at		AB007927	arginine-glutamic acid dipeptide (RE)	KIAA0458 protein
132	549_at	RARS	S80343	arginyl-tRNA synthetase	arginyl-tRNA synthetase
133	39164_at	ARIH2	AF099149	ariadne homolog 2 (Drosophila)	TRIAD1 type I
134	41729_at	ARIH1	AJ009771	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila) putative RING finger protein	putative RING finger protein
135	36057_at	ALEX2	AB011084	armadillo repeat protein ALEX2	KIAA0512 protein
136	40052_at	ACTR1A	X82206	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	alpha-centractin
137	35734 at	ACTR2	A1935551	ARP2 actin-related protein 2 homolog (yeast)	
138		ACTR2	AF006082	ARP2 actin-related protein 2 homolog (veast)	Агр2
				ARP3 actin-related protein 3 homolog	
139	35271_at	ACTR3	AF006083	(yeast)	Arp3
		AHR	L19872	aryl hydrocarbon receptor	AH-receptor
141	36671	ASNS	M27396	asparagine synthetase	asparagine synthetase
	41241	NARS	D84273	asparaginyl-tRNA synthetase	Asparaginyl tRNA Synthetase
<u>इ</u>	38703	DNPEP	AF005050	aspartyl aminopeptidase	aspartyl aminopeptidase
144	34181_at	AGA	X55330	aspartylglucosaminidase	aspartylglucosaminidase



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145	37229_at	ATR	U49844	ataxia telangiectasia and Rad3 related	FRAP-related protein
146	34817_s_at	A2LP	U70671	ataxin 2 related protein	ataxin-2 related protein
				ATP binding protein associated with cell	
147	379_at	APACD	AB006679	differentiation	ATP binding protein
148	148 40881_at	ACLY	X64330	ATP citrate lyase	ATP-citrate (pro-S-)-lyase
				ATP synthase, H+ transporting,	
\$	14000	A #Dr. 74	70000	mitochondrial Fo complex, subunit b,	H. ATD emthace cubinit b
2	41228_r_all	AIPSFI	ABUZZ I	ATD ATD TO THE PROPERTY.	THE SYMMES SUBJECT OF THE
				ATP symnase, n+ transporting, mitochondrial F0 complex, subunit c	mitochondrial ATP synthase subunit 9
150	34811_at	ATP5G3	U09813	(subunit 9) isoform 3	precursor
				ATP synthase, H+ transporting,	
151	35760_at	АТР5Н	AF087135	mitochondrial F0 complex, subunit d	F1FO-type ATPase subunit d
			*	ATP synthase, H+ transporting,	
152	38751_i_at	ATP51	AA426364	mitochondrial F0 complex, subunit e	
				ATP synthase, H+ transporting,	-
153	36107_at	ATP5J	AA845575	mitochondrial F0 complex, subunit F6	
				ATP synthase, H+ transporting,	
154	38693_at	ATP5L	AA917672	mitochondrial F0 complex, subunit g	
				ATP synthase, H+ transporting,	
				mitochondrial F1 complex, gamma	-
155	40115_at	ATP5C1	D16562	polypeptide 1	ATP synthase gamma-subunit
				ATPase, Ca++ transporting, cardiac	ATPase, Ca++ transporting, cardiac muscle,
156	39791_at	ATP2A2	M23114	muscle, slow twitch 2	slow twitch 2
				ATPase, Ca++ transporting, cardiac	ATPase, Ca++ transporting, cardiac muscle,
157	39790_at	ATP2A2	M23115	muscle, slow twitch 2	slow twitch 2
				ATPase, Ca++ transporting, type 2C,	
158	38684_at	ATP2C1	AJ010953	member 1	putative Ca2+-transporting ATPase
159	35831_at	ATP9A	AB014511	ATPase, Class II, type 9A	KIAA0611 protein
- 8	160 40853_at	ATP10D	A1478147	ATPase, Class V, type 10D	
161	36635_at	ATP11B	AB023173	ATPase, Class VI, type 11B	KIAA0956 protein
				ATPase, Cu++ transporting, alpha	
162	36523_at	ATP7A	L06133	polypeptide (Menkes syndrome)	Cu++-transporting P-type ATPase
				ATPase, H+ transporting, lysosomal	
<u>ස</u>	163 33854_at	ATP6M	AA877795	(vacuolar proton pump)	

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				ATPase, H+ transporting, lysosomal	
164	37395_at	ATP6S14	D49400	(vacuolar proton pump) 14kD	vacuolar A I Pase
				ATPase, H+ transporting, lysosomal	
165	36994_at	ATP6L	M62762	(vacuolar proton pump) 16kD	vacuolar H+ ATPase proton channel subunit
				ATPase, H+ transporting, lysosomal	
166	36167_at	ATP6F	D89052	(vacuolar proton pump) 21kD	proton-ATPase-like protein
				ATPase, H+ transporting, lysosomal	
167	37367 at	ATP6E	X76228	(vacuolar proton pump) 31kD	vacuolar H+ ATPase E subunit
				ATPase, H+ transporting, lysosomal	
168	37948_at	ATP6C	J05682	(vacuolar proton pump) 42kD	H+ -ATPase C subunit
				ATPase, H+ transporting, lysosomal	
169	33875_at	ATP6H	AI547262	(vacuolar proton pump) 9kD	
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump) membrane sector	
170	170 40903_at	ATP6M8-9	AL049929	associated protein M8-9	hypothetical protein
L				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump), alpha	
171	34889_at	ATP6A1	AA056747	polypeptide, 70kD, isoform 1	
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump), beta polypeptide,	
172	40568_at	ATP6B2	L35249	56/58kD, isoform 2	vacuolar H+-ATPase 56,000 subunit
				ATPase, H+ transporting, lysosomal	
173	35770_at	ATP6S1	D16469	(vacuolar proton pump), subunit 1	ORF
				ATPase, Na+/K+ transporting, beta 1	
174	37669_s_at	ATP1B1	U16799	polypeptide	Na,K-ATPase beta subunit
				ATPase, Na+/K+ transporting, beta 3	sodium/potassium-transporting ATPase beta-
175	32563_at	ATP1B3	U51478	polypeptide	3 subunit
L				ATP-binding cassette, sub-family A	
176	35717 at	ABCA8	AB020629	(ABC1), member 8	KIAA0822 protein
				ATP-binding cassette, sub-family C	
177	7 38261_at	ABCC3	AF085692	(CFTR/MRP), member 3	multidrug resistance-associated protein 3B
178	3 35648 at	KIAA0442	AB007902	autism-related protein 1	autism-related protein 1
179	38068_at	AMFR	M63175	autocrine motility factor receptor	autocrine motility factor receptor
180	38433_at	AXL	M76125	AXL receptor tyrosine kinase	tyrosine kinase receptor
. ;		+ (2)	75,000		hypothetical protein DKFZp586F1122 similar
181	35268_at	AXOI	AL050171	axotropnin	to axerraphilit

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		9	١		l
182	3535U_at	П	AB0111/0		NIAAUSS protein
				B lymphoma Mo-MLV insertion region	murine leukemia viral (bmi-1) oncogene
183	41562_at	BMI1	L13689		homolog
				B lymphoma Mo-MLV insertion region	murine leukemia viral (bmi-1) oncogene
184	1728_at		L13689	(esnow)	homolog
185	36578_at		U37547	baculoviral IAP repeat-containing 2	MIHB
186	41278_at		AF041474	BAF53	BAF53a
187	33175_at	BBS4	AA156237	Bardet-Biedl syndrome 4	
				basic helix-loop-helix domain containing,	
188	40790_at		AB004066	class B, 2	1-Dec
189	189 40108_at	BZAP45	D13630	basic leucine-zipper protein BZAP45	basic leucine-zipper protein BZAP45
				basic transcription element binding protein	
190	190 40202_at	BTEB1	D31716		GC box binding protein
191	35055_at		X53281	basic transcription factor 3	general transcription factor
192	38364_at	BCE-1	AF068197	BCE-1 protein	BCE-1
				B-cell CLL/lymphoma 6 (zinc finger protein	
193	40091_at	BCL6	U00115	51)	zinc-finger protein
				B-cell translocation gene 1, anti-	
194	37294_at	BTG1	X61123	proliferative	B-cell translocation protein 1
				BCL2/adenovirus E1B 19kD interacting	BCL2/adenovirus E1B 19kD-interacting
195	32060_at	BNIP2	U15173	protein 2	protein 2
				BCL2/adenovirus E1B 19kD interacting	
196	38010_at	BNIP3	AF002697	protein 3	E1B 19K/Bcl-2-binding protein Nip3
				BCL2/adenovirus E1B 19kD interacting	BCL2/adenovirus E1B 19kDa-interacting
197	39436_at	BNIP3L	AF079221	protein 3-like	protein 3a
					glucocortoid receptor-associated protein
198	34798_at	BAG1	Z 35491	BCL2-associated athanogene	RAP46
199	199 35291_at	BAG2	AL050287	BCL2-associated athanogene 2	hypothetical protein
200	200 36463_at	BAGS	AB020680	BCL2-associated athanogene 5	KIAA0873 protein
201	201 38050_at	BTF	D79986	Bcl-2-associated transcription factor	KIAA0164 gene product
202	38101_at	BDG-29	AB011151	BDG-29 proten	KIAA0579 protein
				beclin 1 (coiled-coil, myosin-like BCL2	
203	39378_at	BECN1	U17999	interacting protein)	
				beta subunit; Human pyruvate dehydrogenase (EC 1.2.4.1) beta subunit	
204	204 39160_at	PDHB	D90086	gene, exons 1-10.	pyruvate dehydrogenase (lipoamide) beta

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		В			
205	34644_at	B2M	_		beta 2-microgiopulin
206	206 40601_at	88P	A1057115	beta-amyloid binding protein precursor	
				beta-hexosaminidase alpha chain; Human	
				beta-hexosaminidase alpha chain (HEXA)	
207	39340_at	HEXA	M16424	gene, exon 14.	hexosaminidase A preproprotein
208	208 38126 at	BGN	J04599	biglycan	biglycan preproprotein
509	209 33198 at	BART1	AA206524	binder of Arl Two	
				biotin-amide amidohydrolase; Homo	
				sapiens biotindase (BTD) gene, exons 2,	
210	37274_at	Btd	AF018631		biotinidase
				biphenyl hydrolase-like (serine hydrolase;	
	-			breast epithelial mucin-associated	
211	211 40912_s_at	BPHL	X81372	antigen)	biphenyl hydrolase-related protein
212	212 35267 g at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
213	213 35266_at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
214	37700 at	BLMH	X92106	bleomycin hydrolase	bleomycin hydrolase
				bone morphogenetic protein receptor, type	
215	39565_at	BMPR1A	Z22535		ALK-3
216	39551_at	BHC80	N98667	BRAF35/HDAC2 complex (80 kDa)	
				brain abundant, membrane attached	
217	32607_at	BASP1	AF039656	signal protein 1	neuronal tissue-enriched acidic protein
				brain abundant, membrane attached	
218	32606 at	BASP1	AA135683	signal protein 1	
219	37945 at	ВАСН	U91316	brain acyl-CoA hydrolase	acyl-CoA thioester hydrolase
220	37958 at	BCMP1	AL049257	brain cell membrane protein 1	brain cell membrane protein 1
221	40023 at	BDNF	X60201	brain-derived neurotrophic factor	brain-derived neurotrophic factor
				branched chain keto acid dehydrogenase	
			-	E1, beta polypeptide (maple syrup urine	branched chain alpha-ketoacid
222	41683_i_at	BCKDHB	U50708	disease)	dehydrogenase E1 beta subunit
					breast cancer antiestrogen resistance 3
223	36812_at	BCAR3	U92715	breast cancer anti-estrogen resistance 3	protein
				brefeldin A-inhibited guanine nucleotide-	
224		BIG1	AA477576	exchange protein 1	
225	37947_at	BRD3	D26362	bromodomain containing 3	bromodomain containing protein 3
				BTB and CNC homology 1, basic leucine	BTB and CNC homology 1, basic leucine
526	226 31895_at	BACH1	AB002803	zipper transcription factor 1	zipper transcription factor 1

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227	36634_at	BTG2	U72649		BTG2
	37218_at	BTG3	D64110		ANA
220	41547 at	RIB3	AF047479	BUB3 budding uninhibited by henzimidazoles 3 homolog (veast)	spleen mitatic checkpoint BUB3
			4 C C C C C C C C C C C C C C C C C C C		tastic mitatic chacknoint BI IR3
		BUB3	AF04/4/3		ממום ווווסטים מוסטים מוסטים ווויסטים מוסטים ווויסטים מוסטים מוסטי
231	32781_f_at	BPAG1	AA058762	bullous pemphigoid antigen 1 (230/240kD)	
232	32780_at	BPAG1	AB018271	bullous pemphigoid antigen 1 (230/240kD) KIAA0728 protein	KIAA0728 protein
233	32629_f_at	BTN3A1	U90552	butyrophilin, subfamily 3, member A1	butyrophilin
234	39357_at	C2F	U72514	C2f protein	CZł
235	40709_at	LOC58502	W27601	C2H2 (Kruppel-type) zinc finger protein	
236	37031_at	C9orf10	D80005	C9orf10 protein	C9orf10 protein
237	33856_at	CXX1	Y13374	CAAX box 1	putative prenylated protein
238		CDH11	D21255	cadherin 11, type 2, OB-cadherin (osteoblast)	OB-cadherin-2
				cadherin 11, type 2, OB-cadherin	
239	2087_s_at	CDH11	D21254	(osteoblast)	OB-cadherin-1
240	2053 at	CDH2	M34064	cadherin 2, type 1, N-cadherin (neuronal)	cadherin 2, type 1 preproprotein
				calcium/calmodulin-dependent protein	
241	31670_s_at	CAMK2G	U81554	kinase (CaM kinase) II gamma	CaM kinase II isoform
				calcium/calmodulin-dependent protein	
242	38716_at	CAMKK2	AB018330	Kinase Kinase 2, beta	KIAAU/8/ protein
243	31854_at	CASK	AF035582	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	CASK
244		CALD1	M64110	caldesmon 1	caldesmon
245		CALD1	M83216	caldesmon 1	caldesmon
			.,	calmodulin 1 (phosphorylase kinase,	
\$	41288_at	CALMI	ALU36/44	delia)	
247	911 s at	CALM2	M19311	calmodulin z (pnospnorytase kinase, delta	calmodulin 2 (phosphorylase kinase, delta)
248	4012	CANX	L10284	calnexin	calnexin
249	37001_at	CAPN2	M23254	calpain 2, (m/II) large subunit	neutral protease large subunit
250	36138	CAPNS1	X04106	calpain, small subunit 1	calpain, small subunit 1

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251	41257_at	CAST	D16217	calpastatin	calpastatin
252	33385_g_at	CAST	U31346	calpastatin	calpastatin
	40953_at	CNN3	S80562	calponin 3, acidic	acidic calponin
	37345_at	CALU	AF013759	calumenin	calumein
	·			AMP responsive element binding protein	cAMP responsive element binding protein 1, isoform A: cAMP responsive element binding
255	37535_at	CREB1	M27691		protein 1, isoform B
				cAMP responsive element binding protein	
256	40849_s_at	CREB3	U88528	3 (luman)	transcription factor LZIP
				cAMP responsive element binding protein-	
257	39438_at	CREBL2	AF039081	like 2	Cre binding protein-like 2
970	3206E at	V C C C	C68134	cAMP reconsive element modulator	cyclic AMP-responsive element modulator
259	32067 at	CREM	S68271	cAMP responsive element modulator	cyclic AMP-responsive element modulator
					cyclic AMP-responsive element modulator
260	32066_g_at	CREM	S68134	cAMP responsive element modulator	beta isoform
				capping protein (actin filament) muscle Z-	
261	40910_at	CAPZA1	U56637	line, alpha 1	capping protein alpha subunit isoform 1
				capping protein (actin filament) muscle Z-	
262	36641_at	CAPZA2	U03851	line, alpha 2	capping protein alpha
				capping protein (actin filament) muscle Z-	
263	37012_at	CAPZB	U03271	line, beta	F-actin capping protein beta subunit
				carbohydrate (chondroitin 6)	
264	32094_at	CHST3	AB017915	sulfotransferase 3	chondroitin 6-sulfotransferase
265	265 41447_at	CHSY1	AB023207	carbohydrate (chondroitin) synthase 1	KIAA0990 protein
				carbohydrate (keratan sulfate Gal-6)	
266	41395_at	CHST1	AB003791	sulfotransferase 1	keratan sulfate Gal-6-sulfotransferase
				carbohydrate (N-acetylglucosamine-6-0)	N-acetylglucosamine-6-O-sulfotransferase
267	37960_at	CHST2	AB014679	sulfotransferase 2	(GlcNAc6ST)
568	268 36454_at	CA12	AF037335	carbonic anhydrase XII	carbonic anhydrase precursor
569	34876_at	CPD	U65090	carboxypeptidase D	carboxypeptidase D
270	36606_at	CPE	X51405	carboxypeptidase E	carboxypeptidase E precursor
Ŀ				Cas-Br-M (murine) ectropic retroviral	
271	35632_at	CBLB	U26710	transforming sequence b	cbl-b
272	272 40184_at	CSNK1A1	L37042	casein kinase 1, alpha 1	casein kinase I-alpha
273	36949_at	CSNK1D	U29171	casein kinase 1, delta	casein kinase I delta

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_	A	В	3	O :	1
274	38019_at	CSNK1E	L37043	casein kinase 1, epsilon	casein Kinase I-epsilon
37.0	1011 0 00	CDAD	194389	CASP2 and RIPK1 domain containing	death domain containing protein CBADD
6//2	18 S 1171 C/7	חשאים	004500		
276	1867 at	CFLAR	AF005775	CASP8 and FADD-like apoptosis regulator	CASP8 and FADD-like apoptosis regulator caspase-like apoptosis regulatory protein 2
				caspase 4, apoptosis-related cysteine	
277	195_s_at	CASP4	U28014	protease	cysteine protease
				caspase 8, apoptosis-related cysteine	
278	33774_at	CASP8	X98172	protease	MACH-alpha-1
279	279 41156 g at	CTNNA1	U03100	catenin (cadherin-associated protein), alpha 1 (102kD)	alpha2(E)-catenin
				catenin (cadherin-associated protein),	
280	280 41155_at	CTNNA1	U03100	alpha 1 (102kD)	alpha2(E)-catenin
				catenin (cadherin-associated protein),	
281	2085_s_at	CTNNA1	D14705	alpha 1 (102kD)	'human alpha-catenin'
				catenin (cadherin-associated protein),	
282	282 2069_s_at	CTNNA1	123805	alpha 1 (102kD)	alpha1(E)-catenin
				catenin (cadherin-associated protein),	
283	283 35331_at	CTNNAL1		alpha-like 1	alpha-catenin-like protein
				catenin (cadherin-associated protein),	
284	284 40777_at	CTNNB1	X87838	beta 1 (88kD)	beta-catenin
				catenin (cadherin-associated protein),	
285	285 40444_s_at	CTNND1	AB002382	delta 1	
286	38466_at	CTSK	X82153	cathepsin K (pycnodysostosis)	Cathepsin O
287	37391_at	CTSL	X12451	cathepsin t.	pro-(cathepsin L)
288	36915_at	CTSO	AI810485	cathepsin O	
289	36119_at	CAV1	AF070648	caveolin 1, caveolae protein, 22kD	
230	339_at	CAV2	AF035752	caveolin 2	caveolin-2
	·			Cbp/p300-interacting transactivator, with	
291	33113_at	CITED2	U65093	Glu/Asp-rich carboxy-terminal domain, 2	msg-related gene 1
				CCAAT/enhancer binding protein	
292	1052_s_at	CEBPD	M83667	(C/EBP), delta	NF-IL6-beta protein
293	293 39219 at	CEBPG	U20240	CCAAT/enhancer binding protein (C/EBP), gamma	C/EBP gamma
			21.22.2	6 17	

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	X	a	٥		
294	33861 at	CNOT2	AI123426	CCR4-NOT transcription complex, suburnit	
				CCR4-NOT transcription complex, subunit	
295	32820 at	CNOT4	U71267	4	potential transcriptional repressor NOT4Hp
296		CD164	D14043	CD164 antigen, sialomucin	MGC-24 precursor
297	297 34699_at	CD2AP	AL050105		hypothetical protein
				CU36 antigen (collagen type i receptor, thrombospondin receptor)-like 2	
298	33823 at	CD36L2	D12676	(lysosomal integral membrane protein II)	85kDa human lysosomał sialoglycoprotein
				CD44 antigen (homing function and Indian	
299	2036_s_at	CD44	M59040	blood group system)	cell adhesion molecule
				CD81 antigen (target of antiproliferative	
300	35282_r_at	CD81	M33680	antibody 1)	CD81 antigen
8	39389_at	റ്റോ	M38690	CD9 antigen (p24)	CD9 antigen
				CDC10 cell division cycle 10 homolog (S.	
302	32175_at	CDC10	872008	cerevisiae)	cell division cycle 10
				CDC16 cell division cycle 16 homolog (S.	
303	40404_s_at	CDC16	U18291	cerevisiae)	CDC16Hs
				CDC23 (cell division cycle 23, yeast,	
304	31877_at	CDC23	AF053977	homolog)	cell division cycle protein 23
305	40690 at	CKS2	X54942	CDC28 protein kinase 2	Cks1 protein homologue
306	33362_at	CEP3	AF094521	Cdc42 effector protein 3	MSE55-related protein
307		CLK1	M59287	CDC-like kinase 1	
308		CDK2AP1	AF006484	CDK2-associated protein 1	putative oral tumor suppressor protein
				CDP-diacylglycerol synthase	
309	41343_at	CDS2	Y16521	(phosphatidate cytidytyttransferase) 2	CDS2 protein
				CDP-diacylglycerolinositol 3-	
				phosphatidyftransferase	
310	33397_at	CDIPT	AL050383	(phosphatidylinositol synthase)	
<u>ج</u>	40591	CDC27	S78234	cell division cycle 27	H-NUC
				cell growth regulatory with ring finger	
312	450_g_at	CGR19	U66469	domain	cell growth regulator CGR19
5	000	000	1 156460	cell growth regulatory with ring finger	cell growth regulator CGR19
? ?	30014 at	CGRIS	000403	- AOITEMIL	

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					cellular repressor of E1A-stimulated genes
314	35311_at	CREG	23	cellular repressor of E1A-stimulated genes CREG	CREG
315	41333_at	CENTB2		centaurin, beta 2	centaurin, beta 2
	34676_at	CENTG2	AB029022	centaurin, gamma 2	KIAA 1099 protein
317	38410_at	CETN2	X72964	itein, 2	caltractin
				centrin, EF-hand protein, 3 (CDC31	
318	35232_f_at	CETN3	A1056696	homolog, yeast)	
319		CENPC1	M95724	centromere protein C 1	centromere autoantigen C
320		CAP350	AB007949	centrosome-associated protein 350	KIAA0480 protein
				cerebellar degeneration-related protein	
321	36190_at	CDR2	M63256 ·	(62kD)	major Yo paraneoplastic antigen
322	32262_at	CGI-01	AL049669	CGI-01 protein	hypothetical protein
323	323 40931_at	LOC50999	AL080084	CGI-100 protein	
324	00588	LOC51014	AB002450	CGI-109 protein	
325	34359_at	LOC51020	AA524058	CGI-130 protein	
	38667_at	LOC51031	AA189161	CGI-150 protein	
327	41824	LOC51096	Al140114	CGI-48 protein	
	34862_at	LOC51097	AA005018	CGI-49 protein	
329		LOC51626	AI760932	CGI-60 protein	
330	330 41411_at	LOC51103	AI566877	CGI-65 protein	
331	39814_s_at	LOC51635	A1052724	CGI-86 protein	
				chaperonin containing TCP1, subunit 2	chaperonin-containing TCP-1 beta subunit
332	35759_at	CCT2	AF026166	(beta)	homolog
				chaperonin containing TCP1, subunit 3	
333	40774_at	ССТЗ	X74801	(gamma)	gamma subunit of CCT chaperonin
				chaperonin containing TCP1, subunit 4	chaperonin containing t-complex polypeptide
334	32594_at	CCT4	AF026291	(delta)	1, delta subunit
	0			chaperonin containing TCP1, subunit 6A	
335	38416_at	CCT6A	L27706	(zeta 1)	chaperonin-like protein
				chaperonin containing TCP1, subunit 7	chaperonin containing t-complex polypeptide
336	38720_at	CCT7	AF026292	(eta)	1, eta subunit
				chaperonin containing TCP1, subunit 8	chaperonin containing TCP1, subunit 8
337	39767_at	сств	D13627	(theta)	(theta)
338	338 41000_at	CHES1	U68723	checkpoint suppressor 1	checkpoint suppressor 1
339	339 37855_at	CTBS	M95767	chitobiase, di-N-acetyl-	di-N-acetylchitobiase

Е	ve, 1A Icin protein		cholesterol 25-hydroxylase		chondroitin sulfate proteoglycan 2 (versican)		chondroitin sulfate proteoglycan 2 (versican)		chromosome-associated polypeptide		heterochromatin protein p25						Mi-2 protein			e 17 KIAA0584 protein						0				e 4 hypothetical protein			e 28 G7b protein	_	e 5 hypothetical protein
Q	chloride channel, nucleotide-sensitive, 1A	chloride intracellular channel 4	cholesterol 25-hydroxylase	chondroitin sulfate proteoglycan 2	(versican)	chondroitin sulfate proteoglycan 2	(versican)	chondroitin sulfate proteoglycan 6	(bamacan)	chromobox homolog 1 (HP1 beta homolog	Drosophila)	chromobox homolog 3 (HP1 gamma	nomolog, Urosopnila)	chromobox homolog 3 (HP1 gamma	nomolog, Urosopnila)	chromodomain helicase DNA binding	protein 4	chromodomain protein, Y chromosome	like	chromosome 1 open reading frame 17	chromosome 1 open reading frame 8	chromosome 12 open reading frame 22	chromosome 14 open reading frame 3	chromosome 18 open reading frame 1	chromosome 19 open reading frame 7	chromosome 21 open reading frame 80	chromosome 22 open reading frame 2	chromosome 22 open reading frame 4	chromosome 22 open reading frame 5	chromosome 3 open reading frame 4	chromosome 4 open reading frame 1	chromosome 5 open reading frame 8	chromosome 6 open reading frame 28	chromosome 6 open reading frame 34	chromosome 6 open reading frame 5
ပ	X91788	AL080061	AF059214		X15998		X15998		AF020043		U35451		A1/40522		AA648295		X86691		AL050164	AB011156	Z78368	AF052105	AJ243310	AF009425	AB028987	AB023175	AL050345	AL096779	AL096879	AL080097	AF006621	U10362	AJ245416	W27949	AL050289
8	CLNS1A	CLIC4	CH25H		CSPG2		CSPG2		CSPG6		CBX1		CBX3		CBX3		CHD4		CDYL	C1orf17	C1orf8	C12orf22	C14orf3	C18orf1	C19orf7	C21orf80	C22orf2	C22orf4	C22orf5	C3orf4	C4orf1	C5orf8	C6orf28	C6orf34	Ceorf5
A	38732_at	341 33891_at	32363_at		38112_g_at		38111_at		34763_at		37304_at	4 6	38085_at		38084_at		36137_at		32111_at	3955(39033_at	32217_at	40979_at	40045_g_at	36860_at		33406_at	33778_at	41758_at	38690_at		36955_at	41375_at	41454_at	36139_at
	340	341	342		343		344		345		346	į	45 7	- 3	348		349		350	351	352	353	354	355	356	357	358	329	360	361	362	363	364	365	366

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35193_at CHC1L		AF060219			RCC1-like G exchanging factor HLG
34292_at CXorf12 X92475	off12 X92475		의	open reading frame 12	chromosome X open reading frame 12
41314_at CS AF047042	AF047042	2	ਹ	citrate synthase	citrate synthase
370 41159_at CLTC D21260 c	D21260		ᆰ	clathrin, heavy polypeptide (Hc)	clathrin heavy chain
38657_s_at CLTA M20471 c	M20471		ပ	clathrin, light polypeptide (Lca)	ciatrinn, light polypeptide A, isoform a; clathrin, light polypeptide A, isoform b
372 35743 at CDSE4		1179569	1	cleavage and polyadenylation specific	no arches
			1	cleavage stimulation factor, 3' pre-RNA,	
373 32723_at CSTF1 L02547	L02547			subunit 1, 50kD	cleavage stimulation factor
00+1-1-1	1100		<u> </u>	cleavage stimulation factor, 3' pre-RNA,	olosvana etimilation factor 77kDa eublinit
27	AB014527		1	CLIP-associating protein 2	KIAA0627 protein
36017 at LOC57213	13	AF055016	Т	CLLL6 protein	CLLL6 protein
			Т	clusterin (complement lysis inhibitor, SP-	clusterin (complement lysis inhibitor, SP-
				40,40, sulfated glycoprotein 2,	40,40, sulfated glycoprotein 2, testosterone-
				testosterone-repressed prostate message	
M25915	M25915		_	2, apolipoprotein J)	apolipoprotein J)
_at LOC113251 AL050205	AL050205		Ť	c-Mpl binding protein	
379 40811_at	AB011148		-	coactivator for steroid receptors	KIAA0576 protein
38052_at F13A1 M14539	M14539			coagulation factor XIII, A1 polypeptide	coagulation factor XIII A1 subunit precursor
at		X92098		coated vesicle membrane protein	transmembrane protein
34326_at		X82103	1	coatomer protein complex, subunit beta	beta-Coat protein
			Г	coatomer protein complex, subunit beta 2	
		X70476		(beta prime)	subunit of coatomer complex
384 35205_at COBRA1 AL050280	1	AL050280		cofactor of BRCA1	hypothetical protein
				cofactor required for Sp1 transcriptional	
385 36648_at CRSP9 AF031383		AF031383		activation, subunit 9 (33kD)	hMed7
386 33659_at CFL1 X95404		X95404		cofilin 1 (non-muscle)	cofilin
40879 at		AB014599	Г	coiled-coil protein BICD2	KIAA0699 protein
39864 at CIRBP		D78134	i .	cold inducible RNA binding protein	CIRP
39839 at		M24069		cold shock domain protein A	cold shock domain protein A
32307_s_at		V00503		collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
COL1A2		J03464		collagen, type I, alpha 2	alpha 2 type i collagen preproprotein
		J03464		collagen, type I, alpha 2	alpha 2 type I collagen preproprotein

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COL3A1		A	a	C	2	u
2248B_att COL3A1 X142D collegen, type III, apha 1 (Ehlers-Danlos 38659 at COL4A2 38420_att COL4A2 X05610 collagen, type V, alpha 2 38420_att COL5A2 Y14690 collagen, type V, alpha 2 38722_at COL6A3 X52022 collagen, type V, alpha 1 38077_att COL6A3 X57527 collagen, type V, alpha 1 38072_att COL6A3 X57527 collagen, type VII, alpha 1 37892_att COL16A1 X67527 collagen, type VII, alpha 1 37668_att COL16A1 M92642 collagen, type VII, alpha 1 37668_att COL6A X78947 complement component 1, r 37668_att CTG X78947 complement component 1, r 366538_att CTGF X78947 <th></th> <th></th> <th></th> <th></th> <th></th> <th></th>						
2348B at 1 COL3A1 X14420 syndrome type IV, alpha 2 38639_at 1 COL6A2 X05610 collagan, type IV, alpha 2 38420_at 1 COL6A1 X15880 collagan, type IV, alpha 2 3872_at 1 COL6A3 X52022 collagan, type IV, alpha 1 38077_at 1 COL6A3 X5222 collagan, type VI, alpha 1 37892_at 1 COL16A1 X57527 collagan, type XI, alpha 1 37892_at 1 COL16A1 M92642 collagan, type XI, alpha 1 37892_at 1 COL16A1 M92642 collagan, type XI, alpha 1 37668_at 1 COL16A1 M92642 collagan, type XI, alpha 1 37688_at 1 COL16A1 M92642 collagan, type XI, alpha 1 39409_at 2 C1ABP M69039 subcomponent 1, a 30409_at 2 C1ABP M14058 subcomponent 1, a 34049_at 3 C1ABP M14058 subcomponent 1, a 34049_at 3 C1ABP AF00180 subcomponent 1, a 34049_at 3 CTGF X7894 connective tissue growth factor					collagen, type III, alpha 1 (Ehlers-Danlos	
28629_at COL4A2 XO5610 collagen, type IV, alpha 2 38720_at COL5A2 Y14890 collagen, type V, alpha 2 38720_at COL6A3 X52022 collagen, type VI, alpha 1 38077_at COL6A3 X52022 collagen, type VII, alpha 1 38722_at COL8A1 X57527 collagen, type VII, alpha 1 37459_at COL16A1 M32642 collagen, type VII, alpha 1 37668_at COL16A1 M32642 collagen, type VII, alpha 1 37668_at COL16A1 M69039 subcomponent binding prolein 37668_at C10BP M69039 subcomponent thiding prolein 3409_at C1R M14058 subcomponent thiding prolein 3653_at C1R M14058 subcomponent thiding prolein 40496_at C1R X78947 component thiding prolein 41202_s_at C7R AF00152 connective tissue growth factor 41202_s_at CAP AF00152 conserved helic-toop-helix ubiquitous 4038_at COPSS U65928 kinase	393	32488_at	COL3A1	X14420	syndrome type IV, autosomal dominant)	prepro-alpha-1 type 3 collagen
38420_at COL5A2 Y14690 collagen, type V, alpha 2 38722_at COL6A1 X15890 collagen, type VI, alpha 1 38722_at COL6A3 X52022 collagen, type VII, alpha 1 37859_at COL6A1 X57527 collagen, type VII, alpha 1 37859_at COL16A1 M92642 collagen, type XI, alpha 1 35168_tat COL16A1 M63039 collagen, type XI, alpha 1 37668_at COL16A1 M63039 complement component 1, q 38409_at C1R M14058 subcomponent binding protein 40496_at C1R M14058 subcomponent 1, r 38409_at C1S J04080 subcomponent 1, r 41202_s_at C1S J04080 subcomponent 1, r 33770_at AF000152 conserved gene amplified in 41202_s_at CHUK AF000152 conserved helix-top-helix ubiquitous 41202_s_at COPS U51205 COP9 constitutive photomorphogenic 40138_at COPS U51205 COP9 subunit 6 (MOV34 homolog, 34 KD)	394	36659_at	COL4A2	X05610	collagen, type IV, alpha 2	alpha (2) chain
COLEA1 X15880 collagen, type VI, alpha 1 COLEA3 X52022 collagen, type VII, alpha 1 COLEA1 X67527 collagen, type VII, alpha 1 COL1A1 J04177 collagen, type XII, alpha 1 COL1A1 M92642 complement component 1, appearance of conserved pane amplified in conserved helix-loop-helix ubiquitous of conserved helix-loop-helix ubiquitous of conserved helix-loop-helix ubiquitous of COPS COPS U50925 Kinase COP9 constitutive photomorphogenic conserved helix-loop-helix ubiquitous of COP9 COPS U50928 COP9 constitutive photomorphogenic conserved helix-loop-helix ubiquitous of COP9 homolog COPS U51205 COP9 homolog COPS U51205 COP9 homolog COPS U50928 COP9 homolog	395	38420_at	COL5A2	Y14690	collagen, type V, alpha 2	procollagen alpha 2(V)
COL6A3 X52022 collagen, type VI, alpha 3 COL8A1 X57527 collagen, type VII, alpha 1 COL11A1 J0A177 collagen, type XI, alpha 1 COL16A1 M92642 collagen, type XI, alpha 1 COMP Complement component 1, r complement component 1, r CTG X78947 complement component 1, r CTGF X78947 conserved gene amplified in conserved gene amplified in conserved belix-loop-helix ubiquitous CHUK AF00925 kinase COPS U65928 homolog subunit 5 (Arabidopsis) COPS U65928 homolog subunit 6 (MOV34 homolog, 34 kD) t CPNE3 AB014536 copine 1 COPS COPS COPS	386	38722_at	COL6A1	X15880	collagen, type VI, alpha 1	alpha-1 collagen VI (AA 574-1009)
COLBA1	397	38077_at	COLEA3	X52022	collagen, type VI, alpha 3	collagen type VI, alpha 3 chain
37892_at COL11A1 J04177 collagert, type XI, alpha 1 35168_f at COL16A1 M92642 collagen, type XI, alpha 1 37668_at COL16A1 M69039 subcomponent 1, q 39409_at C1R M14058 complement component 1, r 39409_at C1R M14058 subcomponent 1, r 40496_at C1S J04080 subcomponent 1, r 36538_at C1R X78947 complement component 1, s 41202_s at CTGF X78947 connective tissue growth factor 41202_s at CTGF X78947 conserved gene amplified in conserved belix-toop-helix ubiquitous 41202_s at CHUK AF009225 Kinase COP9 constitutive photomorphogenic 1789_at COPS U65228 homolog subunit 5 (M0V34 homolog, 34 kD) 40138_at COPS U170735 COP9 tomolid 40452_at CPNE3 AB014536 copine 1 39706_at CPO D16611 (coproporphyring producin 41175_at CPO D16611 (coproporphyring	398	37459_at	COL8A1	X57527	collagen, type VIII, alpha 1	alpha 1(VIII) collagen
37892 at COL11A1 J04177 Collagen, type XI, alpha 1						alpha 1 type XI collagen, isoform A
37892_at COL11A1 J0A177 collagent, type XI, alpha 1 35168 f_at COL16A1 M92642 collagen, type XI, alpha 1 37668_at COL16A1 M92642 complement component 1, q 39409_at C1R M14058 complement component 1, r 40496_at C1R M14058 complement component 1, r 39409_at C1R M78947 complement component 1, r 38638_at C1R X78947 complement component 1, r 33770_at C1GF X78947 conserved gene amplified in conserved gene amplified in conserved helix-loop-helix ubiquitous 1, r 41202_s_at CFO AF009225 corserved helix-loop-helix ubiquitous 1, r 33770_at CHUK AF009225 kinase 40138_at COPS COPS conserved helix-loop-helix ubiquitous 1, r 40452_at COPS U57256 COP9 homolog subunit 6 (MOV34 homolog, 34 kD) 40452_at CPNE1 AB014536 copine i 39706_at CPNE3 AB014536 copine i 370999_at CPO AF0046						preproprotein; alpha 1 type XI collagen,
37892_at COL11A1 J04177 collagent, type XI, alpha 1 35168_i_at COL16A1 M92642 collagen, type XII, alpha 1 3768_at COL16A1 M92642 collagen, type XII, alpha 1 3768_at C1QBP M69039 subcomponent binding protein 39409_at C1R M14058 subcomponent component 1, r 39409_at C1R M14050 subcomponent 1 subcomponent 1, subcomponent 2000 40496_at C1R X78947 connective tissue growth factor 41202_s_at CTGF X78947 conserved gene amplified in 2000 41202_s_at CTGF X78947 conserved helix-loop-helix ubiquitous 2000 33770_at AF009225 Sinase conserved helix-loop-helix ubiquitous 2000 40138_at COP9 U51205 COP9 homolog conserved helix-loop-helix ubiquitous 2000 40452_at COP9 U51205 COP9 homolog cOP9 homolog 40452_at CPNE1 AB014536 copine i 39706_at CPO D16611 coproporphyrina, harderoporphyria)		- ,,,		-		isoform B preproprotein; alpha 1 type XI
35168_i_at COL16A1 M92642 collagen, type XVI, alpha 1 37668_at C1GBP M69039 subcomponent 1, q 39409_at C1R M14058 subcomponent 1, r 39409_at C1R M14058 subcomponent 1, r 40496_at C1S J04080 subcomponent 1, s 36538_at CTGF X78947 complement component 1, s 36538_at CTGF X78947 complement component 1, s 36538_at CTGF X78947 complement component 1, s 41202_s_at CTGF X78947 complement component 1, s 41202_s_at CHUK AF000152 conserved gene amplified in 41202_s_at CHUK AF009225 kinase 60P8 U51205 COP9 constitutive photomorphogenic 1789_at COPS U65228 kinase 60P8 U51205 COP9 subunit 6 (MOV34 homolog, 34 kD) 40452_at CPNE3 AB014536 COP9 subunit 6 (MOV34 homolog, 34 kD) 40452_at CPNE3 AB014536 copine I	399	37892	COL11A1	J04177	collagen, type XI, alpha 1	collagen, isoform C preproprotein
37668_at C1QBP M69039 complement component 1, q 39409_at C1R M14058 subcomponent binding protein 39409_at C1R M14058 subcomponent 1, r 40496_at C1S J04080 subcomponent 1, r 36638_at C1S J04080 complement component 1, r 36638_at C1S X78947 complement component 1, s 41202_s_at CTGF X78947 connective tissue growth factor 36638_at CTGF AF000152 conserved gene amplified in conserved belix-loop-helix ubiquitous 41202_s_at CHUK AF009255 kinase COP9 constitutive photomorphogenic 1789_at COPS U51205 COP9 constitutive photomorphogenic 1045928 L070735 COP9 constitutive photomorphogenic 40138_at MOV34-34KD U70735 COP9 subunit 6 (MOV34 homolog, 34 kD) 40452_at CPNE3 AB014536 copine III 39706_at CPO CPP copine III 37026_at CPP AF001461 corpine II parderopoph	400	-	COL16A1	M92642	collagen, type XVI, alpha 1	alpha-1 type XVI collagen
3766B_at C1QBP M69039 subcomponent binding protein 39409_at C1R M14058 complement component 1, r 39409_at C1R M14058 subcomponent 1, r 40486_at C1S J04080 subcomponent 1, s 36638_at C1S J04080 subcomponent 1, s 36638_at C1GF X78947 complement component 1, s 36638_at C1GF X78947 complement component 1, s 36638_at C1GF X78947 complement component 1, s 36638_at C1GF X78947 conserved gene amplified in conserved belaxion b					complement component 1, q	complement component 1, q subcomponent
39409_at C1R M14058 subcomponent component component subcomponent component compon	5	37668_at	C10BP	M69039	subcomponent binding protein	binding protein precursor
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10496_at C1S J04080 subcomponent subcomponent subcomponent subcomponent subcomponent 1262_s_at CTGF X78947 connective tissue growth factor 11202_s_at CTGF AF000152 conserved gene amplified in osteosarcoma 1202_s_at CHUK AF00925 kinase 1789_at CHUK AF00925 kinase 1789_at COPS U65928 homolog subunit 5 (Arabidopsis) 32539_at COPS U70735 COP9 toonstitutive photomorphogenic 40138_at COPS U70735 COP9 toonolog 40452_at CPNE1 U83246 copine I 39706_at CPNE3 AB014536 copine I 37026_at CPO D16611 (coproporphyrine, harderoporphyria) 37026_at COPE AF001461 core promoter element binding protein 41175_at CBFB L2029B core-binding factor, beta subunit 42803_at CNIL AF10439B cornichon-like	402	39409_at	C1R	M14058	subcomponent	complement component 1, r subcomponent
10496_at C1S J04080 subcomponent 36638_at CTGF X78947 connective tissue growth factor 11202_s_at CTGF X78947 conserved gene amplified in osteosarcoma 11202_s_at OS4 AF000152 osteosarcoma 33770_at CHUK AF009225 kinase 1789_at COPS5 U65928 homolog subunit 5 (Arabidopsis) 32539_at COP9 U70735 COP9 homolog 40138_at MOV34-34KD U70735 COP9 homolog 39706_at CPNE1 U83246 copine 1 39706_at CPNE3 AB014536 copine 1 37999_at CPO D16611 (coproporphyrina, harderoporphyria) 37026_at COPE AF001461 core promoter element binding protein 41175_at CBFB L20298 core-binding factor, beta subunit 420380 cornichon-like cornichon-like					complement component 1, s	
36538_at CTGF X78947 connective tissue growth factor 11202_s_at OS4 AF000152 osteosarcoma 33770_at CHUK AF009225 kinase 1789_at COPS5 U65928 homolog subunit 5 (Arabidopsis) 32539_at COP9 U70735 COP9 homolog 40138_at MOV34-34KD U70735 COP9 homolog 39706_at CPNE1 U83246 copine 1 39706_at CPNE3 AB014536 copine 1 37999_at CPO D16611 (coproporphyria, harderoporphyria) 41175_at CBFB L2029B core-binding factor, beta subunit 41175_at CNIL AF10439B cornichon-like	403	40496_at	C1S	J04080	subcomponent	complement component 1, s subcomponent
11202_s_at OS4 AF000152 conserved gene amplified in conserved helix-loop-helix ubiquitous 33770_at CHUK AF00925 kinase conserved helix-loop-helix ubiquitous 1789_at COPS5 U65928 homolog subunit 5 (Arabidopsis) 32539_at COP9 U70735 COP9 homolog 40138_at CPNE1 U83246 COP9 subunit 6 (MOV34 homolog, 34 kD) 39706_at CPNE1 U83246 copine ill 37999_at CPO D16611 (coproporphyrinogen oxidase 37026_at CPO D16611 (coproporphyria, harderoporphyria) 41175_at CBFB L2029B core-binding factor, beta subunit 42029 CONIL AF10439B cornichon-like	404	36638_at	CTGF	X78947	connective tissue growth factor	connective tissue growth factor
11202_s_at OS4 AF000152 osteosarcoma conserved helix-loop-helix ubiquitous 33770_at CHUK AF009225 kinase conserved helix-loop-helix ubiquitous 1789_at COPS5 U65928 homolog subunit 5 (Arabidopsis) 32539_at COP9 U70735 COP9 homolog 40138_at CPNE1 U83246 COP9 subunit 6 (MOV34 homolog, 34 kD) 39706_at CPNE1 U83246 copine ill 37999_at CPO D16611 (coproporphyrinogen oxidase 37026_at CPO D16611 (coproporphyria, harderoporphyria) 41175_at CBFB L2029B core-binding factor, beta subunit 42029 CONIL AF10439B cornichon-like					conserved gene amplified in	
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39706_at CPNE3 AB014536 copine III 37999_at CPO D16611 (coproporphyria, harderoporphyria) 37026_at COPEB AF001461 core promoter element binding protein 41175_at CBFB L20298 core-binding factor, beta subunit 32803_at CNIL AF104398 cornichon-like	4	40452 at	CPNE	U83246	copine I	copine I
37999_at CPO D16611 (coproporphyria, harderoporphyria) 37026_at COPEB AF001461 core promoter element binding protein 41175_at CBFB L20298 core-binding factor, beta subunit 32803_at CNIL AF104398 cornichon-like	4	39706 at	CPNE3	AB014536	copine III	KIAA0636 protein
37999_at CPO D16611 (coproporphyria, harderoporphyria) 37026_at COPEB AF001461 core promoter element binding protein 41175_at CBFB L20298 core-binding factor, beta subunit 32803_at CNIL AF104398 cornichon-like		7			coproporphyrinogen oxidase	
37026_at COPEB AF001461 core promoter element binding protein 41175_at CBFB L20298 core-binding factor, beta subunit 32803_at CNIL AF104398 cornichon-like	412	37999_at	CPO	D16611	(coproporphyria, harderoporphyria)	coproporphyrinogen oxidase
41175_at CBFB L20298 corp-binding factor, beta subunit AF104398 cornichon-like	413	37026_at	COPEB	AF001461	core promoter element binding protein	Kruppel-like zinc finger protein Zf9
32803 at CNIL AF104398 cornichon-like	414	41175_at	CBFB	120298	core-binding factor, beta subunit	transcription factor
	415	32803_at	CNIF	AF104398	cornichon-like	comichon



416 34723_at COX11 417 37907_at F8A; DXS522E 418 38684_at CFDP1 420 36948_at CRI1 421 38148_at CRI1 422 37902_at CRY1 422 37902_at CRY2 423 40167_s_at CRY2 424 38804_at CRY2 425 1768_s_at CRY2 426 41309_g_at CTBP1 427 40780_at CTBP2 428 39723_at CUL1 429 40141_at CUL48 430 31823_at CUL1 431 36872_at ARPP-19 432 41808_at DMTF1 433 38418_at CCND1 434 2020_at CCND1 435 36650_at CCND2 436 40225_at GAK	COX11 homolog, cylochrome c oxidase assembly protein (yeast) CpG island protein; Human nested gene protein gene, complete cds. craniotacial development protein 1 CREB binding protein (Rubinstein-Taybi syndrome) CREBBP/EP300 inhibitory protein 1 cryptochrome 1 (photolyase-like) crystallin, zeta (quinone reductase) CS box-containing WD protein CSE1 chromosome segregation 1-like (yeast) c-src tyrosine kinase C-terminal binding protein 1 C-terminal binding protein 2	COX11 homolog coagulation factor VIII-associated protein craniofacial development protein 1 CREB-binding protein C15orf3 photolyase zeta-crystallin c-src-kinase phosphoprotein CtBP C-terminal binding protein 2
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34723_at COX11 37907_at FBA; DXS522 38664_at CFDP1 38684_at CFDP1 36948_at CRY1 38148_at CRY1 37902_at CRY2 40167_s_at CRY2 40167_s_at CRY2 40780_at CSE1L 40780_at CTBP1 40780_at CTBP2 39723_at CUL1 40780_at CTBP2 39723_at CUL1 40180_at CTBP2 39723_at CUL1 40180_at CTBP2 39723_at CUL1 40180_at CCND1 36872_at CCND1 36872_at CCND1 36872_at GCND1 36872_at GCND1 36872_at GCND1 36872_at GCND1 36872_at GCND1	assembly protein (yeast) CpG island protein; Human nested gene protein gene, complete cds. CREB binding protein (Rubinstein-Taybi syndrome) CREBBP/EP300 inhibitory protein 1 cryptochrome 1 (photolyase-like) Crystallin, zeta (quinone reductase) CS box-containing WD protein CSE1 chromosome segregation 1-like (yeast) C-terminal binding protein 1 C-terminal binding protein 2 C-terminal binding protein 2	coagulation factor VIII-associated protein craniofacial development protein 1 CREB-binding protein C15orf3 photolyase zeta-crystallin cellular apoptosis susceptibility protein c-src-kinase phosphoprotein CIBP C-terminal binding protein 2
37907_at FBA; DXS522 38664_at CFDP1 33831_at CRD1 36948_at CRI1 38148_at CRY1 37902_at CRYZ 40167_s_at CRYZ 40167_s_at CRYZ 40167_s_at CREBP 40780_at CSE1L 40780_at CTBP1 40780_at CTBP2 39723_at CUL1 40780_at CTBP2 39723_at CUL1 40141_at CULL1 36872_at CUTL1 36872_at CUTL1 36872_at CCND1 36872_at CCND1 36872_at CCND1 36872_at GCND1 36872_at GCND1 36872_at GCND1 36872_at GCND1	CpG island protein; Human nested gene protein gene, complete cds. craniolacial development protein 1 CREB binding protein (Rubinstein-Taybi syndrome) CREBBP/EP300 inhibitory protein 1 cryptochrome 1 (photolyase-like) crystallin, zeta (quinone reductase) CS box-containing WD protein CSE1 chromosome segregation 1-like (yeast) C-scr tyrosine kinase C-terminal binding protein 1 C-terminal binding protein 2 C-terminal binding protein 2	coagulation factor VIII-associated protein craniofacial development protein 1 CREB-binding protein C15orf3 photolyase zeta-crystallin c-src-kinase phosphoprotein CtBP C-terminal binding protein 2
37907_at FBA; DXS522 38664_at CFDP1 38664_at CFDP1 38938_at CR11 38148_at CRY1 37902_at CRYZ 40167_s_at CRYZ 40167_s_at CRYZ 40167_s_at CRYZ 40167_s_at CREBP1 40780_at CTBP2 39723_at CUL1 40780_at CTBP2 39723_at CUL1 40141_at CUL1 38672_at DMTF1 36872_at DMTF1 36872_at CCND1 36872_at CCND1 36872_at CCND1 36872_at GCND1 36872_at GCND1 36872_at GCND1	protein gene, complete cds. craniolacial development protein 1 CREB binding protein (Rubinstein-Taybi syndrome) CREBBP/EP300 inhibitory protein 1 cryptochrome 1 (photolyase-like) crystallin, zeta (quinone reductase) CS box-containing WD protein CSE1 chromosome segregation 1-like (yeast) C-src tyrosine kinase C-terminal binding protein 1 C-terminal binding protein 2 C-terminal binding protein 2	coagulation factor VIII-associated protein craniofacial development protein 1 CREB-binding protein C15orf3 photolyase zeta-crystallin c-src-kinase phosphoprotein CtBP C-terminal binding protein 2
38664_at (1) 3831_at (2) 36948_at (3) 38148_at (4) 38148_at (4) 40167_s_at (1) 40780_at (4) 40780_at (4) 40780_at (4) 40780_at (4) 39723_at (4) 39723_at (4) 30872_at (4) 36872_at (4)	craniotacial development protein 1 CREB binding protein (Rubinstein-Taybi syndrome) CREBBP/EP300 inhibitory protein 1 cryptochrome 1 (photolyase-like) crystallin, zeta (quinone reductase) CS box-containing WD protein CSE1 chromosome segregation 1-like (yeast) c-src tyrosine kinase C-terminal binding protein 1 C-terminal binding protein 2 36 cullin 1	craniofacial development protein 1 CREB-binding protein C15orf3 photolyase zeta-crystallin cellular apoptosis susceptibility protein c-src-kinase phosphoprotein CtBP C-terminal binding protein 2
33831_at	CREB binding protein (Rubinstein-Taybi syndrome) CREBBP/EP300 inhibitory protein 1 cryptochrome 1 (photolyase-like) crystallin, zeta (quinone reductase) CS box-containing WD protein CSE1 chromosome segregation 1-like (yeast) c-src tyrosine kinase C-terminal binding protein 1 C-terminal binding protein 2 cullin 1	CREB-binding protein C15orf3 photolyase zeta-crystallin cellular apoptosis susceptibility protein phosphoprotein CtBP C-terminal binding protein 2
33831_at	syndrome) CREBBP/EP300 inhibitory protein 1 cryptochrome 1 (photolyase-like) crystallin, zeta (quinone reductase) CS box-containing WD protein CSE1 chromosome segregation 1-like (yeast) c-src tyrosine kinase C-terminal binding protein 1 C-terminal binding protein 2 cullin 1	CREB-binding protein C15orf3 photolyase zeta-crystallin cellular apoptosis susceptibility protein c-src-kinase phosphoprotein CtBP C-terminal binding protein 2
36948_at 0 38148_at 0 37902_at 0 40167_s_at 1 1768_s_at 0 47309_g_at 0 47309_at 0 47309_at 0 471309_at 0 3723_at 0 41808_at 0 36872_at 0 36872_at 0 36872_at 0 41808_at 0 41808_at	CREBBP/EP300 inhibitory protein 1 cryptochrome 1 (photolyase-like) crystallin, zeta (quinone reductase) CS box-containing WD protein CSE1 chromosome segregation 1-like (yeast) c-src tyrosine kinase C-terminal binding protein 1 C-terminal binding protein 2 cullin 1	c15orf3 photolyase zeta-crystallin cellular apoptosis susceptibility protein c-src-kinase phosphoprotein CtBP C-terminal binding protein 2
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37902_at 0 38804_at 0 38804_at 0 1768_s_at 0 47309_g_at 0 471309_g_at 0 40141_at 0 31823_at 0 31823_at 0 31823_at 0 31823_at 0 31823_at 0 41808_at 0 2020_at 0 36650_at 0 40225_at 0 40125_at 0	crystallin, zeta (quinone reductase) CS box-containing WD protein CSE1 chromosome segregation 1-like (yeast) c-src tyrosine kinase C-terminal binding protein 1 C-terminal binding protein 2 cullin 1	cellular apoptosis susceptibility protein c-src-kinase phosphoprotein CtBP C-terminal binding protein 2
38804_at (1768_s_at (1768_s_at (1768_s_at (1709_at (1709_	CS box-containing WD protein CSE1 chromosome segregation 1-like (yeast) c-src tyrosine kinase C-terminal binding protein 1 C-terminal binding protein 2 cullin 1	cellular apoptosis susceptibility protein c-src-kinase phosphoprotein CtBP C-terminal binding protein 2
38804_at 1768_s_at 41309_g_at 40780_at 39723_at 40141_at 31823_at 36872_at 38418_at 38418_at 41808_at 41808_at 41808_at 41808_at 41808_at 41808_at	CSE1 chromosome segregation 1-like (yeast) c-src tyrosine kinase C-terminal binding protein 1 C-terminal binding protein 2 cullin 1	cellular apoptosis susceptibility protein c-src-kinase phosphoprotein CtBP C-terminal binding protein 2
38804_at 1768_s_at 41309_g_at 40780_at 39723_at 40141_at 40141_at 36872_at 36872_at 38418_at 2020_at 36650_at 40225_at	(yeast) c-src tyrosine kinase C-terminal binding protein 1 C-terminal binding protein 2 cullin 1	cellular apoptosis susceptibility protein c-src-kinase phosphoprotein CtBP C-terminal binding protein 2
1768 s_at 41309 g_at 40780_at 39723_at 40141_at 40141_at 36872_at 36872_at 38418_at 2020_at 36650_at 40225_at	c-src tyrosine kinase C-terminal binding protein 1 C-terminal binding protein 2 cullin 1	c-src-kinase phosphoprotein CtBP C-terminal binding protein 2
41309_g_at 40780_at 39723_at 40141_at 40141_at 31823_at 36872_at 41808_at 38418_at 2020_at 36650_at 40225_at	C-terminal binding protein 1 C-terminal binding protein 2 cullin 1	phosphoprotein CtBP C-terminal binding protein 2
40780_at 39723_at 40141_at 31823_at 36872_at 41808_at 38418_at 2020_at 36650_at 40225_at	C-terminal binding protein 2 cullin 1	C-terminal binding protein 2
39723_at 40141_at 40141_at 31823_at 36872_at 41808_at 41808_at 2020_at 36650_at 40225_at	cullin 1	oullin 1
40141_at 31823_at 36872_at 41808_at 41808_at 28418_at 2020_at 36650_at 40225_at		
31823_at 36872_at 41808_at 38418_at 2020_at 36650_at 40225_at	AB014595 cullin 4B	KIAA0695 protein
31823_at 36872_at 41808_at 38418_at 2020_at 36650_at 40225_at	CCAAT displacement protein	
36872_at 41808_at 38418_at 2020_at 36650_at 40225_at		cut-like 1, CCAAT displacement protein
41808_at 38418_at 2020_at 36650_at 40225_at	AL120559 cyclic AMP phosphoprotein, 19 kD	
41808_at 38418_at 2020_at 36650_at 40225_at	cyclin D binding myb-like transcription	cyclin D binding myb-like transcription factor
38418_at 2020_at 36650_at 40225_at	AF052102 factor 1	
38418_at 2020_at 36650_at 40225_at	cyclin D1 (PRAD1: parathyroid	
	X59798 adenomatosis 1)	cyclin
	cyclin D1 (PRAD1: parathyroid	
	M73554 adenomatosis 1)	bci-1
	D13639 cyclin D2	cyclin D2
	D88435 cyclin G associated kinase	HsGAK
437 37723 at CCNG2	U47414 cyclin G2	cyclin G2
438 1913_at CCNG2	U47414 cyclin G2	cyclin G2
1924_at	U11791 cyclin H	cyclin H
1836_at	D50310 cyclin l	cyclin I
1792_g_at	M68520 cyclin-dependent kinase 2	cdc2-related protein kinase

(7 Sig

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				cyclin-dependent kinase 7 (MO15	
				homolog, Xenopus laevis, cdk-activating	
442	33317_at	CDK7	120320	kinase)	protein serine/threonine kinase
				cyclin-dependent kinase 7 (MO15	
				homolog, Xenopus laevis, cdk-activating	
443	1969_s_at	CDK7	X77743	kinase)	CDK activating kinase
444	35140_at	CDK8	R59697	cyclin-dependent kinase 8	
				cyclin-dependent kinase inhibitor 1A (p21,	
445	2031_s_at	CDKN1A	U03106	Cip1)	cyclin-dependent kinase inhibitor 1A
				cyclin-dependent kinase inhibitor 1B (p27,	
446	33847_s_at	CDKN1B	Al304854	Kip1)	
				cyclin-dependent kinase inhibitor 2C (p18,	
447	36053_at	CDKN2C	AF041248	inhibits CDK4)	cyclin-dependent kinase inhibitor
448	448 38700_at	CSRP1	M33146	cysteine and glycine-rich protein 1	cysteine and glycine-rich protein 1
449	41401_at	CSRP2	U57646	cysteine and glycine-rich protein 2	cysteine and glycine-rich protein 2
450	40936_at	CRIM1	AI651806	cysteine-rich motor neuron 1	
451	38772_at	CYR61	Y11307	cysteine-rich, angiogenic inducer, 61	CYR61 protein
452	40408_at	CARS	L06845	cysteinyl-tRNA synthetase	cysteinyl-tRNA synthetase
				cytidine monophosphate-N-	
2	***		70000	acetymetrammic acid hydroxylase (Civir-	OMD N-ocetyloguspinion in production
433	39317_all	CMAT	U80324	iv-acetyliteuralilliate illoriooxygeriase)	כוגור יוז-מכפולוווסמומווווווכ מכוח וולחוכעלומכם
757	27070	N advo	A 4 17200C	cytochrome be outer mitochondrial	
404	94040 BI	M-coro	AA 1 / 3030	ווופוווחומוום חופרתומחו	
455	35818_at	HCS	D00265	cytochrome c	cytochrome c
456	39921_at	COX5B	AI526089	cytochrome c oxidase subunit Vb	
				cytochrome c oxidase subunit VIa	
457	41206_r_at	COX6A1	AI540925	polypeptide 1	
458	36165_at	coxec	W51774	cytochrome c oxidase subunit VIc	
				cytochrome c oxidase subunit VIIa	
459	39031_at	COX7A1	AA152406	polypeptide 1 (muscle)	
				cytochrome c oxidase subunit VIIa	×
460	41760_at	COX7A2	AA978033	polypeptide 2 (liver)	
		***		cytochrome c oxidase subunit VIIa	
461	34330_at	COX7A2L	AB007618	polypeptide 2 like	COXYRP
462	462 34381_at	COX7C	AI708889	cytochrome c oxidase subunit VIIc	

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463	38080_at	SOX8	AI525665	cytochrome c oxidase subunit VIII	
ঠ	35819_at	CYC1	X06994	cytochrome c-1	cytochrome c-1
465	33389 at	CYP51	U23942	cytochrome P450, 51 (lanosterol 14-alphademethylase)	lanosterol 14-demethylase cytochrome P450
				cytochrome P450, subfamily I (dioxin-	
				eptide 1 (glaucoma 3,	
466	466 859_at	CYP1B1	U03688		cytochrome P450
				cytochrome P450, subfamily I (dioxin-	
				inducible), polypeptide 1 (glaucoma 3,	
467	40071_at	CYP1B1	U03688	primary infantile)	cytochrome P450
468	37509_at	CRLF3	AF046059	cytokine receptor-like factor 3	cytokine receptor related protein 4
469	37306_at	KIAA0068	D38549	cytoplasmic FMRP interacting protein 1	
				cytoplasmic; Human Ser/Thr protein	
470	470 1706_at	A-RAF-1	U01337	kinase (A-RAF-1) gene, complete cds.	Ser/Thr protein kinase
471	471 34338_at	CKAP1	D49738	cytoskeleton-associated protein 1	cytoskeleton associated protein
472	472 32529_at	CKAP4	X69910	cytoskeleton-associated protein 4	P63 protein
473	473 40282_s_at	DF	M84526	D component of complement (adipsin)	adipsin/complement factor D
474	474 40877_s_at	MN7	AF041080	D15F37 (pseudogene)	
				damage-specific DNA binding protein 2	
475	475 1243_at	DDB2	U18300	(48kD)	DDBb p48
476	476 36616_at	DAZAP2	D31767	DAZ associated protein 2	DAZ associated protein 2
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
477	37663_at	DDX1	X70649	polypeptide 1	member of DEAD box protein family
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
478	35306_at	DDX15	AB001636	polypeptide 15	ATP-dependent RNA helicase #46
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
479	40490_at	DDX21	U41387	polypeptide 21	Gu protein
			,	DEAD/H (Asp-Glu-Ala-Asp/His) box	
480	39744_at	DDX3	AF000982	polypeptide 3	dead box, X isoform
				DEAD/H (Asp-Glu-Ala-Asp/His) box	DEAD/H (Asp-Glu-Ala-Asp/His) box
481	34647_at	DDX5	X52104	polypeptide 5 (RNA helicase, 68kD)	polypeptide 5
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
				polypeptide 9 (RNA helicase A, nuclear	
482	482 36153_at	6XQQ	L13848	DNA helicase II; leukophysin)	RNA helicase A
483	483 41872 at	DFNA5	AF073308	deafness, autosomal dominant 5	nonsyndromic hearing impairment protein

DAP3 U18321		4	8	0	Q	Ľ
1356_at DAP3 U18321 C 39114_at DEPP AB022718 c 37638_at DOCK1 D50857 c 38413_at DAD1 D15057 c 38413_at DAD1 D15057 c 32824_at CLN2 AF03504 c 33337_at DEGS AF03519 c 37951_at DLC1 AF03519 c 37951_at DLEU1 Y15227 c 38792_at DEK X64229 c 38791_at DLEU1 Y15227 c 38744_at DSS1 N95406 c 38785_at DSTN S65738 c 38044_at DSTN S65738 c 38003_s_at DGKD D73409 c 37692_at DIAPH1 AF051782 c 37692_at DPYSL2 U97105 c 36149_at DPYSL3 D78014 c 38503_s_at <td< th=""><th></th><th></th><th>1</th><th></th><th></th><th>ionizing radiation resistance conferring</th></td<>			1			ionizing radiation resistance conferring
39114_at DEPP AB022718 of 37638_at DOCK1 D50857 of 38413_at DAD1 D15057 of 32824_at CLN2 AF039704 of 33337_at DEGS AF035119 of 37951_at DLC1 AF035138 of 38032_at DDFP2 AB007860 of 38041_at DGKD D73409 of 38003_s_at DGKD D13409 of 33920_at DPYSL2 D78014 at DBYSL2 D78014 at DPYSL3 DPYSL4 AB006713 af 38220_at DPYSL4 AB006713 af 38220_at DPYSL4 AA0485_at HSA249128 AA176780	484	1356_at	DAP3	U18321		protein
32824_at DEPP AB022718 of 38413_at DAD1 D15057 of 38413_at DAD1 D15057 of 32824_at CLN2 AF039704 of 33337_at DEC			1	1		
37638_at DOCK1 D50857 o 38413_at DAD1 D15057 o 38413_at DAD1 D15057 o 32824_at CLN2 AF039704 o 33337_at DEGS AF03229 o 33791_at DLC1 AF035119 o 33791_at DLC1 AF035119 o 33791_at DLC1 AF035119 o 33791_at DLC1 AF035119 o 33791_at DLEU1 Y15227 o 38785_at DLEU1 Y15227 o 38744_at DSS1 N95406 o 38385_at DSTN S65738 o 38044_at DGKD D73409 o 38003_s_at DGKD D73409 o 38004_sat DGKD D73409 o 3904_at DBN DGKD D73409 3904_at DBN DGKD D794905 3904_at <t< th=""><th><u>왕</u></th><th>39114_at</th><th>UEPP</th><th>AB022/18</th><th>+</th><th>UEFF CONTON</th></t<>	<u>왕</u>	39114_at	UEPP	AB022/18	+	UEFF CONTON
38413_at DAD1 D15057 32824_at CLN2 AF039704 32337_at DEGS AF02268 3892_at DEK X64229 37951_at DLC1 AF035119 37951_at DLC1 AF035119 37951_at DLC1 AF035119 38791_at DLC1 AF035119 38791_at DLEU1 Y15227 3874_at DSS1 N95406 3874_at DSTN S65738 38941_at DSTN S65738 39044_s_at DGKD D73409 38003_s_at DGKZ U94905 33920_at DIAPH1 AF051782 37692_at DIAPH1 AF051782 37692_at DBYSL2 U97105 36149_at DPYSL2 U97105 35041_at DPYSL3 D78014 35503_s_at DPYSL4 AB006713 38503_s_at DPYSL4 AB176780	486	37638_at	DOCK1	D50857	1	DOCK 180 protein
32824_at CLN2 AF039704 33337_at DEGS AF002668 38992_at DEK X64229 37951_at DLC1 AF035119 33791_at DLEU1 Y15227 38744_at DES1 N95406 36629_at DENT AF064603 38985_at DSTN S65738 39044_s_at DGKD D73409 39044_s_at DGKZ U94905 33920_at DIAPH1 AF051782 33920_at DIAPH1 AF051782 36149_at DDYSL2 U97105 36149_at DPYSL2 U97105 36149_at DPYSL3 D78014 39503_s_at DPYSL4 AB006713 39503_s_at DPYSL4 AB006713 39503_s_at DPYSL4 AB006713 39503_s_at DPYSL4 AB006713		38413_at	DAD1	D15057		DAD-1
32824_at CLN2 AF039704 32337_at DEGS AF002668 38992_at DEK X64229 37951_at DLC1 AF035119 33791_at DLEU1 Y15227 38744_at DES1 N95406 36629_at DSIP! AI635895 36829_at DSTN S65738 38385_at DSTN S65738 38003_s_at DGKD D73409 38003_s_at DGKZ U94905 33920_at DIAPH1 AF051782 33920_at DIAPH1 AF051782 36149_at DPYSL2 U97105 36149_at DPYSL2 U97105 36149_at DPYSL3 D78014 38503_s_at DPYSL4 AB006713 38520_at DPYSL4 AB006713 38520_at DPYSL4 AB06713					deficient in late-infantile neuronal ceroid	
32824_at CLN2 AF039704 33337_at DEGS AF002668 38992_at DEK X64229 37951_at DLC1 AF035119 33791_at DLEU1 Y15227 38744_at DSS1 N95406 36629_at DSIPI AF035895 35814_at GA17 AF064603 39044_s_at DGKD D73409 39044_s_at DGKZ U94905 33920_at DGKZ U94905 33920_at DGKZ U94905 33920_at DDAT Y00978 40607_at DPYSL2 U97105 36149_at DPYSL2 U97105 36149_at DPYSL3 D78014 38503_s_at DPYSL4 AB006713 38503_s_at DPYSL4 AB006713 38503_s_at DPYSL4 AB006713 38503_s_at DPYSL4 AB006713					lipofuscinosis; Homo sapiens lysosomal	
32824_at CLN2 AF039704 33337_at DEGS AF02668 38992_at DEK X64229 37951_at DLC1 AF035119 33791_at DLEU1 Y15227 38744_at DSS1 N95406 36629_at DSIPI AI635895 35814_at GA17 AF064603 39044_s_at DGKD D73409 39044_s_at DGKZ U94905 33920_at DGKZ U94905 33920_at DGKZ U94905 33920_at DGKZ U94905 33920_at DDAT Y00978 40607_at DDAT Y00978 36149_at DPYSL2 U97105 36149_at DPYSL3 D78014 38503_s_at DPYSL4 AB006713 38520_at DPYSL4 AB06713 38520_at DPYSL4 AB06713						
3337_at DEGS AF002668 38992_at DEK X64229 3791_at DLC1 AF03519 33791_at DLEU1 Y15227 38744_at DSS1 N95406 3629_at DSIPI AF064603 3629_at DSIPI AF064603 38385_at DSTN S65738 38044_s_at DGKD D73409 39044_s_at DGKZ U94905 33920_at DIAPH1 AF051782 37692_at DIAPH1 AF051782 40607_at DPYSL2 U97105 36149_at DPYSL2 U97105 36149_at DPYSL2 U97105 36149_at DPYSL2 U97105 38503_s_at DPYSL3 D78014 38503_s_at DPYSL4 AB006713 38503_s_at DPYD U20938 40485_at HSA249128 AA176780	488	32824_at	CLN2	AF039704		lysosomal pepstatin insensitive protease
3337_at DEGS AF002668 38992_at DEK X64229 38992_at DLC1 AF03519 33791_at DLEU1 Y15227 38744_at DSS1 N95406 38744_at DSIPI AF064603 35814_at GA17 AF064603 38044_s_at DDEF2 AB007860 39044_s_at DGKD D73409 39042_s_at DGKD D73409 33920_at DIAPH1 AF051782 37692_at DIAPH1 AF051782 39041_at DLAT Y00978 40607_at DPYSL2 U97105 36149_at DPYSL2 U97105 36149_at DPYSL3 D78014 38503_s_at DPYSL3 D78014 38503_s_at DPYSL3 D78014 38503_s_at DPYSL3 D78014 38503_s_at DPYSL3 D78018 40485_at HSA249128 AA176780					atocyte homolog, lipid	
38992_at DEK X64229 37951_at DLC1 AF035119 33791_at DLEU1 Y15227 38744_at DSS1 N95406 3629_at DSIPI AF064603 35814_at GA17 AF064603 35816_at DSTN S65738 39044_s_at DDEF2 AB007860 39042_s_at DGKD D73409 38003_s_at DGKZ U94905 33920_at DIAPH1 AF051782 37692_at DBI AI557240 36149_at DPYSL2 U97105 36149_at DPYSL2 U97105 36149_at DPYSL2 U97105 36149_at DPYSL2 U97105 38503_s_at DPYSL3 D78014 38503_s_at DPYSL4 AB006713 3850_at HSA249128 AA176780	489	33337_at	DEGS	AF002668		MLD
37951_att DLC1 AF035119 33791_att DLEU1 Y15227 38744_at DSS1 N95406 3629_at DSIP1 AI635895 35814_at GA17 AF064603 38385_at DSTN S65738 39044_s_at DGKD D73409 38063_s_at DGKZ U94905 33920_at DIAPH1 AF051782 33920_at DIAPH1 AF051782 36041_at DLAT Y00978 40607_at DPYSL2 U97105 36149_at DPYSL2 U97105 38503_s_at DPYSL3 D78014 38503_s_at DPYSL3 D78014 38503_at DPYSL3 D78018 40485_at HSA249128 AA176780	490	38992_at	DEK	X64229		putative oncogene
33791_at DLEU1 Y15227 38744_at DSS1 N95406 36629_at DSIP! AI635895 35814_at GA17 AF064603 38385_at DSTN S65738 39044_s_at DDEF2 AB007860 39044_s_at DGKD D73409 38003_s_at DGKZ U94905 33920_at DIAPH1 AF051782 37692_at DBI AI557240 36149_at DDAT Y00978 40607_at DPYSL2 U97105 36149_at DPYSL3 D78014 38503_s_at DPYSL3 D78014 38220_at DSY0938 40485_at HSA249128 AA176780	491	37951 at	DLC1	AF035119		deleted in liver cancer-1
38744_at DSS1 N95406 36629_at DSIPI AIG35895 35814_at GA17 AF064603 38385_at DSTN S65738 39044_s_at DDEF2 AB007860 39044_s_at DGKD D73409 38003_s_at DGKZ U94905 33920_at DIAPH1 AF051782 37692_at DBI AI557240 36143_at DLAT Y00978 40607_at DPYSL2 U97105 36143_at DPYSL2 U97105 38503_s_at DPYSL3 D78014 38503_s_at DPYSL3 D78014 38503_s_at DPYSL4 AB006713 38220_at HSA249128 AA176780	492	33791_at	DLEU1	Y15227	1	deleted in lymphocytic leukemia, 1
DSIPI AI635895 GA17 AF064603 GA17 AF064603 DSTN S65738 DDEF2 AB007860 at DGKZ U94905 DIAPH1 AF051782 DBI AI557240 DPYSL2 U97105 DPYSL3 D78014 at DPYSL4 AB006713 DPYD U20938 DPYD U2094 DPYD	493	38744 at	DSS1	N95406	Deleted in split-hand/split-foot 1 region	
DSIP AI635895 GA17					delta sleep inducing peptide,	
GA17 AF064603 DSTN S65738 DDEF2 AB007860 at DGKD D73409 DIAPH1 AF051782 DBI AI557240 DAT Y00978 DPYSL2 U97105 DPYSL3 D78014 DPYSL3 D78014 DPYSL49128 AA176780 HSA249128 AA176780 DATA AB066713 DATA AB066713 HSA249128 AA176780 AB066713 AB066713 AB06713 AB066713 AB06713 AB06713 AB06713 AB067	494	36629_at	DSIPI	A1635895		
DSTN S65738	495	35814_at	GA17	AF064603		GA17 protein
DDEF2 AB007860 DGKD D73409 DGKZ U94905 DIAPH1 AF051782 DBI AI557240 DPYSL2 U97105 DPYSL3 D78014 DPYSL3 D78014 DPYSL4 AB006713 DPYD U20938 HSA249128 AA176780	496	38385_at	DSTN	S65738	destrin (actin depolymerizing factor)	actin depolymerizing factor
DDEF2 AB007860 DGKD D73409 DGKZ U94905 DIAPH1 AF051782 DBI AI557240 DAT Y00978 DPYSL2 U97105 DPYSL3 D78014 DPYSL4 AB006713 DPYSL4 AB006713 DPYSL4 AB006713 DPYSL49128 AA176780					development and differentiation enhancing	development- and differentiation-enhancing
DGKD D73409 diacylglycerol kinase, delta (130kD) DGKZ U94905 diacylglycerol kinase, zeta (104kD) DIAPH1 AF051782 diaphanous homolog 1 (Drosophila) diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A receptor modulator, acyl-Coenzyme A receptor modulator, acyl-Coenzyme A binding protein) Al557240 binding protein) DBI Al557240 binding protein) component of pyruvate dehydrogenase (E2 component of pyruvate dehydrogenase DLAT Y00978 complex) dihydropyrimidinase-like 3 DPYSL2 U97105 dihydropyrimidinase-like 4 DPYSL3 DRWO6713 dihydropyrimidinase-like 4 DPYD U20938 dihydropyrimidinase-like 4 HSA249128 AA176780 DIPB protein	497	39410 at	DDEF2	AB007860	factor 2	factor 2
DGKZ U994905 diacylglycerol kinase, zeta (104kD) DIAPH1 AF051782 diaphanous homolog 1 (Drosophila) diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) A1557240 binding protein) DBI A1557240 binding protein) dihydrolipoamide S-acetyftransferase (E2 component of pyruvate dehydrogenase DLAT Y00978 complex) complex) DPYSL2 U97105 dihydropyrimidinase-like 2 dihydropyrimidinase-like 3 dihydropyrimidinase-like 4 d	498	39044 s_at	DGKD	D73409	diacylglycerol kinase, delta (130kD)	diacylglycerol kinase delta
DIAPH1 AF051782 diaphanous homolog 1 (Brosophila) DBI AI557240 binding protein) DBI AI557240 binding protein) DLAT Y00978 component of pyruvate dehydrogenase DPYSL2 U97105 dihydropyrimidinase-like 2 DPYSL3 D78014 dihydropyrimidinase-like 3 DPYSL4 AB006713 dihydropyrimidinase-like 4 DPYD U20938 dihydropyrimidine dehydrogenase HSA249128 AA176780 DIPB protein	499	38003 s at	DGKZ	U94905	diacylglycerol kinase, zeta (104kD)	diacylglycerol kinase zeta
Al557240 diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A receptor modulator, acyl-Coenzyme A binding protein) Al557240 binding protein) Al557240 dihydrolipoamide S-acetyftransferase (E2 component of pyruvate dehydrogenase (Component of p	20	33920_at	DIAPH1	AF051782	diaphanous homolog 1 (Drosophila)	diaphanous 1
19692_at DBI AI557240 binding protein					diazepam binding inhibitor (GABA	
37692_at DBI AI557240 binding protein) 39041_at DLAT Y0097B component of pyruvate dehydrogenase 40607_at DPYSL2 U97105 dihydropyrimidinase-like 2 39503_s_at DPYSL4 AB006713 dihydropyrimidinase-like 4 38220_at DPYD U20938 dihydropyrimidinase-like 4 40485_at HSA249128 AA176780 DIPB protein		e			receptor modulator, acyl-Coenzyme A	
dihydrolipoamide S-acetyftransferase (E2 20041_at DLAT Y00978 component of pyruvate dehydrogenase 40607_at DPYSL2 U97105 dihydropyrimidinase-like 2 39503_s_at DPYSL4 AB006713 dihydropyrimidinase-like 3 38220_at DPYD U20938 dihydropyrimidinase-like 4 40485_at HSA249128 AA176780 DIPB protein	501		IBO	AI557240	binding protein)	
39041_at DLAT Y00978 component of pyruvate dehydrogenase 40607_at DPYSL2 U97105 dihydropyrimidinase-like 2 39503_s_at DPYSL3 D78014 dihydropyrimidinase-like 3 38220_at DPYSL4 A8006713 dihydropyrimidinase-like 4 38220_at DPYD U20938 dihydropyrimidine dehydrogenase 40485_at HSA249128 AA176780 DIPB protein					dihydrolipoamide S-acetyftransferase (E2	
39041_at DLAT Y00978 complex) 40607_at DPYSL2 U97105 dihydropyrimidinase-like 2 36149_at DPYSL3 D78014 dihydropyrimidinase-like 3 39503_s_at DPYSL4 A8006713 dihydropyrimidinase-like 4 38220_at DPYD U20938 dihydropyrimidine dehydrogenase 40485_at HSA249128 AA176780 DIPB protein					component of pyruvate dehydrogenase	
40607_at DPYSL2 U97105 dihydropyrimidinase-like 2 36149_at DPYSL3 D78014 dihydropyrimidinase-like 3 39503_s_at DPYSL4 AB006713 dihydropyrimidinase-like 4 38220_at DPYD U20938 dihydropyrimidine dehydrogenase 40485_at HSA249128 AA176780 DIPB protein	502		DLAT	Y00978	complex)	PDC-E2 precursor (AA -54 to 561)
36149_at DPYSL3 D78014 dihydropyrimidinase-like 3 39503_s_at DPYSL4 AB006713 dihydropyrimidinase-like 4 38220_at DPYD U20938 dihydropyrimidine dehydrogenase 40485_at HSA249128 AA176780 DIPB protein	503	40607_at	DPYSL2	U97105	dihydropyrimidinase-like 2	N2A3
39503_s_at DPYSL4 AB006713 dihydropyrimidine 4 38220_at DPYD U20938 dihydropyrimidine dehydrogenase 40485_at HSA249128 AA176780 DIPB protein	504	36149_at	DPYSL3	D78014	dihydropyrimidinase-like 3	dihydropyrimidinase related protein-3
38220_at DPYD U20938 dihydropyrimidine dehydrogenase 40485_at HSA249128 AA176780 DIPB protein	505	39503_s_at	DPYSL4	AB006713	dihydropyrimidinase-like 4	dihydropyrimidinase related protein 4
40485_at HSA249128 AA176780	200	38220_at	DPYD	U20938	dihydropyrimidine dehydrogenase	dihydropyrimidine dehydrogenase
	507	40485_at	HSA249128	AA176780	DIPB protein	

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				disabled homolog 2, mitogen-responsive	
508	479_at	DAB2	U53446	phosphoprotein (Drosophila)	DOC-2
				discoidin domain receptor family, member	
509	36643_at	DDR1	120817		tyrosine protein kinase
510	40575_at	DLG5	AB011155	discs, large (Drosophila) homolog 5	KIAA0583 protein
				dishevelled associated activator of	
511	33753_at	DAAM1	AB014566	morphogenesis 1	KIAA0666 protein
512	512 33150_at	SAS10	A1126004	disrupter of silencing 10	,
				dJ635G19.1 (LAMR1 (Laminin Receptor 1	
				(67kD) (RPSA, 40S Ribosomal Protein	
				SA, P40)) pseudogene); match: cDNAs:	
				Em:X15005 Em:J03799 Em:X61156	
				Em:M64923 Em:X06406 Em:AF140348	
				Em:J02870 Em:L16589 Em:Z22749	
				Em:D25224 Em:M14199 Em:M27798;	
513	513 40916_at	dJ635G19.1	AL035494	match: ESTs: Em:AA642	dJ635G19.2.1 (novel protein (isoform 1))
				dJ734P14.1 (KRAB box and C2H2 Zinc	
				finger domain protein pseudogene) match:	
				cDNAs: Em:M27878 Em:M29580	
				Em:U27186 Em:D31763 Em:AB007872	
				Em:U09366 Em:U09413 Em:X17617	
				Em:AF011573 Em:AF020591 Em:X78925	
				match: proteins: Sw:P52736 Sw:Q06730	
				Sw.P51523 Tr.Q14585 Sw.P15620	
				Sw:Q02386 Sw:P51786 Sw:Q99676	
				Tr:O60792 Sw:Q03923 Sw:O75820	dJ734P14.2.1 (snRNP (small nuclear
514	514 38456 s at	dJ734P14.1	AL049650	Tr:Q61116 Tr:Q64247	ribonucleoprotein particle) protein B)

		-	C		
	∢	В	j.	O	U
515	38455 <u>_</u> at	dJ734P14.1	AL049650	dJ734P14.1 (KRAB box and C2H2 Zinc finger domain ptotein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09366 Em:U09413 Em:X17617 Em:U09366 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:P51523 Tr:Q14585 Sw:P15620 Sw:Q0386 Sw:P51786 Sw:Q099676 Tr:O60792 Sw:Q03923 Sw:O75820 Tr:Q61116 Tr:Q64247	dJ734P14.2.1 (snRNP (small nuclear
516	35809 <u>g</u> at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:Q57731 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serine- rich 6 (SRP55-2)(isoform 2))
517	35808_at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P57731 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serine- rich 6 (SRP55-2)(isoform 2))
	518 32433_at	dJ90L6.1	Z97353	dJ90L6.1 (RPL15 (60S Ribosomal Protein L15) pseudogene); match: proteins: Sw:O74895 Sw:P51417 Sw:P39030 Sw:O77445 Sw:P54780 Sw:O23515 Sw:O65050 Wp:CE12148 Sw:P30736 Sw:P641051 Sw:P54060 Sw:O65082 Sw:P52818 Sw:P53074 Sw:P52818 Sw:P79324 Sw:O65082 Sw:O13418 Sw:O82528 Sw:P05748; Human DNA sequence from clone RP1-90L6 on chromosome 22q11.21-11.23 Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence.	

Fig 21

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519	34183_at	DKFZP434C171	AL080169 [DKFZP434C171 protein	hypothetical protein
520	40801_at	DKFZP434C212	_	DKFZP434C212 protein	
521	38400_at	DKFZP434D1335 AI920820		DKFZP434D1335 protein	
522	33392_at		AL080155	DKFZP434J154 protein	hypothetical protein
	39411_at		AL080156 [DKFZP434J214 protein	hypothetical protein
	40564_at		N42007	DKFZP564A043 protein	
525	37000_at	DKFZP564B167		DKFZP564B167 protein	hypothetical protein
526	33433_at	DKFZP564F0522		DKFZP564F0522 protein	hypothetical protein
527	41437_at	DKFZP564F1123		DKFZP564F1123 protein	hypothetical protein
528	39442_at	DKFZP564G0222 AL080115		DKFZP564G0222 protein	hypothetical protein
529	40437_at	DKFZP564G2022		DKFZP564G2022 protein	hypothetical protein
530	36456_at	DKFZP5641052		DKFZP5641052 protein	hypothetical protein
531	38033_at	DKFZP564M1416	116 AL049934	DKFZP564M1416 protein	hypothetical protein
532	36078_at	DKFZP56400423	23 AL080120	DKFZP56400423 protein	hypothetical protein
533	533 38256_s_at	DKFZP5640092	W21827	DKFZP5640092 protein	
534	39034_at	DKFZP5640123	AL080122	DKFZP564O123 protein	hypothetical protein
535	535 41662_at	DKFZP566B183	AL050272	DKFZP566B183 protein	hypothetical protein
536	536 32807_at	DKFZP566C134	AF004292	DKFZP566C134 protein	
537	537 38687_at	DKFZP566D193	AL050051	DKFZP566D193 protein	hypothetical protein
538	538 33776_at	DKFZP566K023	AL050062	DKFZP566K023 protein	hypothetical protein
539	539 41335_at	DC8	AL050084	DKFZP56601646 protein	hypothetical protein
540	540 36961_at	DKFZP586A011	AL050286	DKFZP586A011 protein	hypothetical protein
541	541 38717_at	DKFZP586A0522 AL050159	AL050159	DKFZP586A0522 protein	hypothetical protein
542	542 40831_at	DKFZP586B0923	23 AL050190	DKFZP586B0923 protein	hypothetical protein
543	543 34821_at	DKFZP586D0623 AL050197	AL050197	DKFZP586D0623 protein	hypothetical protein
544	544 39986_at	DKFZP586D0919 AL050100	AL050100	DKFZP586D0919 protein	hypothetical protein
545	545 34269_at	DKFZp586F1019 AL050102	AL050102	DKFZp586F1019 protein	hypothetical protein
546	35736_at	DKFZP586F1918 AL050091	AL050091	DKFZP586F1918 protein	hypothetical protein
547	547 40832_s_at	DKFZP586G011	AL050126	DKFZP586G011 protein	hypothetical protein
548	548 36007 at	DKFZP586L151	AL050137	DKFZP586L151 protein	hypothetical protein
549	34833 at	DKFZP58600120 AL050157	AL050157	DKFZP58600120 protein	hypothetical protein
550	550 37333 at	DNMT1	X63692	DNA (cytosine-5-)-methyttransferase 1	DNA (cytosine-5-)-methyttransferase
				DNA segment on chromosome X (unique)	
551	40891_f_at	DXS9879E	X92896	9879 expressed sequence	ITBA2 protein
25.0	24045 04	DVVS466	1 03426	DNA segment on chromosome X and Y	DNA segment on chromosome X and Y (unique) 155 expressed seguence
200	34215_at	DATSIBBE	LUSAKO	Callonhas passaldva col (anhilin)	South the south

	Α	8	၁	Q	ш
553	553 1252 at	DESAG	M735.47	DNA segment, single copy probe LNS-	colynosis locus-encoded protein
3	1202_at			DNA segment single conv probe pH4	DNA segment single copy, probe pH4
554	37162 at	D10S170	S72869	(transforming sequence, thyroid-1,	(transforming sequence, thyroid-1,
				DnaJ (Hsp40) homolog, subfamily A,	
555	39118_at	DNAJA1	F08069	member 1	DNAJ homologue-2
				DnaJ (Hsp40) homolog, subfamily A,	
556	276_at	DNAJA1	F080e9	member 1	DNAJ homologue-2
				DnaJ (Hsp40) homolog, subfamily B,	
557	41233_at	DNAJB6	AB014888	member 6	MRJ
				DnaJ (Hsp40) homolog, subfamily B,	
558	35799_at	DNAJB9	AL080081	member 9	hypothetical protein
				DnaJ (Hsp40) homolog, subfamily C,	
559	36166_at	DNAJC8	AF083190	member 8	SPF31
				docking protein 1, 62kD (downstream of	
560	816_g_at	DOK1	U70987	tyrosine kinase 1)	GAP binding protein p62dok
				docking protein 1, 62kD (downstream of	
561	34433_at	DOK1	AF035299	tyrosine kinase 1)	docking protein 1
				dolichyl-phosphate mannosyltransferase	
562	34879 at	DPM1	AF007875	polypeptide 1, catalytic subunit	dolichol monophosphate mannose synthase
563	38957_at	DCAMKL1	AB002367	doublecortin and CaM kinase-like 1	doublecortin and CaM kinase-like 1
564	564 32168 s at	DSCR1	U85267	Down syndrome critical region gene 1	Down syndrome critical region protein 1
565	36088_at	DSCR2	AJ006291	Down syndrome critical region gene 2	leucine rich protein
999	35166_at	DSCR3	D87343	Down syndrome critical region gene 3	DCRA
				down-regulator of transcription 1, TBP-	TATA binding protein-associated
267	32621_at	DR1	M97388	binding (negative cofactor 2)	phosphoprotein
268	37981_at	DBN1	D17530	drebrin 1	drebrin E
				dual specific protein; Homo sapiens	
		-		tyrosine phosphatase (cdc14B) mRNA,	
569	40920_at	cdc14B	AF023158	complete cds.	tyrosine phosphatase
				dual specificity phosphatase 11	
570	39727_at	DUSP11	AF023917	(RNA/RNP complex 1-interacting)	PIR1
571	38272_at	DUSP14	AF038844	dual specificity phosphatase 14	MKP-1 like protein tyrosine phosphatase
573	579 41995 at	DI ISP3	AI 049417	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	
7	141665_dt	5 155	20.00		

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A	П	В			<u> </u>
41193_at		DUSP6	AB013382	dual specificity phosphatase 6	DUSPe
36946 at		DYBK1A	DRESSO	dual-specificity tyrosine-(Y)-	serine/Ihreonine protein kinase
1512_at		DYRK1A	D86550	phosphorylation regulated kinase 1A	serine/threonine protein kinase
				dual-specificity tyrosine-(Y)-	dual-specificity tyrosine-(Y)-phosphorylation
760_at		DYRK2	Y09216	kinase 2	regulated kinase 2 isoform 1
				dual-specificity tyrosine-(Y)-	
39931_at		DYRK3		ed kinase 3	Dyrk3 protein
38368_at		DUT	U31930	phatase	deoxyuridine nucleotidohydrolase
38475_at		DCTN2	U50733	dynactin 2 (p50)	dynamitin
34891_at		NIG	AI540958	dynein, cytoplasmic, light polypeptide	
34829_at		DKC1	U59151	dyskeratosis congenita 1, dyskerin	Cbf5p homolog
		į	7.00.0014	dystonia 1, torsion (autosomal dominant;	V. (1997)
32234_al		וואס	AF00/8/1	(orsin A)	Musion
				dystroglycan 1 (dystrophin-associated	
36989_at		DAG1	L19711	glycoprotein 1)	dystroglycan
				dystrophin (muscular dystrophy,	
40488_at		DMD	M18533	Duchenne and Becker types)	dystrophin
40106_at		E18-AP5	AJ007509	E1B-55kDa-associated protein 5	E1B-55kDa-associated protein
33354_at		SMURF2	AA630312	E3 ubiquitin ligase SMURF2	
40375_at		EGR3	X63741	early growth response 3	transcription factor
36135_at		EBNA18P2	U86602	EBNA1 binding protein 2	nucleolar protein p40
37730_at		p100	U22055	EBNA-2 co-activator (100kD)	100 kDa coactivator
33254_at		EVIS	AF008915	ecotropic viral integration site 5	EVI-5 homolog
				ectodermal-neural cortex (with BTB-like	•
39542_at		ENC1	AF059611	domain)	nuclear matrix protein NRP/B
				ectonucleotide	
		00		pyrophosphatase/phosphodiesterase 2	
41124_r_at	at	ENPP2	L35594	(autotaxin)	autotaxin
				ectonucleotide pyrophosphatase/phosphodiesterase 2	
41123_s_at	_at	ENPP2	L35594	(autotaxin)	autotaxin
594 32551 at	-	EFEMP1	U03877	EGF-containing fibulin-like extracellular matrix protein 1	extracellular protein
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	4	a			L
595	36488_at	EGFLS	AB011542	iple 5	MEGF9
596		ETEA	เกสกรล	n, alpha	electron transfer flavoprotein, alpha
				electron-transfer-flavoprotein, beta	
297	36881_at	ЕТЕВ	X71129	polypeptide	electron transfer flavoprotein beta subunit
				elongation factor EF-1-alpha; Human	entendatic translation alongstion factor 1
598	1288_s_at	EEF1A	J04617	complete cds.	alpha 1
599	599 31853_at	EED	AF080227	embryonic ectoderm development	embryonic ectoderm development protein
				ems1 sequence (mammary tumor and	
009	39861 at	EMS1	M98343	squamous cell carcinoma-associated (p80/85 src substrate)	amplaxin
	t:			end of last exon based on GENSCAN	
				prediction presumably this gene and	
				dJ477H23.2 are part of the same gene	
601	41478_at	dJ477H23.1	AL033538	match: ESTs: Em:AA354647	dJ477H23.1 (novel protein)
				endocytic receptor (macrophage mannose	
602	37408_at	ENDO180	AB014609	receptor family)	KIAA0709 protein
				endosome-associated FYVE-domain	
603	37914_at	ENDOFIN	AB002303	protein	endosome-associated FYVE-domain protein
604	39010_at	ENSA.	A1658639	endosulfine alpha	
				endothelial differentiation,	
		i		lysophosphatidic acid G-protein-coupled	
905	40387_at	EDG2	U80811	receptor, 2	lysophosphatidic acid receptor homolog
9	1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	i	, C	the state of the s	t rotaet petalor acitatorostik lailadtokan
900	400/4 al	בותו	WY000CO	onhancer of ridimentary homolog	himse protein bomologous to DROFR
607	607 39079 at	ЕВН	D85758	(Drosophila)	protein
809	608 2035_s_at	EN01	M55914	enolase 1, (alpha)	c-myc binding protein
609	609 34335_at	EFNB2	AI765533	ephrin-B2	
				epidermal growth factor receptor pathway	epidermal growth factor receptor pathway
610	37731_at	EPS15	Z29064	substrate 15	substrate 15
				epidermal growth factor receptor pathway	epidermal growth factor receptor kinase
91	611 1467_at	EPS8	U12535	substrate 8	substrate
612	612 37762_at	EMP1	Y07909	epithelial membrane protein 1	progression associated protein
613	613 39631_at	EMP2	U52100	epithelial membrane protein 2	XMP

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				EPM1 disease gene; cysteine protease	
				inhibitor; Human cystatin B gene,	
614	35816_at	cystatin B	U46692	complete cds.	cystatin B
				erythrocyte membrane protein band 4.1-	
615	615 32585_at	EPB41L2	AF027299	like 2	protein 4.1-G
616		ESD	AF112219	esterase D/formylglutathione hydrolase	esterase D
				estrogen receptor binding site associated,	
617	38283_at	EBAG9	AB007619	antigen, 9	EBAG9
618	618 37161_at		W28948	ESTs	
619	619 40885_s_at		N30151	ESTs	
620	33328_at	C1S	W28612	ESTs	
621	621 33453_at	ATP6S1	A1400326	ESTs	
622	622 31801_at		AI808712	ESTs	
623	623 41598 at		AA890010	ESTs	•
				ESTs, Highly similar to RS21_HUMAN	
				40S RIBOSOMAL PROTEIN S21	
624	32744_at	RPS21	AI526078	[H.sapiens]	
				ESTs, Moderately similar to	
				ALUB_HUMAN ALU SUBFAMILY SX	
				SEQUENCE CONTAMINATION	
625	39750_at	•	W61005	WARNING ENTRY [H.sapiens]	
				ESTs, Moderately similar to	
				GLK5_HUMAN GLUTAMATE	
				RECEPTOR, IONOTROPIC KAINATE 5	
626	34906_g_at		AA977136	PRECURSOR [H.sapiens]	
				ESTs, Moderately similar to T46365	
				hypothetical protein DKFZp434A1518.1	*
627	35787_at		Al986201	[H.sapiens]	
				ESTs, Weakly similar to 0903209A	
628	41463_at		AL042729	peptide PD,basic Pro rich [H.sapiens]	
				ESTs, Weakly similar to N-WASP	
629	41273_at		AL046940	[H.sapiens]	
630	38097_at	PIG8	AF010313	etoposide-induced mRNA	Pig8
				eukaryotic translation elongation factor 1	
83	631 40888_f_at	EEF1A1	W28170	alpha 1	

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				eukaryotic translation elongation factor 1	
83	35175_f_at	EEF1A2	X70940	aipha 2	elongation factor 1 alpha-2
CCC		4	V00.100	eukaryotic translation elongation factor 1	
3	35/48_at	EEF182	X60489	Deta 2	elongation factor-1-beta
				eukaryotic translation elongation factor 1	
634	624 41256 at	בבביוט	701507	idelia (gualilile liucieolide excitatige profein)	Himse along the factor 1-dette
	,		1001	elikaryotic translation elongation factor 1	
635	1676_s_at	EEF1G	M55409	gamma	pancreatic tumor-related protein
989	36587_at	EEF2	Z11692	eukaryotic translation elongation factor 2	human elongation factor 2
637	663_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
638	34278_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
				eukaryotic translation initiation factor 2,	eukaryotic translation initiation factor 2,
639	1154_at	EIF2S1	J02645	subunit 1 (alpha, 35kD)	subunit 1 (alpha, 35kD)
				eukaryotic translation initiation factor 2B,	eukaryotic translation initiation factor 2B,
949	40515_at	EIF2B2	AF035280	subunit 2 (beta, 39kD)	subunit 2 (beta, 39kD)
				eukaryotic translation initiation factor 3,	
641	1644_at	EIF3S2	U36764	subunit 2 (beta, 36kD)	TGF-beta receptor interacting protein 1
				eukaryotic translation initiation factor 3,	
642	35327_at	EIF3S3	U54559	subunit 3 (gamma, 40kD)	translation initiation factor eIF3 p40 subunit
				eukaryotic translation initiation factor 3,	
643	32576_at	EIF3S5	U94855	subunit 5 (epsilon, 47kD)	translation initiation factor 3 47 kDa subunit
		•	,	eukaryotic translation initiation factor 3,	murine mammary tumor integration site 6
644	38681_at	EIF3S6	U62962	subunit 6 (48kD)	(oncogene homolog)
			-	eukaryotic translation initiation factor 3,	
645	35298_at	EIF3S7	U54558	subunit 7 (zeta, 66/67kD)	translation initiation factor eIF3 p66 subunit
				eukaryotic translation initiation factor 3,	
646	646 35323_at	EIF3S9	U78525	subunit 9 (eta, 116kD)	eukaryotic translation initiation factor
				eukaryotic translation initiation factor 4	
647	41785_at	EIF4G2	U73824	gamma, 2	p97
				eukaryotic translation initiation factor 4	
648	648 33907_at	EIF4G3	AF012072	gamma, 3	elF4GII

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Γ				eukaryotic translation initiation factor 4A,	
8	649 1420_s_at	EIF4A2	D30655	isoform 2	eukaryotic initiation tactor 4Atii
650	37752 at	EIF4E	M15353		cap-binding protein
	at	EIF4EBP2	N73769		
652	167_at	EIF5	U49436	eukaryotic translation initiation factor 5	translation initiation factor 5
653	37318 at	ETF1	X81625	eukaryotic translation termination factor 1	C11 protein
				excision repair cross-complementing	excision repair cross-complementing rodent
				rodent repair deficiency, complementation	rodent repair deficiency, complementation repair deficiency, complementation group 3
				group 3' (xeroderma pigmentosum group	(xeroderma pigmentosum group B
654	1885_at	ERCC3	M31899	B complementing)	complementing)
				excision repair cross-complementing	
)	rodent repair deficiency, complementation	
				group 5 (xeroderma pigmentosum,	
				complementation group G (Cockayne	
655	2063_at	ERCCS	L20046	syndrome))	excision repair protein
				over 1.4 beyond this clone, match.	A 1434O14 1 (Hydroxysteroid (11-beta)
656	33734 pt	HSD1181	AL022398	proteins P28845 P50172 P51975 Q29608	
557	667 222 at	EYT1	\$79639	exostoses (multiple) 1	
858 878	36526 at	EXTI 2	AF000416	exostoses (multiple)-like 2	EXT-like protein 2
8	659 38809 s at	EXT.3	AB011091	exostoses (multiple)-like 3	KIAA0519 protein
99	37729 at	XPO1	Y08614	exportin 1 (CRM1 homolog, yeast)	exportin 1
				exportin, tRNA (nuclear export receptor for	_
661	38753_at	XPOT	AF039022	(RNAs)	exportin t
				extracellular matrix protein 2, female	
662	39673 i at	ECM2	AB011792	organ and adipocyte specific	extracellular matrix protein
				extracellular matrix protein 2, female	
အွ	39674 r at	ECM2	AB011792	organ and adipocyte specific	extracellular matrix protein
8	664 35226 at	EYA2	U71207	eyes absent homotog 2 (Drosophila)	Eab1
				family with sequence similarity 8, member	
985	665 38318_at	FAM8A1	AL050128	Al	
999	666 31879 at	FUBP3	U69127	far upstream element (FUSE) binding protein 3	FUSE binding protein 3
	D. C.				

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	A	В	၁	O	נו
				ase (famesyl	farnesyl diphosphate synthase (farnesyl
			-	pyrophosphate synthetase,	pyrophosphate synthetase,
				dimethylallyftranstransferase,	dimethylallyltranstransferase,
299	37325_at	FDPS	D14697	geranyttranstransferase)	geranyltranstransferase)
				famesyl-diphosphate famesyttransferase	
899	34848_at	_	X69141		farnesyl-diphosphate farnesyltransferase
699	1499_at	FNTA	L10413	farnesyltransferase, CAAX box, alpha	farnesyl-protein transferase alpha-subunit
				Fas (TNFRSF6)-associated via death	
670	38755_at	FADD	X84709	domain	mediator of receptor induced toxicity
				fasciculation and elongation protein zeta 1	
671	37743_at	FEZ1	N60060	(zygin I)	FEZ1
				fasciculation and elongation protein zeta 2	
672	38651_at	FEZ2	U60061	(zygin II)	FEZ2
				FAT tumor suppressor homolog 1	
673	40454_at	FAT	X87241	(Drosophila)	homologue of Drosophila Fat protein
				fatty-acid-Coenzyme A ligase, long-chain	
674	674 40082_at	FACL2	D10040	2	long-chain acyl-CoA synthetase
				fatty-acid-Coenzyme A ligase, long-chain	
675	33880_at	FACL3	D89053	3	Acyl-CoA synthetase 3
				fatty-acid-Coenzyme A ligase, long-chain	
676	33881_at	FACL3		3	
677	677 33360_at	FBXL11	AB023221	F-box and leucine-rich repeat protein 11	KIAA1004 protein
678	678 37205_at	FBXL7	AB020647	F-box and leucine-rich repeat protein 7	KIAA0840 protein
629	32854_at	FBXW1B	AB014596	F-box and WD-40 domain protein 1B	KIAA0696 protein
680	680 32169_at	FBX021	AB020682	F-box only protein 21	KIAA0875 protein
681	35337_at	FBXO7	AL050254	F-box only protein 7	hypothetical protein
				EBBNP: hataroganaous ribonucleoprofein	
				homolog: This segments comes from Eig	
				13: D10S102—EBBNP thuman fetal brain	
682	33817 at	D10S102	S63912	o, 0.100.102=1.01 mt. [manual].	FBRNP
683	683 1877 g at	Hie	HG1103-HT1103 Fe protein	Fe protein	dinitrogenase reductase
684	34678 at	FER1L3	AL096713	fer-1-like 3, myoferlin (C. elegans)	hypothetical protein
				FERM, RhoGEF (ARHGEF) and pleckstrin	
685	685 32148_at	FARP1	AI701049	domain protein 1 (chondrocyte-derived)	

Fig 2)

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300		ı	,		ı
989	33943_at	FTH1	120941	ferritin, heavy polypeptide 1	ferritin heavy chain
687	41091_at	FALZ	U05237	fetal Alzheimer antigen	fetal Alzheimer antigen
688	32535_at	FBN1	X63556	fibrillin 1 (Marfan syndrome)	fibrillin
689	39945_at	FAP	U09278	fibroblast activation protein, alpha	fibroblast activation protein
				wth factor 7 (keratinocyte	
<u>6</u>	1380_at	FGF7	M60828	growth factor)	keratinocyte growth factor
					fibroblast growth factor receptor 1, isoform 1
		-		-	precinsor, fibroblast growth factor recentor
		,			1 isoform 2 precursor fibroblast growth
					factor receptor 1, isoform 3 precursor:
				-	fibroblast growth factor receptor 1, isoform 4
					precursor; fibroblast growth factor receptor
					1, isoform 5 precursor; fibroblast growth
					factor receptor 1, isoform 6 precursor;
					fibroblast growth factor receptor 1, isoform 7
				fibroblast growth factor receptor 1 (fms-	precursor; fibroblast growth factor receptor
					1, isoform 8 precursor; fibroblast growth
691	2057_g_at	FGFR1	M34641	(syndrome)	factor receptor 1, isoform 9 precursor
					fibronectin 1, isoform 1 preproprotein;
692	31720_s_at	FN1	M10905	fibronectin 1	fibronectin 1, isoform 2 preproprotein
693	31719_at	FN1	X02761	fibronectin 1	fibronectin precursor
				fibronectin leucine rich transmembrane	fibronectin leucine rich transmembrane
694	34853_at	FLRT2	ĸ	protein 2	protein 2
695	38026_at	FBLN1	U01244	fibulin 1	fibulin-1D
969	39038_at	FBLN5	AF093118	fibulin 5	UP50
202	38078 04	QN II	A E042166	filamin B hote (actin hinding protein 278)	nimeli, eter
3	2007 0 01		21 24 100		
698	38761_s_at	FKBP9	AA487755	FK506 binding protein 9 (63 kD)	
669		FM03	M83772	flavin containing monooxygenase 3	flavoprotein
8	35254_at	FLN29	AB007447	FLN29 gene product	Fln29
L				follistatin precursor; Human follistatin	follistatin isoform FST317 precursor;
701	701 38356_at	FST	M19481	gene, exon 6.	follistatin isoform FST344 precursor

Fig 21

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				forkhead (Drosophila)-like 7; FREAC3; Homo sapiens forkhead/winged helix-like	
5	44007	1	A E0.700.00	actor 7 (FKHL7) gene,	forkhead/winged helix-like transcription
702	703 36319 at	FOXE?	1113220	forkhead box F2	forkhead protein FREAC-2
	37	7 WO.	0.100.0	\top	
704	40570_at	FOX01A	AF032885	(rhabdomyosarcoma)	forkhead protein
705	34740_at	FOXO3A	AF032886		forkhead protein
902	32542_at	FHC	AF063002	four and a half LIM domains 1	LIM protein SLIMMER
707	38422_s_at	FHL2	U29332	four and a half LIM domains 2	heart protein
708	41649_at	FHX	AF038177	FOXJ2 forkhead factor	
709	34997_r_at	FZD5	U43318	frizzled'homolog 5 (Drosophila)	transmembrane receptor
710	34472_at	FZD6	AB012911	frizzled homolog 6 (Drosophila)	Frizzled-6
711	33222_at	FZD7	AB017365	frizzled homolog 7 (Drosophila)	frizzled-7
712	38923_at	FRG1	L76159	FSHD region gene 1	FSHD region gene 1
713	713 38139_at	FPGT	AF017445	fucose-1-phosphate guanylytransferase	GDP-L-fucose pyrophosphorylase
714	41814_at	FUCA1	M29877	fucosidase, alpha-L- 1, tissue	fucosidase, alpha-L- 1, tissue
				Fukuyama type congenital muscular	
715	715 40022_at	FCMD	AB008226	dystrophy (fukutin)	fukutin
716	716 32546_at	FH	U59309	furnarate hydratase	fumarase precursor
717	36145 at	SIAHBP1	U51586	(use-binding protein-interacting repressor siah binding protein 1	siah binding protein 1
718	718 40480_s_at	FYN	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES FYN oncogene related to SRC, FGR, YES
719	2039_s_at	FYN	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES FYN oncogene related to SRC, FGR, YES
720	34288_at	RDC1	U67784	G protein-coupled receptor	orphan G protein-coupled receptor
721	37308_at	GPR107	A1888084	G protein-coupled receptor 107	
722	37298_at	GABARAP	AF044671	GABA(A) receptor-associated protein	MM46
793	26785 of	GABABAPI 1	W28281	GABA(A) receptor-associated protein like	
		17 17 17 17 17 17 17 17 17 17 17 17 17 1	10000	CABA/A) recentor associated protein-like	
724	35767 at	GABARAPL2	A1565760	Andread Secretary associated process med	
725	37825 at	GALK2	M84443	galactokinase 2	galactokinase
726	726 37742_at	GLB1	M34423	galactosidase, beta 1	galactosidase, beta 1

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				gamma-glutamyl hydrolase (conjugase,	
727	37263_at	GGH	U55206	folylpolygammaglutamyl hydrolase)	human gamma-glutamyi hydrolase
				gap junction protein, alpha 1, 43kD	
728	32531_at	GJA1	X52947	(connexin 43)	connexin 43
				GCN1 general control of amino-acid	
729	36603_at	GCN1L1		synthesis 1-like 1 (yeast)	
730	35307_at			GDP dissociation inhibitor 2	GDP dissociation inhibitor beta
				gene predicted from cDNA with a	gene predicted from cDNA with a complete
731	39386_at	KIAA0110	D14811	complete coding sequence	coding sequence
			٠	gene with multiple splice variants near HD	gene with multiple splice variants near HD
732	32180_s_at	RES4-22	AB000461	locus on 4p16.3	locus on 4p16.3
				_	Bruton's tyrosine kinase-associated protein-
733		GTF2I	U77948	general transcription factor II, i	135
734	35450_s_at	GTF2I	AF015553	general transcription factor II, i	TFII-I protein
				general transcription factor IIA, 2 (12kD	
735	37010_at	GTF2A2	AI203737	subunit)	
				general transcription factor IIA, 2 (12kD	
736	869_at	GTF2A2	U14193	subunit)	transcription factor IIA small 12 kDa subunit
				general transcription factor IIE,	-
737	37882_at	GTF2E1	X63468	polypeptide 1 (alpha subunit, 56kD)	TFIIE-alpha
				general transcription factor IIE,	
738	37295_at	GTF2E2	X63469	polypeptide 2 (beta subunit, 34kU)	I FIIE-beta
				general transcription factor IIH,	
739	38782_at	GTF2H1	M95809	polypeptide 1 (62kD subunit)	basic transcription factor 62kD subunit
				general transcription factor IIH,	
740	40754_at	GTF2H3	Z30093	polypeptide 3 (34kD subunit)	basic transcription factor 2, 35 kD subunit
741	36188_at	GTF3A	D32257	general transcription factor IIIA	Xenopus transcription factor IIIA homologue
742	742 35296_at	GGPS1	AB019036	geranylgeranyl diphosphate synthase 1	geranylgeranyl pyrophosphate synthase
743	743 763 at	GMFB	AB001106	glia maturation factor, beta	glia maturation factor
744	39793_at	GBAS	AF029786	glioblastoma amplified sequence	GBAS
				glucan (1,4-alpha-), branching enzyme 1	
				(glycogen branching enzyme, Andersen	
				disease, glycogen storage disease type	
745	745 32643_at	GBE1	L07956	(A)	1,4-alpha-glucan branching enzyme
746	746 34332_at	GNPI	D31766	glucosamine-6-phosphate isomerase	glucosamine-6-phosphate isomerase

	•		C		
	¥	G.	ر		<u> </u>
				glucosaminyl (N-acetyl) transferase 1,	
				core 2 (beta-1,6-N-	
747	38218_at	GCNT1	M97347	acetylglucosaminyftransferase)	beta-1,6-N-acetylgiucosaminyttransferase
748		GPI	K03515	glucose phosphate isomerase	neuroleukin
749		GRP58	249835	glucose regulated protein, 58kD	protein disultide isomerase
750		GePD	X03674	glucose-6-phosphate dehydrogenase	glucose-6-phosphate dehydrogenase
751		GUSB	M15182	glucuronidase, beta	glucuronidase, beta
752		GLUD1	M20867	glutamate dehydrogenase 1	glutamate dehydrogenase 1
753	753 35485_at	GRM4	X80818	glutamate receptor, metabotropic 4	metabotropic glutamate receptor type 4
			-	glutamate-ammonia ligase (glutamine	
754	40522_at	GLUL	X59834	synthase)	glutamateammonia ligase
				glutamate-cysteine ligase, catalytic	
755	31850_at	CCLC	M90656	subunit	gamma-glutamylcysteine synthetase
				glutamate-cysteine ligase, modifier	gamma-glutamylcysteine synthetase light
756	33163_r_at	GCLM	L35546	subunit	subunit
	_		,	glutamic-oxaloacetic transaminase 1,	
757	35343_at	GOT1	M37400	soluble (aspartate aminotransferase 1)	aspartate aminotransferase 1
		1		glutamic-oxaloacetic transaminase 2,	
				mitochondrial (aspartate aminotransferase	
758	40764_at	GOT2	M22632	(2)	aspartate aminotransferase 2 precursor
759	759 34719_at	GLS	AB020645	glutaminase	KIAA0838 protein
				glutamine-fructose-6-phosphate	glutamine:fructose-6-phosphate
760	32626_at	GFPT1	M90516	transaminase 1	amidotransferase
				glutamine-fructose-6-phosphate	Glutamine:fructose-6-phosphate
761	39640_at	GFPT2	AB016789	transaminase 2	amidotransferase
762	35300_at	EPRS	X54326	glutamyl-prolyl-tRNA synthetase	glutaminyf-tRNA synthetase
763	34311_at	GLRX	X76648	glutaredoxin (thiottransferase)	glutaredoxin
764	764 37033_s_at	GPX1	X13710	glutathione peroxidase 1	
765	40508_at	GSTA4	AF025887	glutathione S-transferase A4	glutathione S-transferase A4-4
766	38386_r_at	GSS	U34683	glutathione synthetase	glutathione synthetase
				glutathione-S-transferase like; glutathione	
767	824_at	GSTTLp28	U90313	transferase omega	glutathione-S-transferase homolog
				glyceraldehyde-3-phosphate	
768	768 AFFX-HUMGAPIGAPD	(GAPD	M33197	dehydrogenase	głyceraldehyde-3-phosphate dehydrogenase
760	760 35005 6 21	GAPD	1134995	glyceraldehyde-3-phosphate	
ê	33303_5_8I	GALD	004333	(den) diogentace	

				_	, .										_								_	_	_
3	głyceraldehyde-3-phosphate dehydrogenase	dihydroxyacetone phosphate acyttransferase	glycine cleavage system protein H	(aminometriyi carrier) qivcine receptor beta subunit	protein kinase	glycogenin	glycogenin-2 alpha	glycoprotein (transmembrane) nmb			glycyl-tRNA synthetase	glycyi-tRNA synthetase	lactoyl glutathione lyase		quanine nucleotide binding protein (G	protein), alpha stimulating activity	polypeptide 1, isoform alpha-s-2;	neuroendocrine secretory protein 55;	guanine nucleotide binding protein (G	protein), alpha stimulating activity	polypeptide 1, isoform XL-alpha-s; guanine	nucleotide binding protein (G protein), alpha	stimulating activity polypeptide 1, isoform	alpha-s-1	alpha subunit of GsGTP binding protein
Q	glyceraldehyde-3-phosphate dehydrogenase	glyceronephosphate O-acyltransferase	glycine cleavage system protein H	(aminometry) dycine receptor, beta	glycogen synthase kinase 3 beta	glycogenin	glycogenin 2	glycoprotein (transmembrane) nmb	glycoprotein M6B	glycosyltransferase AD-017	glycyl-tRNA synthetase	glycyl-tRNA synthetase	głyoxalase I	głyoxylate reductase/hydroxypyruvate										GNAS complex locus	GNAS complex locus
O	M33197	AJ002190		U33267	L33801	U31525	U94362	X76534	AF016004	L13435	U09510	U09510	D13315	W28944										X04409	6009SX
8	GAPD	GNPAT	- 1000	GLRB	GSK3B	GYG	GYG2	GPNMB	GPM6B	AD-017	GARS.	GARS	GL01	авнря					-					GNAS	GNAS
A	770 AFFX-HUMGAPIGAPD	39392_at	1000	37.357_at	40645_at	40876_at	35334_at	38379_at	37251_s_at	33126_at	36582_g_at	36581_at	36201_at	40133 s at	m									784 37449 i_at	785 37448 s at
	70	144	-	7/2	774	775	776	177	178	6//	780	781	782	783	3									784	785

Lis 2

					·			_	_		_		_	_	_		_		—,	
2	guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-2; neuroendocrine secretory protein 55; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform XL-alpha-s; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-1	ADP-ribosylation factor binding protein 3, isoform short; ADP-ribosylation factor binding protein 3, isoform long	Golgi complex autoantigen golgin-97	256 kD golgin	unknown protein		putative 13 S Golgi transport complex 90kD subunit brain-specific isoform	KIAA0855 protein		glycosylphosphatidylinositol anchor attachment 1 (GPA41)	G-rich sequence factor-1	growth arrest and DNA-damage-inducible protein GADD45beta		1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	growin arrest-specific 1	grown allest-specific 1	מוסשווו-מוופפר-פספרווני סוסיפווו	growth-arrest-specific protein	growth factor receptor-bound protein 10	
Q	GNAS complex locus	golgi associated, gamma adaptin ear containing, ARF binding protein 3	golgi autoantigen, golgin subfamily a, 1	4		golgi SNAP receptor complex member 2		Т	gp25L2 protein	GPAA1P anchor attachment protein 1	G-rich RNA sequence binding factor 1	growth arrest and DNA-damage-inducible, growth arrest and DNA-damage-inducible beta	growth arrest and DNA-damage-inducible,	Deta	growin arrest-specific 1	grown allest specific 1	giowiii aii asi-spaciiic o	growth arrest-specific 6	growth factor receptor-bound protein 10	growth hormone inducible transmembrane protein
ပ	X04409	D63876	U51587	X82834	AF020762	AA905543	AF058718	AB020662	X90872	AB002135	U07231	AF078077		89168N	13698	1 10700	L13/20	L13720	D86962	W28190
В	GNAS	GGA3	GOLGA1	GOLGA4	GOLPH1	GOSR2	GOLTC1	KIAA0855	HSGP25L2G	GPAA1	GRSF1	GADD45B	0	GADU45B	GASI	GAS I	GASO	GAS6	GRB10	GHITM
Y	37450 <u>_r_</u> at	37959_at	1 32713_at	32150_at	36827_at	38620_at	34737 at	41767_r_at	794 36950_at	36035 at	32595 at			39821_s_at	/99 bol_at	904 41039 at	2/000	_	37615_at	804 41752_at
	786	787	788	789	790	791	792	793	794	795	96/	797		86			3	88	803	804

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	V	ام ا	C	C	
805	#				growth hormone receptor
908		355		GS3955 protein	GS3955
				GTP binding protein overexpressed in	
ğ	3/2/9_at	GEM	010550	SKeletal muscle	Cell
				guanine nucleotide binding protein (G	
a Ca	808 33800 at	NAI1	AI 049933	protein), airtia unibruit acuvity polypaptida 1	hypothetical protein
3	m_0000			guanine nucleotide binding protein (G	quanine nucleotide binding protein (G
				protein), alpha inhibiting activity	protein), alpha inhibiting activity polypeptide
803	37307_at	GNAI2	X04828	polypeptide 2	2
				guanine nucleotide binding protein (G	
810	810 34608_at	GNB2L1	M24194	protein), beta polypeptide 2-like 1	MHC B complex protein 12.3
				guanine nucleotide binding protein (G	
811	811 35272_at		AI541042	protein), gamma 5	
812	812 37735_at	GNG10	U31383	guanine nucleotide binding protein 10	G protein gamma-10 subunit
				guanylate binding protein 1, interferon-	
813	35735_at	GBP1	M55542	inducible, 67kD	guanylate binding protein isoform l
814	814 905 at	GUK1	L76200	guanylate kinase 1	guanylate kinase
815	815 32249_at		M65292	H factor (complement)-like 1	factor H homologue
816	816 32250_at		X07523	H factor 1 (complement)	complement factor H
				H.sapiens ACTH-R gene for	candidate adrenocorticotropic hormone
817	817 420_at	ACTH-R	X65633	adrenocorticotropic hormone receptor.	receptor
818	31673_s_at	sion	regu X65784	H.sapiens CAR gene.	cell matrix adhesion regulator
819	37003 at	CD63: MLA1: ME4	ME4X62654	H.sapiens gene for Me491/CD63 antigen.	ME491 /CD63 antigen
		-}		GEV Total	
820	38076 at	P1 gene for a sub	sub(X69907	H.sapiens gene for milocinomial ATF synthase c subunit (P1 form).	Illucational art o comprex, subdim c (subdim 9), isoform 1
2	35125 at		X67309	H.sapiens gene for ribosomal protein S6.	ribosomal protein S6
822	34646_at	трS7	225749	H.sapiens gene for ribosomal protein S7.	ribosomal protein S7
823	823 31510 s at	hH3.38	248950	H.sapiens hH3.3B gene for histone H3.3.	histone H3.3

			,		
	¥	8	င	Q	u
				H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined	
824	33820_g_at	IdhB	X13794	CDS).	lactate dehydrogenase B
				H.sapiens lactate dehydrogenase B gene	
				exon 1 and 2 (EC 1.1.1.27) (and joined	
825	33819_at	IdhB	X13794	CDS).	lactate dehydrogenase B
826	34787_at	ORF1	X93209	H.sapiens mRNA for NRD1 convertase.	NRD1 convertase
				H.sapiens mRNA for PIBF1 protein,	
827	36012_at	PIBF1	Y09631	complete.	PIBF1 protein
		-		H.sapiens mRNA for tre oncogene (clone	
828	31526_f_at	tre	X63547	213).	oncogene
829	829 40471_at	PxF	Y09048	H.sapiens PxF gene.	PxF protein
				H.sapiens PXMP1 gene, exon 1 (and	70kD peroxisomal integral membrane
830	37038_at	PXMP1	X83467	joined CDS).	protein
				H.sapiens rpS8 gene for ribosomal protein	
831	31583_at	трS8	X67247	58.	ribosomal protein S8
				H.sapiens SPHAR gene for cyclin-related	
832	1685_at	SPHAR	X82554	protein.	S-phase response (cyclin-related)
833	38127_at	syndecan-1	Z48199	H.sapiens syndecan-1 gene (exons 2-5).	syndecan 1
834	37310_at	uPA	X02419	H.sapiens uPA gene.	urokinase-plasminogen activator
835	34308_at	HZAFL	U90551	H2A histone family, member L	histone 2A-like protein
836	39337_at	H2AFZ	M37583	H2A histone family, member Z	H2A histone family, member Z
837	33458_r_at	H2BFL	AI688098	H2B histone family, member L	
838	40818_at	LOC51580	D14041	H-2K binding factor-2	H-2K binding factor-2
839		H3F3A	M11353	H3 histone, family 3A	H3 histone, family 3A
840	39969_at	H4FG	AA255502	H4 histone family, member G	
<u>8</u>	32591_at	HCDI	AI494623	HCDI protein	
842	35215_at	HDCMA18P	AL049996	HDCMA18P protein	hypothetical protein
L				heat shock 10kD protein 1 (chaperonin	
843	39353_at	HSPE1	AI912041	10)	
\$	844 37720_at	HSPD1	M22382	heat shock 60kD protein 1 (chaperonin)	mitochondrial matrix protein
				heat shock 70kD protein 5 (glucose-	heat shock 70kD protein 5 (glucose-
845	36614_at	HSPA5	X87949	regulated protein, 78kD)	regulated protein, 78kD)
970	046 41640 c ot	НСБАОВ	15180	heat shock 70kD protein 9B (mortalin-2)	MTHSP75
ð	41310_s_all	nor year	E13103		

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847	32316_s_at	HSPCA	X15183	heat shock 90kD protein 1, alpha	heat shock 90kD protein 1, alpha
848	848 33984_at	HSPCB	M16660	heat shock 90kD protein 1, beta	heat shock 90kD protein 1, beta
849	31906 at	HSBP1	AF068754	heat shock factor binding protein 1	heat shock factor binding protein 1 HSBP1
					tumor necrosis factor type 1 receptor
850	1468_at	TRAP1	U12595	heat shock protein 75	associated protein
851	851 38054_at	HBXIP	AF029890	hepatitis B virus x interacting protein	hepatitis B virus X interacting protein
				hepatoma-derived growth factor (high-	
852	852 38779_r_at	HDGF	D16431	mobility group protein 1-like)	hepatoma-derived GF
853	853 35644_at	HEPH	AB014598	hephaestin	KIAA0698 protein
				heterogeneous nuclear ribonucleoprotein	
854	38094_at	HNRPAB	M65028	A/B	hnRNP type A/B protein
				heterogeneous nuclear ribonucleoprotein	
855	37334_at	HNRPAO	U23803	A0	heterogeneous ribonucleoprotein A0
		٠		heterogeneous nuclear ribonucleoprotein	
856	34987_s_at	HNRPA1	X79536	A1	hnRNPcore protein A1
					heterogeneous nuclear ribonucleoprotein
				heterogeneous nuclear ribonucleoprotein	A2/B1, isoform A2; heterogeneous nuclear
857	36654_s_at	HNRPA2B1	M29065	A2/B1	ribonucleoprotein A2/B1, isoform B1
					heterogeneous nuclear ribonucleoprotein C,
				heterogeneous nuclear ribonucleoprotein	isoform b; heterogeneous nuclear
828	858 33666_at	HNRPC	M16342	C (C1/C2)	ribonucleoprotein C, isoform a
				heterogeneous nuclear ribonucleoprotein	
				D (AU-rich element RNA binding protein 1,	
859	38016_at	HNRPD	M94630	37kD)	DNA-binding protein
				heterogeneous nuclear ribonucleoprotein	
860	33845_at	HNRPH1	W28483	H1 (H)	
				heterogeneous nuclear ribonucleoprotein	
861	41132_r_at	HNRPH2	U01923	H2 (H')	heterogeneous nuclear ribonucleoprotein H2
					heterogeneous nuclear ribonucleoprotein
			- 1	heterogeneous nuclear ribonucleoprotein	H3, isoform a; heterogeneous nuclear
862	41283_at	HNRPH3	AF052131	H3 (2H9)	nbonucieoprotein H3, isotorm b
863	863 40836 s. at	HNRPH3	W26677	heterogeneous nuclear ribonucleoprotein (H3 (2H9)	
	15-2000L	2: ::::::::::::::::::::::::::::::::::::			

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				heterogeneous nuclear ribonucleoprotein	
864	39415_at	HNRPK	X72727	K	transformation upregulated nuclear protein
598	35201 at	IdaNH	X16135	heterogeneous nuclear ribonucleoprotein	heterogeneous nuclear ribonucleoprotein L
3	10700	4	300	heterogeneous nuclear ribonucleonrotein	
998	37717_at	HNRPM	L03532		M4 protein
				heterogeneous nuclear ribonucleoprotein	
867	39792_at	HNRPR	AF000364	R	heterogeneous nuclear ribonucleoprotein R
				heterogeneous nuclear ribonucleoprotein	
868	38654_at	HNRPU	X65488	U (scaffold attachment factor A)	nnHinP U protein
698	32818_at	HXB	X78565	hexabrachion (tenascin C, cytotactin)	human tenascin-C
870	39827_at	RTP801	AA522530	HIF-1 responsive RTP801	
				high density lipoprotein binding protein	
871	31504_at	HDLBP	M64098	(vigilin)	high density lipoprotein binding protein
				high-mobility group (nonhistone	(
872	32220_at	HMG1	D63874	chromosomal) protein 1	HMG-1
				high-mobility group (nonhistone	high-mobility group (nonhistone
873	306_s_at	HMG14	J02621	chromosomal) protein 14	chromosomal) protein 14
				high-mobility group (nonhistone	
874	35738_at	HMG17L3	AI347088	chromosomal) protein 17-like 3	
				high-mobility group (nonhistone	high-mobility group (nonhistone
875	38065_at	HMG2	X62534	chromosomal) protein 2	chromosomal) protein 2
876	876 38843_at	HMG2L1	AL079310	high-mobility group protein 2-like 1	hypothetical protein
877	35693_at	HPCAL1	AF070616	hippocalcin-like 1	BDP-1 protein
878	878 1009 at	HINT1	U51004	histidine triad nucleotide binding protein 1	protein kinase C inhibitor
879	34231 at	HBOA	AF074606	histone acetyltransferase	histone acetyltransferase
88	880 41855 at	HAT1	AF030424	histone acetyttransferase 1	histone acetyltransferase 1
88	38771_at	HDAC1	D50405	histone deacetylase 1	RPD3 protein
885	2 34368_at	HDAC2	U31814	histone deacetylase 2	transcriptional regulator homolog RPD3
883	3 38271_at	HDAC4	AB006626	histone deacetylase 4	KIAA0288 protein
884	3904	H2AV	AL049324	histone H2A.F/Z variant	
885	39092_at	HZAV	AW007731	histone H2A.F/Z variant	
988	38824_at	HTATIP2	AF039103	HIV-1 Tat interactive protein 2, 30 kD	Tat-interacting protein TIP30
887	7 40220_at	HIS1	AB021179	HMBA-inducible	HEXIM1 protein

	A	8	ပ	Q	ш
888	39809_at	HBP1	AF019214		HMG box containing protein 1
				HMG-domain containing protein which is the 57 kd subunit within SWI/SNF-related	
				BAF complexes; contains a proline-rich N-	
				terminus, a kinesin-like coiled-coil region,	
				and a highly acidic c-terminus; Homo	
				sapiens BAF57 (BAF57) gene, complete	
889	889 33828_at	BAF57	AF035262		BAF57
				HMT1 hnRNP methyltransferase-like 1 (S.	•
890	39348_at	HRMT1L1	X99209	cerevisiae)	arginine methyltransferase
				HMT1 hnRNP methyltransferase-like 2 (S.	
891	32825_at	HRMT1L2	Y10805	cerevisiae)	arginine methyltransferase
				HNRNP Core Protein A1 LIKE	
				pseudogene; match: proteins P04256	
		-		Q28521 P49312 P09651 P51991 P51992	
892	31463_s_at	dJ256G22.1	AL022097	P51968 P17130 P22626	
				holocytochrome c synthase (cytochrome c	
893	38943_at	HCCS	U36787	heme-lyase)	holocytochrome c-type synthetase
894	39610_at	HOXB2	X16665	homeo box B2	homeo box B2
895	40674_s_at	HOXCE	S82986	homeo box C6	homeo box C6
896		HOMER-3	AF093265	Homer, neuronal immediate early gene, 3	homer-3
)			
897	34401 at	UOCRES1	132977	Homo sapiens (clone 117252) ubiquinol cytochrome c reductase Rieske ironsulbhur protein (UQCRFS1) gene, exon 2. Rieske Fe-S protein	Rieske Fe-S protein
	1			Homo sapiens (clone FFE-7) type II	
				(IMPDH2) gene, exons 1-13, complete	inosine monophosphate dehydrogenase type
898	36624_at	IMPDH2	L33842	cds.	=
000	37590 at	AOX1	AE017060	Homo sapiens aldehyde oxidase (AOX1)	aldehyde oxidase
3	1000 to			Homo caniane alnha NAC mRNA	
8	900 39740_g_at	NACA	AF054187	complete cds.	alpha NAC

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	A	В	S	D	ų
100	30730 21	W O VIA	A G0E 4 187	Homo sapiens alpha NAC mRNA,	
5	39739 BI			complete cas.	alpha IANO
902	902 41154_r_at	CTNNA1	AF102803	Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds.	alphaE-catenin
903	41153_f_at	CTNNA1	AF102803	Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds.	alphaE-catenin
904	39324 at		AL050078	Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp56G0746	
905	905 35310 at		D45288	Homo sapiens cDNA FLJ13267 fis, clone OVARC1000964	
906	906 35754_at		L40391	Homo sapiens cDNA FLJ13553 fis, clone PLACE1007454	
				Homo sapiens cDNA FLJ14821 fis, clone OVARC1000556, highly similar to RIBOSOMAL PROTEIN S6 KINASE II	
907	907 33325_at		W26667	ALPHA 2 (EC 2.7.1)	
908	908 38102_at		W28575	Homo sapiens cDNA FLJ25016 fis, clone CBL01574	
606	909 41253_s_at		A1983043	Homo sapiens cDNA FLJ30436 fis, clone BRACE2009037	
910	910 39162_at		AA156987	Homo sapiens cDNA FLJ30544 fis, clone BRAWH2001412	
911	911 41807_at		AL040137	Homo sapiens cDNA FLJ31959 fis, clone NT2RP7007422	
912	38643_at	1	W87466	Homo sapiens cDNA FLJ33151 fis, clone UTERU2000263	
913	34246 at		AA418437	Homo sapiens cDNA: FLJ21175 fis, clone CAS11071	
914	914 40813_at		AI768188	Homo sapiens cDNA: FLJ21243 fis, clone COL01164	

Fig 21

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	V	B	C	Ω	IJ
				Homo sapiens cDNA: FLJ21449 fis, clone COL04483, highly similar to AF010235	
915	915 40923 at		AA290994	Homo sapiens mHNA from chromosome 5q31-33 region	
				Homo sapiens cDNA: FLJ21904 fis, clone	
916	38993_r_at		W27522	HEP03585	
				Homo sapiens cDNA: FLJ21927 fis, clone	
917	917 38093_at		60606N	Human clone 23722 mRNA sequence	-
918	918 34840 at		AIZOOG33	Homo sapiens cDNA: FLJ22642 fis, clone HSI06970	
				Homo sapiens cDNA: FLJ23324 fis, clone	
				HEP12482, highly similar to	
		•		cle myosin	myosin heavy chain isoform
919	919 32838_at	smooth muscle my	le m S67247	heavy chain-B (MYH10) mHNA	
				Homo sapiens cervical cancer suppressor-	
920	920 33737_f_at		AI871359	1 mRNA, complete cds	
				Homo sapiens clone 23570 mRNA	
921	921 41663_at		AF038202	sequence	
			i	Homo sapiens clone 23700 mRNA	
922	36815_at		AF038185	sednence	
				Homo sapiens clone 23718 mRNA	
923	923 41841_at		AF052138	sednence	
				Homo sapiens clone 23903 mRNA	
924	37794_at		AF035281	sednence	
			·	Homo sapiens clone 23938 mRNA	
925	38764_at		AF007142	sednence	
				Homo sapiens clone 24416 mRNA	
926	35342_at		AF052159	sednence	
				Homo sapiens clone 24630 mRNA	
927	31867_at		AF052174	sequence	
				Homo sapiens clone 24674 mRNA	
928	36758_at		AF070578	sednence	
8			A COE0404	Homo sapiens clone 24790 mRNA	
929	929 41864 at		Ar052181	Sequence	

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	A	90	၁	O	ı
				Homo sapiens clone FBD3 Cri-du-chat	
930	38070_at		AL080234	critical region mRNA	
				Homo sapiens cofactor A protein mRNA,	
931	931 34773_at	TBCA	AF038952	complete cds.	cofactor A protein
				Homo sapiens cytochrome c oxidase	
				subunit IV precursor (COX4) gene,	
				nuclear gene encoding mitochondrial	
932	39027_at	COX4	AF017115		cytochrome c oxidase subunit IV precursor
				Homo sapiens D15F37 pseudogene, S4	
933	40878_f_at	D15F37	AF041081	allele, mRNA sequence.	
				Homo sapiens deoxycytidylate deaminase	
934	631_g_at	DCTD	L39874	gene, complete cds.	deoxycytidylate deaminase
				ycytidylate deaminase	
935	630_at	DCTD	L39874	gene, complete cds.	deoxycytidylate deaminase
				Homo sapiens DNA for	
				galactocerebrosidase, exon 17 and	
936	936 33936_at	GALC	D86181	complete cds.	galactocerebrosidase
				Homo sapiens F1Fo-ATPase synthase f	
937	937 40134_at	ATP5J2; ATP5JL; AF047436	AF047436	subunit mRNA, complete cds.	F1Fo-ATPase synthase f subunit
				Homo sapiens gene for LD78 alpha	
938	938 36103_at	SCYA3; LD78ALP D90144	D90144	precursor, complete cds.	LD78 alpha precursor
				Homo sapiens GOS28/P28 protein	
939	939 40725_at	GOSR1; P28; GS2	GS2AF047438	mRNA, complete cds.	GOS28/P28 protein
				Homo sapiens GTP binding protein	
940	940 38708_at	RAN; TC4; ARA24	RA24AF054183	mRNA, complete cds.	GTP binding protein
				Homo sapiens H beta 58 homolog mRNA,	
941	35790_at	VPS26; HB58; HB AF054179	AF054179	complete cds.	H beta 58 homolog
				Homo sapiens histone macroH2A1.2	
942	36576_at	H2AFY; H2A.y; H2	.y; H2AF054174	mRNA, complete cds.	histone macroH2A1.2
				Homo sapiens insulin induced protein 1	
943	35303_at	INSIG1	U96876	(INSIG1) gene, complete cds.	insulin induced protein 1
				Homo sapiens interferon-gamma receptor	
7	044 1038 s. at	interferon-gamma [119247	1119247	cds.	interferon-gamma receptor alpha chain
5	1000-5-m	The second second	20.01		

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945	945 895 at	ЫW	L19686	Homo sapiens macrophage migration inhibitory factor (MIF) gene, complete cds. I macrophage migration inhibitory factor	macrophage migration inhibitory factor
Γ				Homo sapiens mitochondrial proteolipid	
				68MP homolog mRNA, nuclear gene	
				encoding mitochondrial protein, complete	
946	38967_at	C14orf2; MP68; P(AF054175		cds.	mitochondrial proteolipid 68MP homolog
				Homo sapiens mRNA for Hmob33 protein,	
947	947 31881_at		Y14155	3' untranslated region	
948	948 34677_f_at	1132	AJ012755	Homo sapiens mRNA for TL132	TL132 protein
				Homo sapiens mRNA full length insert	
949	38786_at		AL079279	cDNA clone EUROIMAGE 248114	
				Homo sapiens mRNA; cDNA	
				DKFZp434A012 (from clone	
950	950 33418_at		AL096752	DKFZp434A012)	
				Homo sapiens mRNA; cDNA	-
				DKFZp434B102 (from clone	
951	38630_at		AL080192	DKFZp434B102)	
				Homo sapiens mRNA; cDNA	
				DKFZp434M162 (from clone	
952	41529_g_at		W72239	DKFZp434M162)	
				Homo sapiens mRNA; cDNA	
				DKFZp434M245 (from clone	
953	36451_at		AI743299	DKFZp434M245)	
				Homo sapiens mRNA; cDNA	
	· .			DKFZp564A026 (from clone	
954	36821_at	DKFZp564A026	AL050367	DKFZp564A026)	hypothetical protein
				Homo sapiens mRNA; cDNA	
				DKFZp564A072 (from clone	
955	37366_at		AL049969	DKFZp564A072)	
				Homo sapiens mRNA; cDNA	
				DKFZp564B222 (from clone	
926	39506_at		AA933984	DKFZp564B222)	
				Homo sapiens mRNA; cDNA	
				DKFZp564D016 (from clone	
957	957 39748_at		AL050021	DKFZp564D016)	

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				Homo sapiens mRNA; cDNA DKFZp564D156 (from clone	
958	38357_at		AL049321	DKFZp564D156)	
				Homo sapiens mRNA; cDNA	
040	99716 04		NOFAAS	DKFZp564E122 (from clone	
3	10 10 N		OH-CON.	Homo sapiens mRNA: cDNA	
				DKFZp564E2222 (from clone	
096	35301_at		AL049941	DKFZp564E2222)	
				Homo sapiens mRNA; cDNA	
001	9E940 04		AI 040265	DKFZp564F053 (from clone	
	SOTE AL		ALCT3£00	Homo sapiens mRNA CONA	
	,			DKFZp564F112 (from clone	
962	40552_s_at		AL049987	DKFZp564F112)	·
				Homo sapiens mRNA; cDNA	
				DKFZp564J0323 (from clone	-
963	39170_at		AL049957	DKFZp564J0323)	
				Homo sapiens mRNA; cDNA	_
				DKFZp564L0822 (from clone	
964	964 34303_at		AL049949	DKFZp564L0822)	
				Homo sapiens mRNA; cDNA	
				DKFZp564L222 (from clone	
965	965 36509_at		AL049998	DKFZp564L222)	
				Homo sapiens mRNA; cDNA	
				DKFZp564P0823 (from clone	-
996	40353_at		AL049962	DKFZp564P0823)	
				Homo sapiens mRNA; cDNA	
				DKFZp566J2146 (from clone	
967	35290_at	•	AL050081	DKFZp566J2146)	
,				Homo sapiens mRNA; cDNA	
				DKFZp586B0918 (from clone	-
968	38079_at		AL049367	DKFZp586B0918)	
				Homo sapiens mRNA; cDNA	
Ġ	20106		AL OADAED	UKFZD58681922 (from clone	
202	132 195_at		ALCHEROO	ייין באסטט ואבר/	

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39379_at 37575_at 34283_at 34752_at 39103_s_at 35187_at	89	ပ	D	
39379_at 37575_at 34283_at 39752_at 39103_s_at 35187_at				
39379_at 37575_at 34283_at 39500_at 39103_s_at 35187_at		<u></u> .	Homo sapiens mRNA; cDNA	
39379_at 37575_at 34283_at 39600_at 34752_at 35167_at 35187_at			DKFZp586C1019 (from clone	
37575_at 34283_at 39600_at 34752_at 36092_at 35187_at		AL049397	DKFZp586C1019)	
37575_at 34283_at 39600_at 34752_at 36092_at 35187_at			Homo sapiens mRNA; cDNA	
37575_at 34283_at 39600_at 34752_at 39103_s_at 35187_at			DKFZp586C1723 (from clone	
39600_at 39600_at 34752_at 39103_s_at 35187_at		AL050192	DKFZp586C1723)	
34283_at 39600_at 34752_at 39103_s_at 36092_at 35187_at			Homo sapiens mRNA; cDNA	
34283_at 39600_at 34752_at 39103_s_at 36092_at 35187_at			DKFZp586F071 (from clone	
39600_at 34752_at 39103_s_at 36092_at 35187_at		AL050125	DKFZp586F071)	
39600_at 34752_at 39103_s_at 36092_at 35187_at			Homo sapiens mRNA; cDNA	
39600_at 34752_at 39103_s_at 36092_at 35187_at			DKFZp586G1922 (from clone	
34752_at 39103_s_at 36092_at 35187_at		AL080110	DKFZp586G1922)	
39103_s_at 36092_at 35187_at			Homo sapiens mRNA; cDNA	
39103_s_at 36092_at 35187_at			DKFZp586G2222 (from clone	
39103_s_at 36092_at 35187_at		AL080111	DKFZp586G2222)	
39103_s_at 36092_at 35187_at 35363_at			Homo sapiens mRNA; cDNA	
39103_s_at 36092_at 35187_at			DKFZp58610523 (from clone	
35092_at		H98552	DKFZp586l0523)	
35092_at			Homo sapiens mRNA; cDNA	
35092_at			DKFZp58611823 (from clone	
35187_at 35363_at		AL080213	DKFZp586l1823)	
35187_at 35363_at			Homo sapiens mRNA; cDNA	
35187_at 35363_at			DKFZp586K1123 (from clone	
		AL080216	DKFZp586K1123)	
			Homo sapiens mRNA; cDNA	
			DKFZp586K2322 (from clone	
	DDX17	AL080113	DKFZp586K2322)	
			Homo sapiens mRNA; cDNA	
			DKFZp586M2022 (from clone	
979 41013_at		AL080114	DKFZp586M2022)	
			Homo sapiens mRNA; cDNA	
			DKFZp586N012 (from clone	
980 41690_at		AL049471	DKFZp586N012)	
			Homo sapiens mRNA; cDNA	
			DKFZp586N1720 (from clone	
981 40349_at		AL049442	DKFZp586N1720)	

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				Homo sapiens mRNA; cDNA	
9			100004	DKFZp586N1918 (from clone	
382	320/2_BI		ALU4938/	UNIZEDOGINI 3 19)	
				me b5	
983	36668_at	DIA1	M28713		NADH-cytochrome b5 reductase
				Homo sapiens nucleophosmin	
				phosphoprotein (NPM) gene, 3' flanking	
984	38542_at		U89322	sequence.	-
				Homo sapiens p18 protein mRNA,	
985	985 40587_s_at	EEF1E1; P18	AF054186	complete cds.	p18 protein
				Homo sapiens PAC clone RP1-170019	even-skipped homeo box 1 (homolog of
986	986 41448_at	HOXA4	AC004080	from 7p15-p21, complete sequence.	Drosophila)
				Homo sapiens prion protein (PrP) gene,	
987	987 36159_s_at	PrP	U29185	complete cds.	prion protein
				Homo sapiens putative dienoyl-CoA	
				isomerase (ECH1) gene, exons 7-10, and	
988	988 32756_at	ECH1	AF030249	complete cds.	putative dienoyl-CoA isomerase
				Homo sapiens RP58 gene, complete	
989	35824_at	RP58	AJ223321	CDS.	RP58 protein
				Homo sapiens Sec61 gamma mRNA,	
980	39169_at	SEC61G	AF054184	complete cds.	Secol gamma
				Homo sapiens signal transducer and	
			-	activator of transcription 6 (STAT6) gene,	signal transducer and activator of
991	41222 at	STATE	AF067575	exons 15 through 23 and complete cds.	transcription 6
				Homo sapiens sperm acrosomal protein	
992	38817_at	SPAG7; ACRP; F	RP; F\$AF047437	mRNA, complete cds.	sperm acrosomal protein
				Homo sapiens splicing factor,	
603	36033 at		AI 049309	complete cds	
				Homo sapiens thymosin beta-10 gene,	•
994	31481_s_at	TMSB10	M92383	3'end.	thymosin beta-10
				Homo sapiens TIMP gene for tissue	
995	995 1693_s_at	TIMP	D11139	inhibitor of metalloproteinases, partial cds. Itissue inhibitor of metalloproteinases	Itissue inhibitor of metalloproteinases

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				Homo sapiens transaldolase-related	
				protein gene, exons 3-8 and complete	
966	37311_at	TALDO1; TAL-H; AF010400	AF010400	cds.	transaldolase-related protein
		,		Homo sapiens translation initiation factor	
997	32229_at	EIF4EL3; 4EHP; 4	IP; 4AF038957	4e mRNA, complete cds.	translation initiation factor 4e
988	998 1323_at	UBB	X04803	Homo sapiens ubiquitin gene.	ubiquitin
666	999 32153_s_at		U49869	Homo sapiens ubiquitin gene.	ubiquitin
8	1000 38372_at		U66042	Homo sapiens unknown mRNA	
3			7 100001	Homo sapiens vacuolar H(+)-ATPase	Tourist H(+) ATDage
3	1001 38814_at	AIP6VIGT; AIP6	1 PG AF038954	Subunit marka, complete cus.	אמרתטומו דו(ד)-איזר מספ סעטעווווג
ξ		4.000	A 5047440	Homo sapiens vesicle trafficking protein	vasirla trafficking protein sec22b
300	1003 34957 at	X5I	V18504	Homo sabiens X5L dene.	XAP-5-like protein
				Homo sapiens, clone IMAGE:3028427,	
1004	1004 38662 at		AL047596	mRNA, partial cds	
				Homo sapiens, clone IMAGE:3140802,	
1005	1005 38312_at		AL050002	mRNA	
				Homo sapiens, clone IMAGE:3855224,	
1006	1006 33388 at		AL080223	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4132509,	
1007	1007 38676 at		AA059408	mRNA	
				Homo sapiens, clone IMAGE:4150198,	
1008	1008 40238_at		AI674208	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4182947,	
1009	1009 32119_at		AL049423	mRNA	
				Homo sapiens, clone IMAGE:4183312,	
1010	1010 38650_at	IGFBP5	127560	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4183312,	
101	1011 1396 at	IGFBP5	127560	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4391536,	
1012	1012 40432_at		AA522891	mRNA	
				Homo sapiens, Similar to RNA helicase-	
5	1012 26130 4 24	MT1E	B92331	related protein, cione McC:3246 IMAGE:3892441 mRNA, complete cds	
2	30130_1_at	101116	1135001		

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				Homo sapiens, Similar to serine (or	
				cysteine) proteinase inhibitor, clade E	
			•	(nexin, plasminogen activator inhibitor	
	•			type 1), member 2, clone MGC:23129	
1014	1014 41246_at		AI743134	IMAGE:4578406, mRNA, complete cds	
				Homo sapiens, similar to unknown, clone	
				MGC:39325 IMAGE:5440447, mRNA,	
1015	1015 41533_at		U79298	complete cds	
				-inducible, endoplasmic	homocysteine-inducible, endoplasmic
		٠	-	0	reticulum stress-inducible, ubiquitin-like
1016	1016 39733_at	HERPUD1	AF055001	domain member 1	domain member 1
				homolog of yeast mutL gene; Human	
				homolog of yeast mutL (hPMS1) gene,	
1017	1017 525 g_at	hPMS1	U13695		postmeiotic segregation 1
				homologous to mouse Rsu-1; putative;	
		-		Human RSU-1/RSP-1 mRNA, complete	
1018	1018 32545_r_at	RSU-1	L12535		ras suppressor protein 1
				homologous to mouse Rsu-1; putative;	
				Human RSU-1/RSP-1 mRNA, complete	
1019	1019 32544_s_at	RSU-1	L12535	cds.	ras suppressor protein 1
1020	1020 39800_s_at	HAX1	U68566	HS1 binding protein	HAX-1
				Human 2,4-dienoyl-CoA reductase gene,	
1021	1021 38104_at	DECR1; NADPH	JPH U78302	exon 10 and complete cds.	2,4-dienoyl-CoA reductase
				Human alcohol dehydrogenase chi	
				polypeptide (ADH5) gene exons 8-9,	
1022	1022 37708_r_at	ADH5	M81118	complete cds.	alcohol dehydrogenase
				Human alcohol dehydrogenase chi	
				polypeptide (ADH5) gene exons 8-9,	
1023	1023 37707_i_at	ADHS	M81118	complete cds.	alcohol dehydrogenase
				Human alpha-1 collagen type IV gene,	
1024	1024 39333_at	COL4A1	M26576	exon 52.	alpha-1 type IV collagen
	1		000707	AND a conjunct ONA	Hamber and description (AMDO) (AMDO)
	1025 38417_at	AMPUZ	MSTOZS	חחווומו אואור טפמווווומסס (אואור טב) ווויזוא.	Aire dealinease solonne spheing variant
1026	1026 37747 at	ANX5	005770	Human annexin V (ANX5) gene, exon 13.	annexin V

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1027	1027 41143 at	CALM1	U12022	Human caimodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds.	calmodulin
				Human cathepsin D (catD) gene, exons 7,	
1028 1028	1028 239_at	CTSD	M63138	8, and 9.	carnepsin U
				Human cellular oncogene c-fos (complete v-fos FBJ murine osteosarcoma viral	v-fos FBJ murine osteosarcoma viral
1029	1029 1916_s_at	c-fos	V01512	sequence).	oncogene homolog
				Human cellular oncogene c-fos (complete v-fos FBJ murine osteosarcoma vira	v-fos FBJ murine osteosarcoma viral
1030	1030 1915_s_at	c-tos	V01512	sequence).	oncogene homolog
				Human c-jun proto oncogene (JUN),	v-jun avian sarcoma virus 17 oncogene
1031	1031 32583_at	NOS	J04111	complete cds, clone hCJ-1.	homolog
				Human c-jun proto oncogene (JUN),	v-jun avian sarcoma virus 17 oncogene
1032	1032 1895_at	NOC	J04111	complete cds, clone hCJ-1.	homolog
1033	1033 41604_at		U79297	Human clone 23589 mRNA sequence	
				Human clone A9A2BRB5 (CAC)n/(GTG)n	
1034	1034 32185_at		U00946	repeat-containing mRNA	
				Human cyclophilin gene for cyclophilin	
1035	1035 33667_at	PPIA	X52851	(EC 5.2.1.8).	peptidylprolyl isomerase
				Human cytochrome b5 (CYB5) gene, exon	_
1036	1036 38459_g_at	CYB5	L39945	6 and complete cds.	cytochrome b5
				Human cytochrome b5 (CYB5) gene, exon	
1037	1037 38458_at	CYB5	L39945	6 and complete cds.	cytochrome b5
				Human dihydrolipoamide dehydrogenase	
1038	1038 36163_at	DLD; E3; LAD; DL	; DLL13761	gene, exon 14.	dihydrolipoamide dehydrogenase
				Human DNA for 14-3-3 protein eta chain,	
1039	1039 1424_s_at	YWHAH; YWHA1	HA1 D78577	exon2 and complete cds.	14-3-3 protein eta chain
				Human DNA sequence from clone 73H22	
	-			on chromosome 6q23, complete	
1040	1040 31797 at	dJ73H22.1	AL035699	sequence.	dJ73H22.1 (TBP-like protein)
				Human ENO2 gene for neuron specific	•
1041	1041 40193_at	EN02	X51956	(gamma) enolase.	human gamma enolase
		000	00000	in the second of	cietary COO
2	1042 36326_at	2005	MOSTES	ruman door protein gene, comprete cas.	
1043	1043 40567 at	TUBA3: Ft.J25113X01703	X01703	Human gene for alpha-tubulin (b alpha 1). alpha-tubulin	alpha-tubulin

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1044	1044 39775 at	O		Human gene for C1-inhibitor.	C1 inhibitor
1045	1045 40862_i_at	скв; сквв		Human gene for creatine kinase B (EC 2.7.3.2).	creatine kinase B
				gene for hepatitis C-associated ular aggregate protein p44, exon	hepatitis C-associated microtubular
1046	1046 37641_at	IF144; p44; MTAP4	AP4D28915	9 and complete cds.	aggregate protein p44
				Human gene for heterogeneous nuclear ribonucleoprotein (hnRNP) core protein	
1047	1047 40211_at	HNRPA1; HNRNP X12671		A1.	hnrnp a1 protein
1048	1048 408 at	MGSA	X54489	Human gene for melanoma growth stimulatory activity (MGSA).	melanoma growth stimulatory activity preprotein
1049	1049 36203 at	0003	X16977	Human gene for omithine decarboxylase	omithine decerboxylase (ODC)
1050	1050 36873 at		Diego	Human gene for very low density	y y y y y y y y y y y y y y y y y y y
1051	1051 34759_at		U68494	Human hbc647 mRNA sequence	
5	1050	AKD404. DD4. D	100004	Human hepatic dihydrodiol	Constitution of the second of
7001	32003_all		000001	Himan HMG-17 dana for non-histona	Hebanc diliyardada deliyardada de
1053	1053 41231_f_at	HMG17; MGC562	562 X13546	chromosomal protein HMG-17.	put. HMG-17 protein
1054	1054 38294 at	HOXD4: HOX4: H X17360	X17360	Human HOX 5.1 gene for HOX 5.1 protein.	hox 5.1 protein
	1			Human hsc70 gene for 71 kd heat shock	
165	1055 40637_at	HSP73 HSC70 HS	0 HS Y00371	cognate protein.	71 Kd heat shock cognate protein
1056	1056 232_at	LAMB2	M55210	Human laminin B2 chain gene, exon 28.	laminin B2 chain
				Human lipoprotein-associated coagulation inhibitor (LACI) gene, exon 9 and	
1057	1057 40767_at	TFPI	M59499	complete cds.	lipoprotein-associated coagulation inhibitor
1058	1058 38637_at	ГОХ	L16895	Human lysyl oxidase (LOX) gene, exon 7. lysyl oxidase	lysyl oxidase
1059	1059 37532_at	MCAD	M91432	Human medium-chain acyl-CoA dehydrogenase (MCAD) gene, exon 12.	medium-chain acyl-CoA dehydrogenase
1060	1060 870_f_at	MT3; GIF; GIFB	M93311	Human metallothionein-III gene, complete cds.	metallothionein-III

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				Human metaxin (MTX) gene, complete	
1061	1061 40890_at	MTX	U46920	cds.	metaxin
1062	1062 32145_at	ADD1	X58141	Human mRNA for enythrocyte adducin alpha subunit.	erythrocyte alpha adducin
553	1063 37381 9 91	TESB	X50268	Human mRNA for general transcription	IIB protein
<u>8</u>	1064 33683_at	Ŧ	D50525	Human mRNA for TI-227H.	
				Human myocyte-specific enhancer factor 2A (MEF2A) gene, last coding exon, and	myocyte-specific enhancer factor 2A, C9 form; myocyte-specific enhancer factor 2A,
1065	1065 41747_s_at	MEF2A	U49020	complete cds.	C4 form
1000			000707	Human NAD(P)H:quinone oxireductase	
2	1066 38066 at	- DON	M81600	gene, exon b.	INAD(r)n:quinone oxireduciase
1067	39729_at	NKEFB	L19185	Human natural killer cell enhancing tactor (NKEFB) mRNA, complete cds.	enhancer protein
				Human nonmuscle/smooth muscle alkali	non-muscle myosin light chain; smooth
1068	1068 33994_g_at	MLC	M22919	myosin light chain gene, complete cds.	muscle myosin light chain
				Human nucleic acid binding protein gene,	
1069	1069 32841_at	9; DM2;	CNB(U19765	complete cds.	nucleic acid binding protein
1070	1070 32590_at	NCL	M60858	Human nucleolin gene, complete cds.	nucleolin
				Human oncoprotein 18 (Op18) gene,	
1071	1782_s_at	Op18	M31303	complete cds.	oncoprotein 18
1072	1072 216_at	PTGDS	M98539	Human prostaglandin D2 synthase gene, exon 7.	prostaglandin D2 synthase (21kD, brain)
<u> </u>				Human protein phosphatase 2A catalytic	protein phosphatase-2A catalytic subunit-
1073	1073 237_s_at	PPP2CA	M60483	subunit-alpha gene, complete cds.	alpha
				Human protein phosphatase inhibitor 2 (PPP1R2) gene, exon 6 and complete	
1074	1074 812_at	PPP1R2	U68111	cds.	protein phosphatase inhibitor 2
			. 13	Human protein phosphatase inhibitor 2 (PPP1R2) gene, exon 6 and complete	
1075	1075 33180_at	PPP1R2	U68111	cds.	protein phosphatase inhibitor 2
1076	1076 35356_at		W21884	Human putative ribosomal protein S1 mRNA	

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		-		Human receptor tyrosine phosphatase	
1077	1077 491_at	PTPRG	U46116		receptor tyrosine phosphatase gamma
				Human receptor tyrosine phosphatase	
				gamma (PTPRG) gene, exon 30 and	
1078	1078 492 g at	PTPRG	U46116	complete cds.	receptor tyrosine phosphatase gamma
				Human red cell-type low molecular weight	
				acid phosphatase (ACP1) gene, exon 6	red cell-type low molecular weight acid
1079	1079 36611_at	ACP1	U25849	and 7, complete cds.	phosphatase
		-		Human SH3 domain-containing protein	
1080	1080 174_s_at	SH3P18	U61167	SH3P18 mRNA, complete cds	SH3 domain-containing protein SH3P18
				Human spermidine synthase gene,	
1081	1081 241_g_at	SRM	M64231	complete cds.	spermidine synthase
				Human sterol carrier protein-X/sterol	
				carrier protein-2 (SCP-X/SCP-2) gene,	
1082	1082 36688_at	SCP-X/SCP-2 U11313	U11313	exon 16, and complete cds.	sterol carrier protein-X/sterol carrier protein-2
1083	1083 32587_at	ZFP36L2; BRF2; I	U07802	Human Tis11d gene, complete cds.	Tis11d
1084	1084 31680_at	TOP1P2	M55630	Human topoisomerase I pseudogene 2.	
				Human transformation-related protein	
1085	1085 36446_s_at	HMG1L2	L24521	mRNA, 3' end	transformation-related protein
				Human transmembrane protein (CD59)	
1086	1086 39351_at	CD59	M84349	gene, exon 4.	CD59 protein
1087	1087 38727_at	11111	M23161	Human transposon-like element mRNA	
				Human vascular cell adhesion molecule-1	
1088	1088 41433_at	VCAM1	M73255	(VCAM1) gene, complete CDS.	vascular cell adhesion molecule-1
1089	40121_at	HIP2	U58522	huntingtin interacting protein 2	huntingtin interacting protein
1000	1090 35973_at	НУРН	AB023163	Huntingtin interacting protein H	KIAA0946 protein
1091	1091 40196_at	HYA22	D88153	HYA22 protein	HYA22
				hydroxyacyl-Coenzyme A	
				dehydrogenase/3-ketoacyl-Coenzyme A	enoyl-CoA hydratase/3-hydroxyacyl-CoA
1092	1092 36952_at	НАДНА	D16480	(trifunctional protein), alpha subunit	protein

(Fig 2)

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1093	1093 39741_at	НАОНВ	D16481	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein
1094	1094 36626_at	HSD1784	X87176	hydroxysteroid (17-beta) dehydrogenase 4 17beta-hydroxysteroid dehydrogenase	17beta-hydroxysteroid dehydrogenase
				Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypotetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans] and (Z70271) KNATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy relatedprotein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy	
1095	1095 41583 at	E Z	AC004770	related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.	BC269730_1; BC269730_2; FEN1_HUMAN; BC269730_4

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ш	BC269730_1; BC269730_2; FEN1_HUMAN;	BC269730_4	hypothetical protein CG018	hypothetical protein AF038182
٥	Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypotetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans] and (Z70271) KAD2.4 [Caenorhabditis elegans]. DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1		hypothetical gene CG018	hypothetical gene supported by AF038182; BC009203
ပ		AC004770	U50527	AF038182
ക		FEN1	CG018	LOC90355
∢	·	1096 34224_at	1097 1527_s_at	1098 33466_at
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Fig 21

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E	R32184_1; R32184_3		hypothetical protein, similar to (AC007017) putative RNA helicase A (Arabidopsis	manana			
Q	Hypothetical human protein (partial CDS); CDS constructed from combination of BLASTX, EST matches and Xgrail predictions. N-terminus of protein likely encoded in flanking cosmid R29942. Predicted protein exhibits weak similarity to hypothetical protein PIDIe1226191 (AL021106) from Drosophila melanogaster, Hypothetical human protein most similar to Rat ionotropic glutamate receptor (L34938); CDS constructed primarity from XGRAIL predictions and BLASTX similarity to (L34938) ionotropic glutamate receptor [Rattus norvegicus] and gil2160125 (U29873) NMDAR-L [Rattus norvegicus]. Also exhibits similarity to PIDIe258718 (Z78413) T01C3.10 [Caenorhabditis elegans]. C-terminus of hypothetical protein is ill-defined at this point; definition will require identification and characterization of appropriate cDNAs; Hypothetical 59.8 kDa human protein; CDS constructed from EST matches and Xgrail predictions. C- terminus of predicted protein not fully confirmed by EST or cDNA coverage. Hypothetical protein exhibits no significant database similarities when queried against R32184_2; R32184_3.	hypothetical protein			hypothetical protein 23851	hypothetical protein 24636	
ပ	AC004528	AA015605		AL0/9292	AF035313	AI651368	
8	MGC2436	FLJ20811		LOC54505	LOC54104	LOC55977	
A	099 35983 at	100 38440 s at		1101 39140_at	1102 37819_at	1104 41561 s at	
	8	12			2 2	12	



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1105 41128_at	LOC92703	AF070537	hypothetical protein BC013073	
1106 38972_at	LOC115207	AF052169	hypothetical protein BC013764	
1107 34864_at	CGI-57	AF070638	hypothetical protein CGI-57	hypothetical protein CGI-57
1108 39960_at	CL640	AF091086	hypothetical protein CL640	hypothetical protein CL640
1109 38837_at	DJ971N18.2	W26226	hypothetical protein DJ971N18.2	
1110 35142_at	72	AF070617	hypothetical protein DKFZp564D172	
1111 34830_at)822 W25986	hypothetical protein DKFZp564K0822	
1112 31852_at	DKFZP5640043	343 AL050390	hypothetical protein DKFZp5640043	
1113 33895_at	DKFZP586F1318	318 AL050373	hypothetical protein DKFZP586F1318	hypothetical protein
1114 39692 at	DKFZP586F2423	423 AL080209	hypothetical protein DKFZp586F2423	
1115 35682_at	FLB6421	Al133727	hypothetical protein FLB6421	
1116 36647_at	FLJ10326	AA526812	hypothetical protein FLJ10326	
1117 34804_at	FLJ10618	AL049246	hypothetical protein FLJ10618	
1118 36840_at	FLJ10737	AF052158	hypothetical protein FLJ10737	
1119 35283_at	FLJ10738	H05692	hypothetical protein FLJ10738	
1120 37610_at	FLJ10803	AI765280	hypothetical protein FLJ10803	
1121 33173_g_at	FLJ10849	T75292	hypothetical protein FLJ10849	
1122 39923_at	FLJ10971	A1935420	hypothetical protein FLJ10971	
			hypothetical protein FLJ11021 similar to	
1123 38105_at	FLJ11021	W26521	splicing factor, arginine/serine-rich 4	
1124 33394_at	FLJ11126	AA034074	hypothetical protein FLJ11126	
1125 35709_at	FLJ11149	AF038172	hypothetical protein FLJ11149	
1126 38141_at	FLJ11193	AF038176	hypothetical protein FLJ11193	
1127 40859_at	FLJ11806	Al561196	hypothetical protein FLJ11806	
1128 41177_at	FLJ12443	AW024285	hypothetical protein FLJ12443	
1129 41434_at	FLJ12552	AF070557	hypothetical protein FLJ12552	hypothetical protein FLJ12552
1130 36580_at	FLJ13910	AL050139	hypothetical protein FLJ13910	hypothetical protein FLJ13910
1131 32222_at	FLJ14639	AA152202	hypothetical protein FLJ14639	
1132 38710_at	FLJ20113	AL096714	hypothetical protein FLJ20113	
1133 38652_at	FLJ20154	AF070644	hypothetical protein FLJ20154	
1134 40868_at	FLJ20274	AA442799	hypothetical protein FLJ20274	
1135 34739_at	FLJ20275	W26023	hypothetical protein FLJ20275	
1136]34857_at	FLJ20986	224724	hypothetical protein FLJ20986	
1137 32251_at	FLJ21174	AA149307	hypothetical protein FLJ21174	
1138 40615_at	FLJ21439	AA780049	hypothetical protein FLJ21439	The state of the s
1139 33915_at	FLJ23027	W22655	hypothetical protein FLJ23027	

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1140	1140 35198_at	LOC57146	AF070596	4796	hypothetical protein from clone 24796
1141	1141 38483_at	HSA011916	AJ011916	3	hypothetical protein
1142	1142 41236_at	HSU79252	U79252		hypothetical protein HSU79252
1143	1143 38443_at	MGC14433	U79291	hypothetical protein MGC14433	
1144	1144 39811_at	MGC2749	AA402538	hypothetical protein MGC2749	
			-	hypothetical protein MGC2840 similar to a	
1145	1145 32051_at	MGC2840	AJ224875	putative glucosyttransferase	glucosyltransferase
1146	1146 35219_at	MGC3047	AL050202	hypothetical protein MGC3047	
1147	1147 41696_at	MGC3077	AI620381	hypothetical protein MGC3077	
				hypothetical protein MGC4276 similar to	hypothetical protein MGC4276 similar to
1148	1148 41147_at	MGC4276	AF038186	CG8198	CG8198
1149	1149 37242_at	MGC5149	U79260	hypothetical protein MGC5149	
1150	1150 36975_at	MGC8721	W26659	hypothetical protein MGC8721	
1151	1151 35677_at	MGC9084	AL035369	hypothetical protein MGC9084	hypothetical protein
1152	1152 32504_at	MY014	AW024812	hypothetical protein My014	
1153	1153 38106_at	YR-29	AJ012409	hypothetical protein YR-29	hypothetical protein
7.5	07020	F	70,000	hypoxanthine phosphoribosyttransferase 1	the second transferse
1154	1154 37540_at	וואאוו	M31642	(Lesch-Nynan syndrome)	וואסטאמווווווום שווספטווסווספטווו ווואססאמוו
1155	1155 1039_s_at	HIF1A	U22431	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) hypoxia-inducible factor 1 alpha	hypoxia-inducible factor 1 alpha
				IGF binding protein-4; Human insulin-like	
1				growth factor binding protein-4 (IGFBP4)	Laiotora paileaid referê descene edil elimei
126	39/81_at	IGFBP4	020982	gene, promoter and complete cus.	HISURIFIED GLOWIN IACIO DINGING PIOCORI-4
1157	1157 38046_at	¥	AJ005579	IK cytokine, down-regulator of HLA II	Prer protein
1158	1158 218_at	¥	S74221	IK cytokine, down-regulator of HLA II	IK factor
1159	1159 37690_at	ILVBL	U61263	ilvB (bacterial acetolactate synthase)-like	acetolactate synthase homolog
1160	1160 36097_at	ETR101	M62831	immediate early protein	immediate early protein
1161	1161 1237_at	IER3	S81914	immediate early response 3	immediate early response 3, isoform short; immediate early response 3, isoform long
1162	1162 34391 at	IGBP1	Y08915	immunoglobulin (CD79A) binding protein 1 alpha 4 protein	l alpha 4 protein

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		c g	, 0,0004	immunoglobulin superfamily containing	a ē
1163	1163 38636_at	ISLH	AB003184	leucine-rich repeat	שומו
				IMP (inosine monophosphate)	IMP (inosine monophosphate)
100	1164 40695_at	IMPDH1	J05272	dehydrogenase 1	dehydrogenase 1
1165	1165 36875_at	IBTK	AL050018	inhibitor of Bruton's tyrsoine kinase	hypothetical protein
				inhibitor of DNA binding 1, dominant	inhibitor of DNA binding 1, dominant
1166	1166 36617_at	5	X77956	negative helix-loop-helix protein	negative helix-loop-helix protein
				inhibitor of DNA binding 2, dominant	
1167	1167 41215_s_at	ID2	D13891	negative helix-loop-helix protein	Id-2H
				inhibitor of kappa light polypeptide gene	
			-	enhancer in B-cells, kinase complex-	•
1168	1168 34344_at	IKBKAP	AF044195	associated protein	IkappaB kinase complex associated protein
				inner membrane protein, mitochondrial	
1169	1169 37659_at	IMMT	L42572	(mitofilin)	transmembrane protein
					human type 1 inositol 1,4,5-trisphosphate
1170	1170 755_at	ITPR1	D26070	inositol 1,4,5-triphosphate receptor, type 1	receptor
					human type 1 inositol 1,4,5-trisphosphate
1171	1171 32778 at	ITPR1	D26070	inositol 1,4,5-triphosphate receptor, type 1	receptor
1172	1172 36154 at	IHPK1	D87452	inositol hexaphosphate kinase 1	KIAA0263 protein
					lithium-sensitive myo-inositol
1173	1173 32697_at	IMPA1	AF042729	inositol(myo)-1(or 4)-monophosphatase 1	monophosphatase A1
					•
1174	1174 36496_at	IMPA2	AF014398	inositol(myo)-1(or 4)-monophosphatase 2 myo-inositol monophosphatase 2	myo-inositol monophosphatase 2
1175	1175 35833_at	LOC51141	AL080184	insulin induced protein 2	
1176	1176 41049_at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
1177	1177 851_s_at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
			×	insulin-like growth factor 1 (somatomedin	
1178	1178 38737_at	IGF1	X57025	(c)	insulin-like growth factor l
				insulin-like growth factor 1 (somatomedin	
1179	1179 1501_at	1GF1	X57025	(0)	insulin-like growth factor l
1180	1180 160027_s_at	IGF2R	Y00285	insulin-like growth factor 2 receptor	insulin-like growth factor 2 receptor
				insulin-like growth factor binding protein 2	insulin-like growth factor binding protein 2
1181	1181 40422_at	IGFBP2	X16302	(36kD)	(36kD)
100	4707 0 04	7001	Mendo	insulin-like arowth factor hinding protein 4	isseulin. like grouth factor binding protein 4. instilin-like growth factor binding protein 4
	1162 1/3/_s_ai	larar4	INI02405	אינויים פוויים אינו ושכנסו פוויוים אינויים אינויים אינויים פוויים אינויים אינו	Thomas and the control of the contro

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1102	1183 2062 of	IGEBD7	10182	ineline growth factor hinding protein 7	
3		ימיטי /	L1310£	וויייועם אוריווים וויייון ווייים אוריווים אוריווים	
1184	1184 37991_at	ITM1	L38961	integral membrane protein 1	integral membrane protein 1
				internal mambrana protain: ewice-prot	
				accession: O04901: may play role in cell	
1185	1185 37326 at	Δ4	1193305	differentiation in intestinal epithelium	LIM domain only 6
1186	1186 41163 at	P24R	AI 109672	integral two I protein	b24B protein
	500		=		integrin beta 1 isoform 1A precursor; integrin
					beta 1 isoform 1B precursor; integrin beta 1
					Isoform 1C-1 precursor; integrin beta 1
				integrin beta 1 subunit precursor; Human	isoform 1D precursor; integrin beta 1 isoform
1187	1187 32808_at	ITGB1; CD29; FN X07979	87670X	mRNA for integrin beta 1 subunit.	1C-2 precursor
				integrin cytoplasmic domain-associated	integrin cytoplasmic domain associated
1188	188 1195_s_at	ICAP-1A	AF012024	protein 1	protein
1189	189 120_at	ITGA1	X68742	integrin, alpha 1	
1190	1190 37484_at	ITGA1	X68742	integrin, alpha 1	
1191	1191 36892 at	ITGA7	AF032108	integrin, alpha 7	integrin alpha-7
				integrin, alpha V (vitronectin receptor,	integrin, alpha V (vitronectin receptor, alpha
1192	1192 39071_at	ITGAV	M14648	alpha polypeptide, antigen CD51)	polypeptide, antigen CD51)
1193	39754 at	ITGB5	X53002	integrin, beta 5	
1194	1194 2058 s at	ITGB5	M35011	integrin, beta 5	integrin, beta 5
				integrin, beta-like 1 (with EGF-like repeat	
1195	1195 40681_at	ITGBL1	AB008375	domains)	osteoblast specific cysteine-rich protein
1196	1196 35365_at	불	U40282	integrin-linked kinase	integrin-linked kinase
				interacts with adenovirus E3-14.7KDa, a	
				TNF-alpha cytolysis antagonist; leucine	
				zipper protein; alternatively translated;	
				long form; interacts with adenovirus E3-	
				14.7KDa, a TNF-alpha cytolysis	
				antagonist; leucine zipper protein;	
				alternatively translated; short form; Homo	
			- A CO 60 0 1	sapiens FIP2 atternatively translated	Sa
<u> </u>	119/41/43_1_Bt	OPIN NAP FIR	FIFZAFUOIUSA	minita, complete cas.	2 11 2

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				interacts with adenovirus E3-14.7KDa, a	-
			•	TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated;	
				long form; interacts with adenovirus E3-	
				14.7KDa, a TNF-alpha cytolysis	
				antagonist; leucine zipper protein;	
				atternatively translated; short form; Homo	
				sapiens FIP2 alternatively translated	
1198	1198 41742_s_at	OPTN; NRP; FIP2	FIP2 AF061034	mRNA, complete cds.	FIP2
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 1
1199	1199 676_g_at	IFITM1	J04164	1 (9-27)	(9-27)
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 1
1200	1200 675_at	IFITM1	J04164	1 (9-27)	(9-27)
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 3
1201	1201 41745_at	IFITM3	X57352	3 (1-8U)	(1-8U)
1202	1202 1456_s_at	IFI16	M63838	interferon, gamma-inducible protein 16	interferon-gamma induced protein
1203	925_at	IF130	J03909	interferon, gamma-inducible protein 30	interferon, gamma-inducible protein 30
1204	1204 39728_at	IF130	J03909	interferon, gamma-inducible protein 30	interferon, gamma-inducible protein 30
				interferon-induced protein with	interferon-induced protein with
1205	1205 32814_at	IFIT1	M24594	tetratricopeptide repeats 1	tetratricopeptide repeats 1
				interferon-related developmental regulator	
1206	1206 37679_at	IFRD1	Y10313		PC4 protein
1207	1207 1368_at	IL1R1	M27492	interleukin 1 receptor, type l	interleukin 1 receptor, type l
1208	1208 33228 g at	IL 10RB	A1984234	interleukin 10 receptor, beta	
1209	1209 33227_at	IL10RB	Al984234	interleukin 10 receptor, beta	
1210	1210 38969_at	127	Al828168	interleukin 27	
1211	1211 38299_at	IL6	X04430	interleukin 6 (interferon, beta 2)	interleukin 6 (interferon, beta 2)
1212	1212 35372 r_at	11.8	M17017	interleukin 8	interleukin 8
				interleukin enhancer binding factor 2,	
1213	1213 36189 at	ILF2	U10323	45kD	NF45 protein
1214	1214 36030 at	DKFZP58612223	AL080214	intermediate filament-like MGC:2625	hypothetical protein
1215	1215 35776_at	ITSN1	AF064243	intersectin 1 (SH3 domain protein)	intersectin short form
1216	1216 41431_at	ΣĘ	AB023153	intestinal cell kinase	KIAA0936 protein
				IQ motif containing GTPase activating	
1217	1217 1825_at	IQGAP1	L33075	protein 1	ras GTPase-activating-like protein

Fig 21

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1218	1218 39023 at	IDH1	AF020038	isocitrate dehydrogenase 1 (NADP+), soluble	NADP-dependent isocitrate dehydrogenase
1219	1219 40112_at	IDH3B	AA522698	isocitrate dehydrogenase 3 (NAD+) beta	
0	, , , , , ,				NAD+specific isocitrate dehydrogenase
1220	1220 40111 g at	ПНЗВ	U49283	isocitrate dehydrogenase 3 (NAD+) beta	beta precursor
1221	1221 40478_at	KIAA1162	AL021396	isoform 1 match: proteins: Tr:Q9UJA1	hypothetical protein
1222	1222 32695_at	dJ196E23.1	297632	isoform 2 match: protein Q99991	bombesin-like receptor 3
1223	1223 40827_at	IARS	U04953	isoleucine-tRNA synthetase	isoleucyl-tRNA synthetase
1224	1224 36985 at	IDI	X17025	isopentenyl-diphosphate delta isomerase	isopentenyl-diphosphate delta isomerase
				isoprenylcysteine carboxyl	
1225	1225 41775_at	ICMT	AF064084	methyltransferase	prenylcysteine carboxyl methyltransferase
1226	1226 34877 at	JAK1	AL039831	Janus kinase 1 (a protein tyrosine kinase)	
1227	1227 34318_at	JM4	AJ005896	JM4 protein	JM4 protein
1228	1228 40957_at	JJAZ1	D63881	joined to JAZF1	joined to JAZF1
1229	1229 41250_at	JTV1	U24169	JTV1 gene	JTV-1
1230	1230 41483_s_at	JUND	X56681	jun D proto-oncogene	junD protein
1231	1231 1612_s_at	DNUC	X56681	jun D proto-oncogene	junD protein
1232	1232 40464_g_at	KPNB2	U70322	karyopherin (importin) beta 2	transportin
1233	39028_at	KPNB3	Y08890	karyopherin (importin) beta 3	Ran_GTP binding protein 5
1234	35725_at	KPNA3	D89618	karyopherin alpha 3 (importin alpha 4)	karyopherin alhph 3
1235	1235 32487_s_at	KPNA4	AB002533	karyopherin alpha 4 (importin alpha 3)	Qip1
				katanin p60 (ATPase-containing) subunit	
1236	1236 32708_g_at	KATNA1	Al191768	A1	
		i	1	KDEL (Lys-Asp-Glu-Leu) endoplasmic	Ü
) (27 1	123/ 3/386_1_at	NUELE1	A55885	reticulum protein retention receptor 1	NUEL receptor
1238	1238 39080 at	KDEL R2	M88458	rolet (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	KDEL receptor 2
				KDEL (Lys-Asp-Glu-Leu) endoplasmic	
1239	1239 33402_at	KDELR3	AL035081	reticulum protein retention receptor 3	hypothetical protein
1240	1240 37150_at	AB026190	AB026190	Kelch motif containing protein	Kelch motif containing protein
1241	1241 32329_at	KRTHB6	X99142	keratin, hair, basic, 6 (monilethrix)	type II intermediate filament of hair keratin
1242	1242 39346 at	KHDBBS1	MBR108	KH domain containing, RNA binding, signal transduction associated 1	292
			20120		

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1243 32679	2679_at	KIAA0009	D13634	KIAA0009 gene product	KIAA0009 gene product
12443	1244 34760_at	KIAA0022	D14664	KIAA0022 gene product	KIAA0022 gene product
1245 41129	.1129_at	KIAA0033	D26067	KIAA0033 protein	
1246 38797	18797_at	KIAA0062	D31887	KIAA0062 protein	
12473	1247 36978_at	KIAA0077	D38521	KIAA0077 protein	
12483	1248 37718_at	KIAA0096	D43636	KIAA0096 protein	
12493	1249 37293_at	KIAA0097	D43948	KIAA0097 gene product	KIAA0097 protein
				KIAA0098 is a human counterpart of	
			-	mouse chaperonin containing TCP-1	
				gene. Start codon is not identified.	
•				ha01413 cDNA clone for KiAA0098 has a	
				2-bp insertion between 736-737 of the	
				sequence of KIAA0098.; Homo sapiens	
1250 40417	10417_at	KIAA0098	D43950	mRNA for KIAA0098 protein, partial cds.	KIAA0098 protein
1251	39783_at	KIAA0100	D43947	KIAA0100 gene product	KIAA0100 protein
1252	37359_at	KIAA0102	D14658	KIAA0102 gene product	KIAA0102 gene product
1253 38031	38031_at	KIAA0111	D21853	KIAA0111 gene product	KIAA0111 gene product
1254	1254 40279_at	KIAA0121	D50911	KIAA0121 gene product	KIAA0121 protein
1255	1255 36845_at	KIAA0136	D50926	KIAA0136 protein	
1256	1256 32099_at	KIAA0138	D50928	KIAA0138 gene product	KIAA0138 gene product
1257	1257 38472_at	KIAA0143	D63477	KIAA0143 protein	
1258	1258 41728_at	KIAA0152	D63486	KIAA0152 gene product	KIAA0152 gene product
1259	1259 37642_at	KIAA0157	D63877	KIAA0157 protein	KIAA0157 protein
1260	1260 32661_s_at	KIAA0170	D79992.	KIAA0170 gene product	KIAA0170 gene product
1261	1261 37225_at	KIAA0172	D79994	KIAA0172 protein	
1262	36942_at	KIAA0174	D79996	KIAA0174 gene product	KIAA0174 gene product
1263	1263 31863_at	KIAA0179	D80001	KIAA0179 protein	
1264	1264 37734_at	KIAA0184	D80006	KIAA0184 protein	
1265	1265 41669_at	KIAA0191	D83776	KIAA0191 protein	
1266	1266 36192_at	KIAA0193	D83777	KIAA0193 gene product	KIAA0193 gene product
1267	38056_at	KIAA0195	D83779	KIAA0195 gene product	KIAA0195 gene product
1268	1268 38419_at	KIAA0196	D83780	KIAA0196 gene product	KIAA0196 gene product
1269	1269 38067_at	KIAA0202	D86957	KIAA0202 protein	
1270	1270 32586_at	KIAA0217	D86971	KIAA0217 protein	
1271	38728_at	KIAA0225	D86978	KIAA0225 protein	

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KIAA0229 D86982 KIAA0229 protein KIAA0222 D86985 KIAA0229 protein KIAA0221 D87445 KIAA0225 protein KIAA0255 D87445 KIAA0255 protein KIAA0256 D87454 KIAA0256 protein KIAA0265 D87456 KIAA0256 protein KIAA0276 D87456 KIAA0266 gene protein KIAA0276 D87456 KIAA0266 gene protein KIAA0276 D87456 KIAA0266 gene protein KIAA0284 AB002306 KIAA0284 protein KIAA0383 AB002319 KIAA0286 protein KIAA0385 AB002347 KIAA0380 protein KIAA0385 AB002348 KIAA0385 protein KIAA0385 AB002348 KIAA0386 protein KIAA0386 AB002336 KIAA0386 protein KIAA0386 AB002368 KIAA0386 protein KIAA0386 AB002368 KIAA0386 protein KIAA0386 AB002368 KIAA0386 protein KI KIAA0388 KIAA0386 protein KI KIAA0388	Ą	<u>«</u>	O	Q	3
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at KIAA0376 AB002374 KIAA0423 protein at KIAA0423 AB007893 KIAA0433 protein at KIAA0438 AB007898 KIAA0433 protein at KIAA0440 AB007900 KIAA0446 gene product at KIAA0447 AB007916 KIAA0447 gene product at KIAA0451 AB007920 KIAA0447 gene product at KIAA0469 AB007925 KIAA0456 gene product at KIAA0469 AB007938 KIAA0469 gene product at KIAA0470 AB007939 KIAA0470 gene product at KIAA0476 AB007940 KIAA0476 gene product at KIAA0476 AB007944 KIAA0476 gene product at KIAA0476 AB007944 KIAA0476 gene product at KIAA0483 AB007945 KIAA0476 gene product at KIAA0483 AB007945 KIAA0476 gene product at KIAA0483 AB007943 KIAA04816 gene product	1291 40517_at	KIAA0372	AB002370	KIAA0372 gene product	KIAA0372 gene product
at KIAA0423 AB007883 KIAA0433 protein at KIAA0433 AB007893 KIAA0433 protein at KIAA0440 AB007900 KIAA0440 protein. at KIAA0446 AB007915 KIAA0447 gene product at KIAA045 AB007916 KIAA0447 gene product at KIAA0451 AB007920 KIAA0451 gene product at KIAA0451 AB007926 KIAA0456 protein at KIAA0470 AB007928 KIAA0470 gene product at KIAA0470 AB007939 KIAA0470 gene product at KIAA0471 AB007940 KIAA0475 gene product at KIAA0476 AB007940 KIAA0476 gene product at KIAA0476 AB007944 KIAA0476 gene product at KIAA0476 AB007944 KIAA0476 gene product at KIAA0483 AB007945 KIAA0483 protein	1292 34837_at	KIAA0376	AB002374	KIAA0376 protein	
at KIAA0433 AB007893 KIAA0433 protein at KIAA0440 AB007900 KIAA0440 protein. at KIAA0446 AB007915 KIAA0446 gene product at KIAA0447 AB007916 KIAA0447 gene product at KIAA0451 AB007920 KIAA0451 gene product at KIAA0451 AB007926 KIAA0456 protein at KIAA0469 AB007928 KIAA0469 gene product at KIAA0470 AB007939 KIAA0471 gene product at KIAA0471 AB007940 KIAA0475 gene product at KIAA0476 AB007944 KIAA0476 gene product at KIAA0476 AB007944 KIAA0476 gene product at KIAA0476 AB007945 KIAA0476 gene product at KIAA0483 AB007945 KIAA0483 protein	1293 41457 at	KIAA0423	AB007883	KIAA0423 protein	
at KIAA0438 AB007898 KIAA0443 gene product at KIAA0440 AB007900 KIAA0446 gene product at KIAA0447 AB007915 KIAA0447 gene product at KIAA0451 AB007920 KIAA0451 gene product at KIAA0452 AB007925 KIAA0456 protein at KIAA0469 AB007938 KIAA0469 gene product i at KIAA0470 AB007939 KIAA0470 gene product i at KIAA0475 AB007940 KIAA0475 gene product i at KIAA0476 AB007944 KIAA0476 gene product i at KIAA0476 AB007945 KIAA0476 gene product i at KIAA0483 AB007945 KIAA0483 protein	1294 35167 at	KIAA0433	AB007893	KIAA0433 protein	KIAA0433 protein
KIAA0440 AB007900 KIAA0446 gene product KIAA0446 AB007915 KIAA0446 gene product KIAA0447 AB007916 KIAA0451 gene product KIAA0451 AB007920 KIAA0451 gene product SRGAP2 AB007926 KIAA0456 protein KIAA0469 AB007938 KIAA0469 gene product KIAA0470 AB007940 KIAA0471 gene product KIAA0475 AB007940 KIAA0475 gene product KIAA0476 AB007945 KIAA0476 gene product KIAA0483 AB007952 KIAA0483 protein KIAA0483 AB007963 KIAA0484 gene product		KIAA0438	AB007898	KIAA0438 gene product	KIAA0438 gene product
KIAA0446 AB007915 KIAA0446 gene product KIAA0447 AB007916 KIAA0447 gene product KIAA0451 AB007920 KIAA0451 gene product SRGAP2 AB007925 KIAA0456 protein KIAA0469 AB007938 KIAA0469 gene product AB007940 KIAA0470 gene product KIAA0475 AB007940 KIAA0475 gene product KIAA0476 AB007944 KIAA0476 gene product KIAA0483 AB007945 KIAA0483 protein KIAA0483 AB007952 KIAA048 gene product KIAA0494 AB007963 KIAA0494 gene product	1296 40805 at	KIAA0440	AB007900	KIAA0440 protein	KIAA0440 protein
KIAA0447 AB007916 KIAA0447 gene product KIAA0451 AB007920 KIAA0451 gene product SRGAP2 AB007925 KIAA0466 protein KIAA0469 AB007938 KIAA0469 gene product AB007939 KIAA0470 gene product KIAA0471 AB007940 KIAA0471 gene product KIAA0475 AB007944 KIAA0475 gene product KIAA0483 AB007945 KIAA0483 protein KIAA0483 AB007952 KIAA0483 gene product KIAA0494 AB007963 KIAA0494 gene product	1297 32091_at	KIAA0446	AB007915	KIAA0446 gene product	KIAA0446 protein
at KIAA0451 AB007920 KIAA0451 gene product at SHGAP2 AB007925 KIAA0456 protein at KIAA0469 AB007938 KIAA0469 gene product r at KIAA0470 AB007939 KIAA0470 gene product at KIAA0475 AB007940 KIAA0475 gene product at KIAA0476 AB007945 KIAA0476 gene product at KIAA0483 AB007952 KIAA0483 protein at KIAA0494 AB007963 KIAA0494 gene product	1298 41243_at	KIAA0447	AB007916	KIAA0447 gene product	KIAA0447 protein
at SHGAP2 AB007925 KIAA0456 protein at KIAA0469 AB007938 KIAA0469 gene product r_at KIAA0470 AB007939 KIAA0470 gene product at KIAA0471 AB007940 KIAA0471 gene product at KIAA0476 AB007944 KIAA0476 gene product at KIAA0483 AB007945 KIAA0483 protein at KIAA0494 AB007963 KIAA0494 gene product	1299 32206_at	KIAA0451	AB007920	KIAA0451 gene product	KIAA0451 protein
at KIAA0469 AB007938 KIAA0469 gene product r at KIAA0470 AB007939 KIAA0470 gene product at KIAA0471 AB007940 KIAA0471 gene product at KIAA0476 AB007945 KIAA0476 gene product at KIAA0483 AB007952 KIAA0483 protein at KIAA0494 AB007963 KIAA0494 gene product	1300 36069 at	SRGAP2	AB007925	KIAA0456 protein	KIAA0456 protein
r_at KIAA0470 AB007939 KIAA0470 gene product at KIAA0471 AB007940 KIAA0471 gene product at KIAA0475 AB007944 KIAA0476 gene product at KIAA0483 AB007952 KIAA0483 protein at KIAA0494 AB007963 KIAA0494 gene product	1301 37230 at	KIAA0469	AB007938	KIAA0469 gene product	KIAA0469 protein
at KIAA0471 AB007940 KIAA0471 gene product at KIAA0475 AB007944 KIAA0475 gene product at KIAA0476 AB007945 KIAA0476 gene product at KIAA0483 AB007952 KIAA0483 protein at KIAA0494 AB007963 KIAA0494 gene product	33893 r	KIAA0470	AB007939	KIAA0470 gene product	KIAA0470 protein
at KIAA0475 AB007944 KIAA0475 gene product at KIAA0483 AB007945 KIAA0483 protein at KIAA0484 AB007963 KIAA0494 gene product	34445	KIAA0471	AB007940	KIAA0471 gene product	KIAA0471 protein
at KIAA0476 AB007945 KIAA0483 product at KIAA0483 AB007952 KIAA0483 protein at KIAA0494 AB007963 KIAA0494 gene product		KIAA0475	AB007944	KIAA0475 gene product	KIAA0475 protein
at KIAA0483 AB007952 KIAA0483 protein at KIAA0494 AB007963 KIAA0494 gene product	35786	KIAA0476	AB007945	KIAA0476 gene product	KIAA0476 protein
at KIAA0494 AB007963 KIAA0494 gene product	, ,	KIAA0483	AB007952	KIAA0483 protein	KIAA0483 protein
		KIAA0494	AB007963	KIAA0494 gene product	KIAA0494 protein

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1308 35534_at	KIAA0514	AB011086	KIAA0514 gene product	KIAA0514 protein
1309 38724_at	KIAA0515	AB011087	KIAA0515 protein	KIAA0515 protein
1310 34192_at	KIAA0532	AB011104	KIAA0532 protein	KIAA0532 protein
1311 33787_at	KIAA0537	AB011109	KIAA0537 gene product	KIAA0537 protein
1312 35184_at	KIAA0546	AB011118	KIAA0546 protein	KIAA0546 protein
1313 31849_at	KIAA0564	AB011136	KIAA0564 protein	KIAA0564 protein
1314 39434_at	KIAA0592	AB011164	KIAA0592 protein	KIAA0592 protein
1315 41379_at	KIAA0594	AB011166	KIAA0594 protein	KIAA0594 protein
1316 32866_at	KIAA0605	AB011177	KIAA0605 gene product	KIAA0605 protein
1317 39852_at	KIAA0610	AB011182	KIAA0610 protein	KIAA0610 protein
1318 40160_at	KIAA0618	AL080109	KIAA0618 gene product	hypothetical protein
1319 40083_at	KIAA0625	AB014525	KIAA0625 protein	KIAA0625 protein
1320 33241_at	KIAA0626	AB014526	KIAA0626 gene product	KIAA0626 protein
1321 39376_at	KIAA0630	AB014530	KIAA0630 protein	KIAA0630 protein
1322 34353_at	KIAA0648	AB014548	KIAA0648 protein	KIAA0648 protein
1323 38082_at	KIAA0650	AB014550	KIAA0650 protein	KIAA0650 protein
1324 39117_at	KIAA0662	AB014562	KIAA0662 gene product	KIAA0662 protein
1325 41170_at	KIAA0663	AB014563	KIAA0663 gene product	KIAA0663 protein
	KIAA0674	AB014574	KIAA0674 protein	KIAA0674 protein
1327 39403_at	KIAA0678	AB014578	KIAA0678 protein	KIAA0678 protein
1328 39519_at	KIAA0692	AB014592	KIAA0692 protein	KIAA0692 protein
1329 39380_at	KIAA0697	AB014597	KIAA0697 protein	KIAA0697 protein
1330 39705_at	KIAA0700	AB014600	KIAA0700 protein	KiAA0700 protein
1331 41620_at	KIAA0716	AB018259	KIAA0716 gene product	KIAA0716 protein
1332 33835_at	KIAA0721	AB018264	KIAA0721 protein	KIAA0721 protein
1333 35177_at	KIAA0725	AB018268	KIAA0725 protein	KIAA0725 protein
1334 41218_at	KIAA0729	AB018272	KIAA0729 protein	KIAA0729 protein
1335 38694_at	K!AA0738	AB018281	KIAA0738 gene product	KIAA0738 protein
1336 39771_at	KIAA0740	AB018283	KIAA0740 gene product	KIAA0740 protein
1337 41585_at	KIAA0746	AB018289	KiAA0746 protein	KIAA0746 protein
1338 38424_at	KIAA0747	AB018290	KIAA0747 protein	KIAA0747 protein
1339 40848_g_at	KIAA0750	AB018293	KIAA0750 gene product	KIAA0750 protein
1340 32224_at	KIAA0769	AB018312	KIAA0769 gene product	KIAA0769 protein
1341 36474_at	KIAA0776	AB018319	KIAA0776 protein	KIAA0776 protein
1342 33251_at	KIAA0779	AB018322	KIAA0779 protein	KIAA0779 protein
1343 35999_r_at	KIAA0781	AB018324	KIAA0781 protein	KIAA0781 protein

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KIAA	KIAA0788	AB018331	KIAA0788 protein	KIAA0788 protein
KIAA0795	0795	AB018338	KIAA0795 protein	KIAA0795 protein
KIAA0802	0802	AB018345	KIAA0802 protein	KIAA0802 protein
KIAA	KIAA0810	AB018353	KIAA0810 protein	KIAA0810 protein
ΚIA	KIAA0826	AB020633	KIAA0826 protein	KIAA0826 protein
KIA	KIAA0830	AB020637	KIAA0830 protein	KIAA0830 protein
KIA	KIAA0831	AB020638	KIAA0831 protein	KIAA0831 protein
МК	KIAA0841	AB020648	KIAA0841 protein	KIAA0841 protein
KA	KIAA0843	AB020650	KIAA0843 protein	KIAA0843 protein
KIA	KIAA0854	AB020661	KIAA0854 protein	KIAA0854 protein
Σ¥	KIAA0864	AB020671	KIAA0864 protein	KIAA0864 protein
X	KIAA0877	AB020684	KIAA0877 protein	KIAA0877 protein
ΣĀ	KIAA0878	AB020685	KIAA0878 protein	KIAA0878 protein
춫	KIAA0882	AB020689	KIAA0882 protein	KIAA0882 protein
КIA	KIAA0893	AB020700	KIAA0893 protein	KIAA0893 protein
X	KIAA0903	AB020710	KIAA0903 protein	KIAA0903 protein
Ž	KIAA0909	AB020716	KIAA0909 protein	KIAA0909 protein
Κľ	KIAA0911	AB020718	KIAA0911 protein	KIAA0911 protein
X	KIAA0916	AF075587	KIAA0916 protein	protein associated with Myc
X	KIAA0931	AB023148	KIAA0931 protein	KIAA0931 protein
K	KIAA0934	AB023151	KIAA0934 protein	KIAA0934 protein
X	KIAA0937	AB023154	KiAA0937 protein	KIAA0937 protein
오	KIAA0938	AB023155	KIAA0938 protein	KIAA0938 protein
ď	Rab11-FIP2	AB023158	KIAA0941 protein	KIAA0941 protein
K	KIAA0942	AB023159	KIAA0942 protein,	KIAA0942 protein
X	KIAA0947	AB023164	KIAA0947 protein	KIAA0947 protein
\mathbf{Z}	KIAA0970	AB023187	KIAA0970 protein	KIAA0970 protein
호	KIAA0978	AB023195	KIAA0978 protein	KIAA0978 protein
K	KIAA0981	AB023198	KIAA0981 protein	KIAA0981 protein
오	KIAA0982	AB023199	KIAA0982 protein	KIAA0982 protein
K	KIAA0993	AB023210	KIAA0993 protein	KIAA0993 protein
X	KIAA0997	A1970189	KIAA0997 protein	
Y	KIAA0999	AB023216	KIAA0999 protein	KIAA0999 protein
ᆂ	KIAA1001	AW052084	KIAA1001 protein	
¥	KIAA1012	AB023229	KiAA1012 protein	KIAA1012 protein
×	KIAA1014	AB023231	KIAA1014 protein	KIAA1014 protein



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1380 39615	1 1	KIAA1026	AB028949	KIAA1026 protein	KIAA1026 protein
13813	1381 34089_at	KIAA1030	AB028953	KIAA1030 protein	KIAA1030 protein
13824	1382 41651_at	KIAA1033	AB028956	KIAA1033 protein	KIAA1033 protein
13834	1383 41708_at	KIAA1034	AB028957	KIAA1034 protein	KIAA1034 protein
13843	1384 35163_at	KIAA1041	AB028964	KIAA1041 protein	KIAA1041 protein
13853	1385 38778_at	KIAA1046	AB028969	KIAA1046 protein	KIAA1046 protein
13864	1386 41268 g_at	KIAA1049	AB028972	KIAA1049 protein	KIAA1049 protein
13874	1387 40855_at	KIAA1053	AB028976	KIAA1053 protein	KIAA1053 protein
13883	1388 39400_at	KIAA1055	AB028978	KIAA1055 protein	KIAA1055 protein
1389 33877	33877_s_at	KIAA1067	AB028990	KIAA1067 protein	KIAA1067 protein
1390	1390 34688_at	KIAA1078	AB029001	KIAA1078 protein	KIAA1078 protein
1391	1391 33924_at	KIAA1091	AB029014	KIAA1091 protein	KIAA1091 protein
1392	1392 32508_at	KIAA1096	AL096857	KIAA 1096 protein	hypothetical protein
13934	1393 41179_at	KIAA1100	AB029023	KIAA1100 protein	KIAA1100 protein
1394	1394 34839_at	KIAA1104	AB029027	KIAA1104 protein	KIAA1104 protein
1395	1395 33457_at	RAP140	AB029028	KIAA1105 protein	KIAA1105 protein
1396	1396 36814_at	KIAA1109	AB029032	KIAA1109 protein	KIAA1109 protein
1397	1397 34274_at	KIAA1116	AB029039	KIAA1116 protein	KIAA1116 protein
1398 37617	37617_at	KIAA1128	U90912	KIAA1128 protein	
1399	1399 33358 at	KIAA1157	W29087	KIAA1157 protein	
1400	1400 40308_at	KIAA1240	AI830496	KIAA1240 protein	
1401	1401 33811_at	KIAA1254	AI761567	KIAA1254 protein	
1402	1402 38674_at	KIAA1354	AA115140	KIAA1354 protein	
1403	1403 32730 at	KIAA1750	AL080059	KIAA1750 protein	
140 <u>4</u>	1404 32171_at	KIAA1856	AL080102	KIAA1856 protein	hypothetical protein
1405	1405 39897_at	KIAA1966	N36997	KIAA1966 protein	
1406	1406 32846_s_at	KTN1	D13629	kinectin 1 (kinesin receptor)	kinectin 1
1407	39057_at	KNS2	L04733	kinesin 2 (60-70kD)	kinesin light chain
1408	1408 32079 at	KIF13B	AB014539	kinesin family member 13B	KIAA0639 protein
1409	1409 33345_at	KIF3C	AF035621	kinesin family member 3C	kinesin-related protein
1410	1410 34294_at	KIFC3	AL041493	kinesin family member C3	
1411	1411 41474 at	KIF2	Y08319	kinesin heavy chain member 2	kinesin-2
1412	1412 40779 at	KIFAP3	U59919	kinesin-associated protein 3	SMAP
1413	1413 34216_at	KLF7	AA478904	Kruppel-like factor 7 (ubiquitous)	
		00.00		L-3-hydroxyacyl-Coenzyme A	2 highway Col dehidranese
1414	1414 38768_at	HADHSC	X36/52	denydrogenase, snort chain	S-riyuloxyacyr-con deliyulogellase

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1415	1415 41485 at	LDHA	X02152	A	lactate dehydrogenase A
1416	1416 288 s at	LBR	125931		lamin B receptor
				laminin receptor 1 (67kD, ribosomal	
1417	1417 256 s at	LAMR1	M14199		laminin receptor 1
1418	1418 37671_at	LAMA4	S78569	ha 4	laminin alpha 4 chain
1419	1419581 at	LAMB1	M61916		laminin B1
				LanC lantibiotic synthetase component C-	
1420	1420 39441 at	LANCL1	Y11395	like 1 (bacterial)	lanthionine synthetase C-like protein 1
				latent transforming growth factor beta	latent transforming growth factor beta
1421	1421 1495_at	LTBP1	M34057	binding protein 1	binding protein 1 precursor
				latent transforming growth factor beta	
1422	1422 37906 at	LTBP2	237976	binding protein 2	LTBP-2 precursor
				lectin, galactoside-binding, soluble, 1	
1423	1423 33412_at	LGALS1	AI535946	(galectin 1)	
				lectin, galactoside-binding, soluble, 3	
1424	1424 35367_at	LGALS3	AB006780	(galectin 3)	galectin-3
				lectin, galactoside-binding, soluble, 3	
1425	37754_at	LGALS3BP	L13210	binding protein	Mac-2 binding protein
				lectin, galactoside-binding, soluble, 8	•
1426	1426 1846 at	LGALS8	L78132	(galectin 8)	prostate carcinoma tumor antigen
1427	1427 34267 r at	LEPR	U50748	leptin receptor	leptin receptor
1428	1428 33830 at	HSOBRGRP	AW026535	leptin receptor gene-related protein	
1429	1429 33829 at	HSOBRGRP	Y12670	leptin receptor gene-related protein	leptin receptor gene-related protein
	2000	- IFOOD	AFOESEDE	lentin zezenter overlanning transcript-like 1 brain mv047 protein	brain mv047 protein
2	30300_al	ברו ווכן ורי	20000	leucine rich repeat (in FLII) interacting	
1431	1431 41320_s_at	LRRFIP1	60969N	protein 1	transcription repressor
1433	1432 30067 of	1 0003	4R019527	leucine zipper down-regulated in cancer 1 LDOC1 protein	LDOC1 protein
1433	1433 41754 at	LAPPAC	M92439	leucine-rich PPR-motif containing	leucine-rich PPR-motif containing protein
434	1434 37470 at	LAIR1	AF013249	leukocyte-associated lg-like receptor 1	leukocyte-associated Ig-like receptor-1
1435	1435 38081 at	LTA4H	J03459	leukotriene A4 hydrolase	leukotriene A4 hydrolase
1438	1436 36062 at	LPXN	AF062075	leupaxin	leupaxin
1437	1437 35278 at	RPS29	AI541542	libtest16.A02.r bvnorm Homo sapiens CDNA 5', mRNA sequence.	
1438	1438 39687 at	E46L	AI524873	like mouse brain protein E46	
	: - 3.2.3				

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6	at	E46L	AL050282	like mouse brain protein E46	hypothetical protein
(2)	1440 39685_at	E46L	AL050282	like mouse brain protein E46	hypothetical protein
				likely homolog of rat kinase D-interacting	
(1)	1441 39163_at	KIDINS220	W27233	substance of 220 kDa	
				likely ortholog of mouse suppressors of	
		ທຸ	AB014571		KIAA0671 protein
. ~ .	1443 40555_at	TC10	AL043108	likely ortholog of mouse TC10-alpha	
				likely ortholog of mouse TPR-containing,	
	1444 40844_at	TSBP	D63875		KIAA0155 gene product
	1445 41248_at	CSTF2T	AB014589	polyadenylation protein CSTF-64	KIAA0689 protein
				likely ortholog of rat golgi stacking protein	
	1446 35805_at	GRASP55	AA447263	homolog GRASP55	
		-		LIM and senescent cell antigen-like	
	1447 39232_at	LIMS1	U09284		PINCH protein
	36181_at	LASP1	X82456	LIM and SH3 protein 1	LIM and SH3 domain protein
	1449 38617_at	LIMK2	D45906	LIM domain kinase 2	LIMK-2
	1450 1452_at	LMO4	U24576	LIM domain only 4	breast turnor autoantigen
	1451 31936_s_at	LKAP	AB007890		KIAA0430 protein
				lipase A, lysosomal acid, cholesterol	
	1452 38745_at	LIPA	X76488	esterase (Wolman disease)	lysosomal acid lipase
	1453 38098_at	LPIN1	D80010	lipin 1	
	37542_at	LHFPL2	D86961	lipoma HMGIC fusion partner-like 2	
	1455 41209_at	LP.	M15856	lipoprotein lipase	lipoprotein lipase precursor
	1456 1798_at	LIV-1	U41060	LIV-1 protein, estrogen regulated	estrogen regulated LIV-1 protein
				liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and	
	1457 37215 at	PYGL	AF046798	complete cds.	glycogen phosphorylase

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1458	1458 40493_at	CD44	L05424 M63959	long tailed isoform; individual exons 6-14 are atternative exons any of which can be spliced out of the mRNA.; putative; long tailed isoform; putative; long tailed isoform; epithelial form; putative; Human cell surface glycoprotein CD44 (CD44) gene, 3' end of long tailed isoform.	long tailed isoform; individual exons 6-14 spliced out of the mRNA.; putative; long tailed soform; putative; long tailed isoform; putative; long tailed isoform; epithelial form; putative; Human cell surface glycoprotein CD44 (CD44) gene, 3' end of long tailed isoform. coll surface glycoprotein cell surface glycoprotein CD44 low density lipoprotein-related protein-associated protein alpha-2-macroglobulin receptor-associated protein alpha-2-macroglobulin receptor-associated protein alpha-1-macroglobulin receptor-associated protein alpha-2-macroglobulin
1460	1460 34400_at	QP-C	AI540957	low molecular mass ubiquinone-binding protein (9.5kD)	
1462	1461 37025_at 1462 39017_at	PIG7 LSM1	AL120815 AJ238094	LPS-induced INF-alpha factor Lsm1 protein	Lsm1 protein
1463	1463 38038_at	LUM	U21128	lumican	lumican
1464	1464 38115_at	FUS1	AF055479	lung cancer candidate	lung cancer candidate FUS1
1465 1466	1465 39428 at	LYPLA1	AF05581 AF081281	lymphocyte adaptor protein lysophospholipase I	kadaptor protein Link lysophospholipase
1467	1467 33788_at	LYSAL1	AB002390	lysosomal apyrase-like 1	lysosomal apyrase-like 1
1468	1468 39758_f_at	LAMP1	J04182	lysosomal-associated membrane protein 1 lysosomal membrane glycoprotein-1	lysosomal membrane glycoprotein-1
1469	1469 38403_at	LAMP2	X77196	lysosomal-associated membrane protein 2	lysosomal-associated membrane protein 2 lysosome-associated membrane protein-2
1470	1470 38402_at	LAMP2	U36336	lysosomal-associated membrane protein 2	lysosomal-associated membrane protein 2 lysosome-associated membrane protein-2b
1471	1471 39019_at	LAPTM4A	D14696	lysosomal-associated protein transmembrane 4 alpha	lysosomar-associated protein transmembrane 4 alpha
1472	1472 33127_at	LOXL2	U89942	lysyl oxidase-like 2	lysyl oxidase-related protein
1473	1473 34336_at	KARS	D32053	lysyl-tRNA synthetase	Lysyl tRNA Synthetase
1474	1474 32832_at	MAEA	AF084928	macrophage erythroblast attacher	erythroblast macrophage protein EMP
1475	1475 36174_at	MACMARCKS	X70326	macrophage mynstoylated alanine-rich C kinase substrate	macropnage mynstoylated alanine-rich C. kinase substrate

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				MAD, mothers against decapentaplegic	
1476	1476 1453_at	MADH2	U68018	homolog 2 (Drosophila)	mad protein homolog
			Э	MAD, mothers against decapentaplegic	
1477	1477 38944_at	MADH3	U68019	homolog 3 (Drosophila)	mad protein homolog
				MAD, mothers against decapentaplegic	
1478	1478 1433_g_at	MADH3	U68019	homolog 3 (Drosophila)	mad protein homolog
				MAD, mothers against decapentaplegic	
1479	1479 36953_at	MADH4	U44378	homolog 4 (Drosophila)	Dpc4
				MAD, mothers against decapentaplegic	
1480	1480 1013_at	MADH5	U59913	homolog 5 (Drosophila)	Smad5
				MAD, mothers against decapentaplegic	
1481	1481 1955_s_at	MADH6	AF035528	homolog 6 (Drosophila)	Smad6
				MAD, mothers against decapentaplegic	
1482	1482 1857_at	MADH7	AF010193	homolog 7 (Drosophila)	MAD-related gene SMAD7
				major histocompatibility complex, class I,	
1483	1483 41237_at	HLA-A	D32129	А	HLA-A26
				major histocompatibility complex, class II,	
1484	1484 41609_at	HLA-DMB	U15085	DM beta	HLA-DMB
				major histocompatibility complex, class II,	
1485	1485 38096_f_at	HLA-DPB1	M83664	DP beta 1	HLA-DPB1
				major histocompatibility complex, class II,	
1486	1486 38095_i_at	HLA-DPB1	M83664	DP beta 1	HLA-DPB1
				major histocompatibility complex, class II,	_
1487	1487 37039_at	HLA-DRA	J00194	DR alpha	DR alpha precursor
				major histocompatibility complex, class II,	
1488	1488 33261_at	HLA-DRB1	M16941	DR beta 1	
				major histocompatibility complex, class I-	
1489	1489 34425_at	HLALS	AF031469	like sequence	MHC class I-related protein 1 isoform D
				major receptor for HIV-1; member of	
				immunoglobulin supergene family; T cell	
1490	1490 34003_at	CD4	U47924	surface glycoprotein T4	protein 'A', isoform 1
140	1401 26609 01	יחטא	DEFCEA	majata dahi dramanasa 1 NAD (saluhla)	consolic malate debydronenses
2	20000 at		2000	maiate dell'acceptation (1) della (2)	chicago in a contract of the c
1492	1492 837_s_at	ME1	U43944	mailc enzyme 1, NADP (+)-dependent, cytosolic	cytosolic NADP(+)-dependent malic enzyme

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				malic enzyme 2, NAD(+)-dependent,	mitochondrial NAD(P)+ -dependent malic
1493	1493 36599_at		M55905	mitochondrial	өпzуте
1494	1494 36673_at	MPI	X76057	mannose phosphate isomerase	phosphomannose isomerase
				MAP kinase-interacting serine/threonine	
1495	1495 35299 at	MKNK1	AB000409		MNK1
				MAP/microtubule affinity-regulating kinase	
1496	1496 40826_at	MARK3	M80359		protein p78
				MAPK-activated protein kinase; PRK;	
			-	e.	
				kinase activated protein kinase gene,	mitogen activated protein kinase activated
1497	1497 41506_at	MAPKAPK5; PRA	PRA AF032437	complete cds.	protein kinase
				match proteins: Sw:P04040 Sw:P04762	
				C Do 4070 T Ceneso C DO 400	
				SW:P242/0 1f:U62839 SW:PU0432	
				Sw:P17336 Tr:P90682 Tr:Q27487	
			-	Sw:O61235 Tr:O18193 Tr:O77229	
				Tr:Q49133 Sw:P26901 Sw:P55306	
				Sw:P30263 Tr:P95631 Sw:P44390	
				Tr:Q27710 Sw:Q96528 Sw:O13289	
				Sw:P07820 Sw:P30265 Sw:P77872	
				Tr:Q59602 Tr:P77924 Sw:Q59170	
				Sw:P15202 Tr:Q59296 Tr:O33613	
				Sw:Q92405 Sw:Q59635 Sw:P81138	
1498	1498 37009 at	CAT	AL035079	match ESTs: W94164 N28621	dJ53C18.1 (Catalase)
				match to ESTs AA316181	
				(NID:g3165221), AA032221	
				(NID:g1502183), and AI167942	
				(NID:g3701112); H_RG041D11.1; Homo	
				sapiens BAC clone CTB-41D11 from	six transmembrane epithelial antigen of the
149	1499 40297 at	WUGSC:H RGO	1G04 AC005053	7q21, complete sequence.	prostate

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1500	500 34860_g_at		Z98046	match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283 D38535 D38595 match: proteins Q06033 P97280 O54882 O35802 Q61704 Q14624 P79263 Q63416 O42141 P19823 O02668 Q61703 P97279 Q29052	match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283 D38535 D38595 match: proteins Q06033 P97280 O54882 O35802 Q61704 Q14624 P79263 Q63416 Q42141 P19823 Q02668 hepatocellular carcinoma associated protein; Q61703 P97279 Q29052 breast cancer associated gene 1
				match: cDNAs: Em:AL050345 match: ESTs: Em:AA304885 Em:AA447346 Em:AA314213 Em:AA209368 Em:AA209372 Em:T84723 Em:H23039	
1501	501 35336_at	HS508115A	AL021707	Em:AA342123 Em:W41050 Em:AA384854 Em:AA492678	chromosome 22 open reading frame 2
1502	502 32658_at	dJ1033B10.1	AL031228	match: protein O15214	BING4
1503	1503 31545_at	dJ1033B10.1		match: protein 015214	BING4
1504	1504 36986_at	dJ886K2.1	AL031295	match: protein SPTREMBL; Q14241	UUP-galactose-4-epimerase
				match: proteins CE02000 059733 CE01999; supported by FGENES and	×
1505	1505 38072_at	dJ465N24.1	AL031432	GENSCAN	hypothetical protein dJ465N24.2.1
				match: proteins O15037 CE16881 supported by GENSCAN possibly this	
				partial gene and dJ281H8.1 are part of	dJ281HB.2 (PUTATIVE novel protein similar
1506	1506 32478_f_at	dJ281H8.1	AL031133	one gene	to KIAA0323 and worm C30F12.1)

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cytochrome с oxidase subunit Vla polypeptide 1	match: proteins P13182 P12074 P10818 P43024 Q02221 P07471 P10817 P43023 cytochrome c oxidase subunit Vla P13182 O13085 O13082 polypeptide 1	AL021546	COX6A	1509 32573_at	15.
dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-7 (isoform 3))	match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6426-27. Contains the 3 part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.	AL031781	dJ51J12.1	1508 39760_at	<u>, , , , , , , , , , , , , , , , , , , </u>
dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-77 (isoform 3))	match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the atternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.	AL031781	dJ51J12.1	507 39759 <u>a</u> t	150
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510	1510 33443_at	HSF2	299129	match: proteins P38533 Q03933 P38530 P41154 Q00613 P38529 P38531 Q63717 P38532 Q99472	heat shock transcription factor 2
				match: proteins Q14189 P15924 Q03001 P97395 P97396 P97394; Human DNA	
				the , STSs	
1511	1511 36133_at	dJ512B11.1	AL031058		dJ512B11.1 (Desmoplakin I (DPI))
				match: proteins Q14209 Q16254 O35261 000716 Q61501 Q90977 Q01094	
1512	1512 37043_at	E2F-2	AL021154	Q27368	E2F transcription factor 2
				match; proteins Q15774; match: protein Q01968 P32019; Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the	
				OCRL1 gene for Lowe Oculocerebrorenal dJ454M7.1.2 (Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains Syndrome protein OCRL-1) (isoform 2)	dJ454M7.1.2 (Lowe Oculocerebrorenal Syndrome protein OCRL-1) (isoform 2);
1513	1513 41227_at	OCRL1	AL022162	ESTs, STSs and GSSs, complete sequence.	dJ454M7.1.1 (Lowe Oculocerebrorenal Syndrome protein OCRL-1) (isoform 1)
				² 20793 Q04859	
1514	1514 38990_at	dJ341E18.1	AL031178	Q39423 P43294 O49669	Q62726))

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1515	1515 34782 <u>_</u> at	ICMONJI	AŁ021938	match: proteins Q92833 Q62315; protein Q92833 has a different stop codon 19 as further downstream because it jumps frame twice, circumventing the stopcodon in this entry. This could be due to a sequence error in the cDNA sequence; Homo sapiens DNA sequence from PAC 232K4 on chromosome 6p22.3. Contains the JUMONJI gene for a hypothetical 141.7 kD protein. Contains ESTs, STSs, a CA repeat polymorphism and genomic marker D6S260', complete sequence.	dJ232K4.1 (hypothetical 141.7 kD protein JUMONJI)
1516	1516 37350. at	dJ889N15.1	AL031177	match: proteins Q99795 Q91665 Q91664 C09052 P78310 P97792 Q91667 C60939 P54900 Q62861 Q61148 C00426 P06907 P25189 Q92677 P20938 P27573 P10522 P37301 match: patented sequence 180040 dJ889N15.1 (novel protein similar to X. supported by GENSCAN and FGENES laevis Cortical Thymocyte Marker CTX	dJ889N15.1 (novel protein similar to X. laevis Cortical Thymocyte Marker CTX)
1517	1517 39738_at	APOL2	Z 82215	П	apolipoprotein L
1518	1518 31824_at	ME1	AL049699	match: proteins: Sw:P06801 Sw:P28227 Sw:Q29558 Sw:P13697 Sw:P40927 Sw:Q16798 Tr:Q16797 Sw:P48163	dJ747H23.1 (malic enzyme 1, soluble (NADP-dependent malic enzyme, malate oxidoreductase, EC 1.1.1.40))
1519	1519 32766_at	OTK27 SSFA1	Z83840	match: proteins; Sw:P12956	non-histone chromosome protein 2 (S. cerevisiae)-like 1
1520	1520 39756 G at	XBP	793930	match: proteins. Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA-292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete	bK292E10.1 (X-box binding protein 1
350	337 30 - 9 - at	- 100	230300	204 2010	<i>"</i>

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ш	bK292E10.1 (X-box binding protein 1 (TREB5))	dJ376D21.1 (Moesin (Membrane-organizing Extension Spike protein))	ribosomal protein L3	C358B7.1 (ubiquitin-conjugating enzyme E2I (homologous to yeast UBC9))	septin 3 small nuclear ribonucleoprotein polypeptide
Q	match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA- 292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete sequence.	match: proteins: Sw:P26038 Tr:O35763 Sw:P26041 Sw:P26042 Sw:P26044 Sw:P35241 Sw:P26043 Sw:P15311 Sw:P31976 Sw:P26040 Tr:O26520 Tr:O24788 Tr:O24796 Tr:O94815; Human DNA sequence from clone 376D21 on chromosome Xq11.1-12 Contains the MSN gene for Moesin (Membrane- organizing Extension Spike protein), ESTs, STSs, GSSs, genomic marker DXS8029 and a putative CpG island, complete sequence.	match: proteins: Sw:P39023 Sw:O16797 Sw:P21531 Sw:P39872 Sw:P27659 Sw:Q92901 Sw:P49149 Sw:P22738 Sw:P35684 Sw:P17094 Wp:CE05598	match: proteins: Sw:P50550 Sw:O09181 Tr:O62622 Sw:P40984 Sw:P50623 Tr:O42551 Tr:O24240 Tr:Q42973 Sw:P52478 Sw:Q02159 Sw:P15732 Sw:C00102 Tr:O76542 Sw:P27949 Sw:P49427 Tr:O17424 Sw:P25867	match: proteins: Sw:Q12772 Sw:Q60429 Sw:P36956 Sw:Q60416 Tr:O15352 match: proteins: Sw:Q28038 Sw:Q16674
C	Z93930	298946	AL022326	AL031714	299716
8	XBP1	MSN	RPL3	UBE21	bK250D10.3
A	1521 39755_at	1522 40771_at	1523 31722_at	1524 33136_at	1525 36607_at
	1521	1522	1523	1524	1525

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				match: proteins: Tr:O54791 Sw:Q90595	
				Sw. 061827 Sw. 090596 Tr. 054790	
				Tr:O15525 Sw:Q90889 Tr:O73679	
1527	1527 36711_at	HS506A DKFZP5 AL021977	AL021977		chromosome 22 open reading frame 5
1528	1528 39561 at	DNAL4	AL008583		chromobox homolog 6
				Tr:Q9QYC8 Tr:Q9WUZ9 Tr:O70214	dJ738P15.2 (CD39-like 2 (a nucleoside
1529	1529 39876 at	dJ738P15.1	AL035252	Tr:Q9QYC9	phosphatase))
				match: proteins: Tr:094136 Sw:Q99798	
				Sw:P49609 Sw:P20004 Sw:P16276	dJ347H13.1 (aconitase 2, mitochondrial
			•	Tr:075809 Tr:074699 Wp:CE00516	(Aconitate Hydratase, EC 4.2.1.3, Citrate
1530	1530 37189 at	ACO2	AL023553	Sw.P19414 Tr.O75944 Sw.O13966	Hydrolyase))
				match: proteins: Tr:P70386 Sw:Q02527	
1531	1531 41235_at	TAXREB67 TXRE	XRE AL022312	Sw:Q10470 Sw:Q09327	activating transcription factor 4
					dJ117516.1 (Ras inhibitor JC265 (Ras
				match: proteins: Tr:Q00425 Sw:Q13671	association (RalGDS/AF-6) domain
1532	1532 36550 at	dJ1175l6.1	AL049538	Tr:O15010 Tr:P97680	containing protein))
				match: proteins: Tr:Q14621 Tr:Q64012	
				Sw:P07910 Sw:P19600 Tr:O60812	RNA-binding protein (autoantigenic) long
1533	1533 39368 at	P542	AL031668	Sw:Q14011 Sw:P26686	isoform
				match: proteins: Tr:Q9Y3M0 Tr:Q9WU14	
1534	1534 33821 at	dJ483K16.1	AL034374	Sw:P39540 Tr:Q9Y396	dJ483K16.1.1 (novel protein (isoform 1))
1535	1535 39029 at	G10	U11861	maternal G10 transcript	matemal G10 transcript
1536	1536 35145 at	MNT	X96401	MAX binding protein	ROX protein
					MAX interacting protein 1, isoform a; MAX
1537	1537 39072 at	MX!1	L07648	MAX interacting protein 1	interacting protein 1, isoform b
					MAX interacting protein 1, isoform a; MAX
1538	1538 654_at	MXI1	L07648	MAX interacting protein 1	interacting protein 1, isoform b
				MCM2 minichromosome maintenance	
1539	1539 35312_at	MCM2	D21063	deficient 2, mitotin (S. cerevisiae)	
				MCM3 minichromosome maintenance	
			-	deficient 3 (S. cerevisiae) associated	
1540	1540 40469_at	MCM3AP	AB011144	protein	KIAA0572 protein

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				MCM6 minichromosome maintenance	
				deficient 6 (MIS5 homolog, S. pombe) (S.	
1541	1541 40117_at	MCM6	D84557	\neg	HsMcm6
				Meis1, myeloid ecotropic viral integration	
1542	1542 41388_at	MEIS2	AF017418		homeobox protein MEIS2
				Meis1, myeloid ecotropic viral integration	
1543	1543 37486_f_at	MEIS3	U68385	site 1 homolog 3 (mouse)	Meis1-related protein 2
				mel transforming oncogene (derived from	
1544	1544 35340_at	MEL	AI819948	cell line NK14)- RAB8 homolog	
				melanoma antigen, family A, 2, copy a;	
				similar to GenBank Accession Number	
1545	1545 36500_at	MAGEA2A	AF027974	L18920	melanoma antigen family A2a
1546	1546 41139_at	MAGED1	W26633	melanoma antigen, family D, 1	
1547	1547 39327_at	D2S448	D86983	Melanoma associated gene	
				membrane cofactor protein (CD46,	membrane cofactor protein (CD46,
				trophoblast-fymphocyte cross-reactive	trophoblast-lymphocyte cross-reactive
1548	1548 38441_s_at	MCP	X59408	antigen)	antigen)
				membrane component, chromosome 11,	
1549	1549 39471_at	M11S1	248042	surface marker 1	GPI-anchored protein p137
				membrane component, chromosome 17,	
		-		surface marker 2 (ovarian carcinoma	membrane component, chromosome 17,
1550	1550 33444_at	M17S2	D30756	antigen CA125)	surface marker 2
				membrane metallo-endopeptidase	
				(neutral endopeptidase, enkephalinase,	
1551	1551 1389_at	MME	J03779	CALLA, CD10)	membrane metallo-endopeptidase
				mesenchyme homeo box 2 (growth arrest-	
1552	552 40399_r_at	MEOX2	AI743406	specific homeo box)	
				Met at bp 326 also used as initiation	
				codon in vitro; Met at bp 248 also used as	
				initiation codon in vitro; Homo sapiens	_
			-	porin (por) mRNA, complete cds and	
1553	1553 37697_s_at	por	L08666	truncated cds.	porin
1554	1554 40244 s at	MPPE1	AI743654	metallo phosphoesterase	

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				gene; H.sapiens onein and	
1555	1555 31975_at			ement.	metallolinonelli
1556	1556 39081_at	MT2A	8		
1557	1557 38945_at	MTF1	X78710	ption factor 1	metal-regulatory transcription factor
1558	1558 1643 g_at	MTA1	U35113		metastasis associated protein
1559	1559 35642_at	MTX2	AF053551		metaxin 2
1560	1560 39342 at	MARS	X94754	methionine-tRNA synthetase	yeast methionyl-tRNA synthetase homolog
1561	1561 37619 at	METAP1	D42084		
1562	41828_at	MBD1	Y10746		methyl-CpG binding protein
1563	1563 33905_at	MBD2	AF072242		methyl-CpG binding protein MBD2
1564	34386_at	MBD4	AF072250	methyt-CpG binding domain protein 4	methyl-CpG binding protein MBD4
		·		methylene tetrahydrofolate	methylene tetrahydrofolate dehydrogenase
		į			(NAD+ dependent), methenyitetrahydrotolate
156	1565 40074_at	MTHFD2	X16396	methenyitetranydrofolate cyclonydrofase	cyclonydrolase, precursor
				methylenetetrahydrofolate dehydrogenase methylenetetrahydrofolate dehydrogenase	methylenetetrahydrofolate dehydrogenase
				(NADP+ dependent),	(NADP+ dependent),
				methenyttetrahydrofolate cyclohydrolase,	methenyltetrahydrofolate cyclohydrolase,
1566	5 674_g_at	MTHFD1	J04031	formyttetrahydrofolate synthetase	formyltetrahydrofolate synthetase
156	1567 40105_at	MUT	M65131	methylmalonyl Coenzyme A mutase	methylmalonyl-CoA mutase
				MHC class I chain related gene B; cDNA	
				sequence deposited under GenBank	
				Accession Number X91625; Human MHC	
_			*	class I molecule (MICB) gene, complete	
156	1568 35937_at	MICB	U65416	cds.	MHC class I molecule
156	1569 36535 at	MFAP1	U04209	microfibrillar-associated protein 1	associated microfibrillar protein
				microphthalmia-associated transcription	A-type microphthalmia associated
157	1570 38228 g_at	MITF	AB006909	factor	transcription factor
157	1571 820_at	MGST2	U77604	microsomal glutathione S-transferase 2	microsomal glutathione S-transferase 2
157	1572 38704_at	MACF1	AB007934	microtubule-actin crosslinking factor 1	KIAA0465 protein
157	1573 35917_at	MAP1A	W26631	microtubule-associated protein 1A	
157	1574 33850_at	MAP4	W28892	microtubule-associated protein 4	

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				ciated protein, RP/EB	
1575	1575 33456_at	MAPRE1	U24166		E81
				microtubule-associated proteins 1A/1B	
1576	1576 39370_at	MAP1A/1BLC3	W28807		
1577	1577 34296_at	MID1	AF041210		midline 1 fetal kidney isoform 3
1578	1578 34403_at	MFGE8	U58516		BA46
				mitochondrial ATP synthase regulatory	
1579	1579 40027_at	ATPW	W52999	component factor B	
1580	1580 37174_at	MRPL19	D14660		mitochondrial ribosomal protein L19
1581	37726 at	MRPL3	X06323		mitochondrial ribosomal protein L3
1582	1582 39717 g at	MRPL33	AI597616	mitochondrial ribosomal protein L33	
1583	1583 32221 at	MRPS18B	AL050361	mitochondrial ribosomal protein S18B	mitochondrial ribosomal protein S18B
1584	1584 38899 s at	MFN1	U95822		putative transmembrane GTPase
1585	1585 34369 at	MFN2	D86987	mitofusin 2	KIAA0214 protein
1586	36577 at	MIG2	Z24725	mitogen inducible 2	mitogen inducible gene mig-2
1587	1587 37733 at	MAPK14	L35263	mitogen-activated protein kinase 14	CSaids binding protein
1588	1588 36926 at	MAPK6	X80692	mitogen-activated protein kinase 6	p97mapk
1589	1589 38431 at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1590	1590 1238_at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1591	1591 1130_at	MAP2K1	L11284	mitogen-activated protein kinase kinase 1	mitogen-activated protein kinase kinase 1
L				mitogen-activated protein kinase kinase	
1592	1592 1327_s_at	MAP3K5	U67156	kinase 5	mitogen-activated kinase kinase kinase 5
				mitogen-activated protein kinase kinase	
1593	1593 36905_at	MAP3K7	AB009356	kinase 7	I GF-beta activated Kinase 1a
				mitogen-activated protein kinase kinase	
1594	1594 38980_at	MAP3K7IP2	AB018276	kinase 7 interacting protein 2	KIAA0733 protein
				mitogen-activated protein kinase kinase	
1595	1595 35694_at	MAP4K4	AB014587	kinase kinase 4	KIAA0687 protein
				mitogen-activated protein kinase-activated	
1596	1596 36179_at	MAPKAPK2	U12779	protein kinase 2	MAP kinase activated protein kinase 2
L				mitogen-activated protein kinase-activated	
1597	1597 1637_at	MAPKAPK3	U09578	protein kinase 3	MAPKAP kinase
1598	1598 41220_at	MSF	AB023208	MLL septin-like fusion	KIAA0991 protein
1595	1599 38437_at	MLN51	X80199	MLN51 protein	MLN51 protein

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				MMS19-like (MET18 homolog, S.	
1600	1600 35273_at	MMS19L	AF007151	сегеvisiае)	MMS19 (MET18 S. cerevisiae)-like
1601	1601 34767_at	MAP-1	Al670788	modulator of apoptosis 1	
1602	1602 41771_g_at	MAOA	AA420624	monoamine oxidase A	
1603	1603 41772_at	MAOA	M68840	monoamine oxidase A	monoamine oxidase A
1604	1604 41770 at	MAOA	AA420624	monoamine oxidase A	
1605	1605 37628 at	MAOB	M69177	monoamine oxidase B	monoamine oxidase B
				ige differentiation-	monocyte to macrophage differentiation-
1606	1606 37565_at	MMD	X85750		associated, precursor
1607	1607 40861 at	MRGX	D14812	MORF-related gene X	MORF-related gene X
				M-phase phosphoprotein 10 (U3 small	
1608	1608 33797_at	MPHOSPH10	X98494	nucleolar ribonucleoprotein)	M phase phosphoprotein 10
1609	1609 34306_at	MBNL	AB007888	muscleblind-like (Drosophila)	muscleblind (Drosophila)-like
1610	1610 35992_at	MSC	AF087036	musculin (activated B-cell factor-1)	musculin
1611	1611 31884_at	MLH3	L40399	mutL homolog 3 (E. coli)	mutL homolog 3
				mutS homolog 2, colon cancer,	
1612	1612 860_at	MSH2	U03911	nonpolyposis type 1 (E. coli)	mutS homolog 2
1613	1613 2003 s at	MSH6	U28946	mutS homolog 6 (E. coli)	G/T mismatch binding protein
1614	1614 33769 at	MPZL1	AF087020	myelin protein zero-like 1	protein zero related protein
				myeloid cell leukemia sequence 1 (BCL2-	myeloid cell leukemia sequence 1 (BCL2-
1615	33146_at	MCL1	L08246	related)	related)
				myeloid cell leukemia sequence 1 (BCL2-	myeloid cell leukemia sequence 1 (BCL2-
1616	1616 277_at	MCL1	L08246	related)	related)
L				myeloid/lymphoid or mixed-lineage	myeloid/lymphoid or mixed-lineage leukemia
				leukemia (trithorax homolog, Drosophila);	(trithorax homolog, Drosophila); translocated
1617	1617 39037_at	MLLT2	L13773	transfocated to, 2	to, 2
1618	1618 41637_at	MYLE	AF108145	MYLE protein	DEXI
1619	1619 41439_at	MYO1B	AJ001381	myosin IB	myh-1c
1620	1620 35729_at	MYO1D	AB018270	myosin ID	KIAA0727 protein
1621	37631_at	MYO1E	U14391	myosin IE	myosin-IC
1622	1622 38251_at	MLC1SA	AI127424	myosin light chain 1 slow a	
1623	۱ ۱	MLC-B	U26162	myosin regulatory light chain	Imyosin regulatory light chain
1624	35362_at	MYO10	AB018342	myosin X	KIAA0799 protein
100	10 2047 01	a) M	VE4304	myosin, light polypeptide, regulatory, non-	myosin, light polypeptide, regulatory, non- sarcomeric (20kD)
300	35730 of	MTMD2	ABOOSEO	myntinhilarin related protein 3	myotirbilarin ralated protein 3
1020	1626 33/39_8(MIMIN	ADVICTOR	Illyotubulatili Tokatod protein o	injoing polatical process

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1	A	æ	S		١
1627 39707	39707_at	MTMR4	AB014547		KIAA0647 protein
1628	1628 38035_at	MTMR6	AF072928	myotubularin related protein 6	myotubularin related protein 6
16291	1629 39607_at	MTMR8	AL080178	myotubularin related protein 8	hypothetical protein
1630	1630 36692_at	MTMR8	AF052099	myotubularin related protein 8	
				myristoylated alanine-rich protein kinase C	
183	1631 32434_at	MARCKS	D10522	substrate	80K-L protein
1632	1632 39267 at	AGM1	AF102265	N-acetylglucosamine-phosphate mutase	N-acetylglucosamine-phosphate mutase
				N-acylsphingosine amidohydrolase (acid	
1633	1633 36938 at	ASAH	U70063	ceramidase)	acid ceramidase
				N-acylsphingosine amidohydrolase (acid	
1634	1634 461_at	ASAH	U70063	ceramidase)	acid ceramidase
				NADH dehydrogenase (ubiquinone) 1	
1635	1635 36169_at	NDUFA1	N47307	alpha subcomplex, 1 (7.5kD, MWFE)	
				NADH dehydrogenase (ubiquinone) 1	NADH-ubiquinone oxidoreductase subunit CII
1636	1636 40546_s_at	NDUFA2	AF047185	alpha subcomplex, 2 (8kD, B8)	B8
				NADH dehydrogenase (ubiquinone) 1	NADPH:ubiquinone oxidoreductase subunit
1637	1637 38462_at	NDUFAS	U64028	alpha subcomplex, 5 (13kD, B13)	B13
				NADH dehydrogenase (ubiquinone) 1	
1638	1638 32752_at	NDUFA7	W72440	alpha subcomplex, 7 (14.5kD, B14.5a)	
				NADH dehydrogenase (ubiquinone) 1 beta	
1639	1639 38605_at	NDUFB1	AI345944	subcomplex, 1 (7kD, MNLL)	
				NADH dehydrogenase (ubiquinone) 1 beta	
1640	1640 38981_at	NDUFB3	AA203354	subcomplex, 3 (12kD, B12)	
				NADH dehydrogenase (ubiquinone) 1 beta	NADH dehydrogenase (ubiquinone) 1 beta NADH-ubiquinone oxidoreductase subunit CI
1641	1641 32232_at	NDUFBS	AF047181	subcomplex, 5 (16kD, SGDH)	SGDH
	_			NADH dehydrogenase (ubiquinone) 1 beta	
1642	1642 32774_at	NDUFB8	AI541050	subcomplex, 8 (19kD, ASHI)	
				NADH dehydrogenase (ubiquinone) 1,	
1643	1643 38485_at	NDUFC1	AA760866	subcomplex unknown, 1 (6kD, KFYI)	
				NADH dehydrogenase (ubiquinone) Fe-S	
				protein 1 (75kD) (NADH-coenzyme Q	75 kDa subunit NADH dehydrogenase
1644	1644 38395_at	NDUFS1	X61100	reductase)	precursor
				NADH dehydrogenase (ubiquinone) Fe-S	
1645	1645 38695 at	NDUESA	AA203303	protein 4 (18kD) (INADA-coenzyme G reductase)	
}	12-0000	1000	22222	,	

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9		В	ر		
- 070				NADH dehydrogenase (ubiquinone) Fe-S	
Š	1646 38060 at	NDUFS5	A 541336	protein 5 (15kD) (NADR-coetzyme Greductase)	
				NADH dehydrogenase (ubiquinone)	
1647 3	1647 34893_at	NDUFV2	AI557064	flavoprotein 2 (24kD)	
-				natriuretic peptide receptor C/guanylate	
				cyclase C (atrionatriuretic peptide receptor	
16483	1648 34519_at	NPR3	M59305	_	atrial natriuretic peptide clearance receptor
				3	
1649	1649 34234_f_at	NKTR	AI688640	sognition sequence	
1650 41795	1795_at	NCK1	X17576		NCK adaptor protein 1
1651 33	33357_at	NCKAP1	AB011159	NCK-associated protein 1	KIAA0587 protein
1652 36073	6073_at	NON	U35139	necdin homolog (mouse)	NECDIN related protein
1653 34202	4202_at	DKFZP566B0846	AL050071	nectin 3	hypothetical protein
1654 34264	4264_at	NESCA	AB026894	nesca protein	NESCA
16553	1655 38719_at	NSF	U03985	N-ethylmaleimide-sensitive factor	N-ethylmaleimide-sensitive factor
				neural precursor cell expressed,	
16563	1656 39356_at	NEDD4L	AB007899	developmentally down-regulated 4-like	ubiquitin-protein ligase NEDD4-like
H					neural precursor cell expressed,
1657 40281	10281_at	NEDDS	D63878	developmentally down-regulated 5	developmentally down-regulated 5
				neural precursor cell expressed,	
1658 1695	1695_at	NEDD8	D23662	developmentally down-regulated 8	ubiquitin-like protein
-	 			neuroblastoma, suppression of	neuroblastoma, suppression of
1659 37005	37005_at	NBL1	D28124		tumorigenicity 1
16603	1660 31896_at	NAG	AL050281	neuroblastoma-amplified protein	hypothetical protein
16613	1661 37286_at	NHCAM	AB002341	neuronal cell adhesion molecule	neuronal cell adhesion molecule
				neutral sphingomyelinase (N-SMase)	
16623	1662 37673_at	NSMAF	X96586	activation associated factor	FAN protein
				NGFI-A binding protein 1 (EGR1 binding	
16633	1663 38692_at	NAB1	AF045451	protein 1)	transcriptional regulatory protein p54
16643	1664 34835_at	NCSTN	D87442	nicastrin	
16653	1665 37032_at	NNMT	U08021	nicotinamide N-methyltransferase	nicotinamide N-methyltransferase
, 000,	10027	FINA	007071		Coordinate of the colour objection
000	1000 41/22 al	INIM	040430	mcomamue nacieonae nanshyangenase	III.COIII IAITII GE II GLEGOLI GE II SII Y CI GOLI IAITII GE II GLEGOLI GE II SII Y CI GOLI GE II GE I
1667	1667 35366_at	QIN	M30269	nidogen (enactin)	nidogen
1668 753_at	753_at	NID2	D86425	nidogen 2	osteonidogen

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		2	3		Micmon Dick O disease profein
1669 37047	7047_at	LOAN	AFOUZUZU	Niemann-Pick disease, type C1	Melitaliii-Fich C disease ploteiii
1670 980_at	80_at	NPC1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1671 3	1671 39345_at	NPC2	AI525834	Niemann-Pick disease, type C2	
16723	1672 35153_at	NBS1	AF058696	Nijmegen breakage syndrome 1 (nibrin)	cell cycle regulatory protein p95
				NIMA (never in mitosis gene a)-related	
1673	1673 36047_at	NEK1	AL050385	kinase 1	
16743	1674 35843 at	Nek8	L40402	NIMA-related kinase Nek8	
1675 4	1675 40866_at	NIPSNAP1	AJ001258	nipsnap homolog 1 (C. elegans)	NIPSNAP1 protein
16763	1676 33916_at	NISCH	AB023192	nischarin	KIAA0975 protein
16773	1677 39165_at	NIFU	U47101	nitrogen fixation cluster-like	NitU-like protein
16783	1678 36472_at	IMN	U32849	N-myc (and STAT) interactor	Nmi
1679 36933	6933_at	NDRG1	D87953	N-myc downstream regulated gene 1	RTP
1680 41656	1656_at	NMT2	AF043325	N-myristoyftransferase 2	N-myristoyttransferase 2
				non-canonical ubquitin conjugating	
1681	1681 39040_at	NCUBE1	W28360	enzyme 1	
				non-canonical ubquitin conjugating	
16823	1682 39039_s_at	NCUBE1	AI557497	enzyme 1	
				non-metastatic cells 1, protein (NM23A)	
1683 1	1683 1521_at	NME1	X17620	expressed in	Nm23 protein
				non-metastatic cells 2, protein (NM23B)	
16843	1684 33415_at	NME2	X58965	expressed in	NM23-H2 protein
				non-metastatic cells 2, protein (NM23B)	
1685	1685 1980_s_at	NME2	X58965	expressed in	NM23-H2 protein
				non-POU domain containing, octamer-	
16863	1686 38527_at	ONON	U02493	binding	54 kDa protein
1687	1687 38750_at	NOTCH3	U97669	Notch homolog 3 (Drosophila)	Notch3
1688	1688 34781_at	WS-3	D84145	novel RGD-containing protein	novel RGD-containing protein
1689	1689 40122 at	NSAP1	AF037448	NS1-associated protein 1	Gry-rbp
1690	1690 33752 at	NS1-BP	AB020657	NS1-binding protein	KIAA0850 protein
				N-sulfoglucosamine sulfohydrolase	
1691	1691 35626_at	SGSH	U30894	(sulfamidase)	N-sulphoglucosamine sulphohydrolase
1692	37352_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1693	1693 37353_g_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1694 40901	ו ו	GS2NA	U17989	nuclear autoantigen	GSZNA
1695	1695 32789 at	NCBP2	AA149428	nuclear cap binding protein subunit 2, 20kD	
	- CO - CI	2.001	22.01.10.7		

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				listribution gene C homolog (A.	istribution ge
1696	1696 35836_at	C	AB019408		homolog
1697	1697 39782_at		X95592	nuclear DNA-binding protein	C1D protein
1698	1698 40063_at	NDP52	U22897	nuclear domain 10 protein	NDP52
1600	1600 853 at	NEE21 2	274017	niclear factor (anthroid-derived 2)-like 2	
				1_	CCAAT/enhancer binding protein (C/EBP),
1700	1700 38354_at	CEBPB; LAP; CRI	CRIX52560		beta
					nuclear factor of activated T-cells,
1701	1701 40822_at	NFATC3	L41067	1	cytoplasmic, calcineurin-dependent 3
				nuclear factor of kappa light polypeptide	
1702	1702 38438_at	NFKB1	M58603	gene enhancer in B-cells 1 (p105)	nuclear factor Kappa-B DINA binding subunit
001,		7071	0000	nuclear factor of kappa light polypeptide	nictor factor Fanna, B DNA hinding cubinnit
1733	1703 1377 at	NFKB1	M58603	gene enhancer in B-cells 1 (p105)	nuciear factor kappa-b DIVA billullig subutili
				nuclear factor of kappa light polypeptide	nuclear factor of kappa light polypeptide
1704	1704 1461_at	NFKBIA	M69043	gene enhancer in B-cells inhibitor, alpha	gene enhancer in B-cells inhibitor, alpha
1705	37544_at	NFIL3	X64318	nuclear factor, interleukin 3 regulated	nuclear factor, interleukin 3 regulated
1706	1706 38648_at	CIZ	080760	nuclear matrix transcription factor 4	CAGH1 alternate open reading frame
				nuclear phosphoprotein similar to S.	
1707	1707 40816_at	PWP1	L07758	cerevisiae PWP1	IEF SSP 9502
1708	1708 34312_at	NCOA2	Ai040324	nuclear receptor coactivator 2	
1709	1709 33381_at	NCOA3	AF012108	nuclear receptor coactivator 3	Amplified in Breast Cancer
1710	1710 39174_at	NCOA4	X77548	nuclear receptor coactivator 4	Ret fused gene
1711	1711 40088_at	NRIP1	X84373	nuclear receptor interacting protein 1	nuclear factor RIP140
				nuclear receptor subfamily 2, group F,	
1712	1712 39397_at	NR2F2	M64497	member 2	apolipoprotein Al regulatory protein-1
				nuclear receptor subfamily 3, group C,	nuclear receptor subfamily 3, group C,
1713	1713 36690_at	NR3C1	M10901	member 1	member 1
1714	1714 35302 at	NXF1	AJ132712	nuclear RNA export factor 1	nuclear RNA export factor 1
1715	1715 37928_at	NFYB	AA621555	nuclear transcription factor Y, beta	
				nuclear transcription factor, X-box binding	
126	1716 34667_at	NFX1	U15306		NFX1
		ī		nuclear; Homo sapiens tyrosine	
	1717 33413_at	PRL-1	AF051160	phosphatase (PRL-1) gene, complete cds. tyrosine phosphatase	lyrosine phosphatase

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1718	1718 32340 s. at	NSEP1	M85234	nuclease sensitive element binding protein	nuclease sensitive element binding protein-1
1719	1719 35643 at	NUCB2	X76732	nucleobindin 2	NEFA protein
					udo
1720	1720 36597_at	NOLC1	D21262	Spriprotein	
1721	1721 37520_at	HSA6591	AJ006591	rich protein	cysteine-rich protein
1722	1722 36930_at	HUMAUANTIG	L05425	nucleolar GTPase	nucleolar GTPase
1723	39390_at	NUP133	AF052123	nucleoporin 133kD	
1724	1724 32850_at	NUP153	Z25535	nucleoporin 153kD	nuclear pore complex protein hnup153
1725	1725 39024 at	NUP98	AF042357	nucleoponin 98kD	
1726	1726 571_at	NAP1L1	M86667	nucleosome assembly protein 1-like 1	nucleosome assembly protein 1-like 1
1727	1727 743_at	NAP1L3	D50370	nucleosome assembly protein 1-like 3	nucleosome assembly protein
1728	1728 32575 at	NAP1L4	U77456	nucleosome assembly protein 1-like 4	nucleosome assembly protein 2
1729	1729 36127 g_at	NBP	U18919	nucleotide binding protein	nucleotide binding protein
				nudix (nucleoside diphosphate linked	diphosphoinositol polyphosphate
1730	1730 41584 at	NUDT3	AF062529	moiety X)-type motif 3	phosphohydrolase
1731	1731 37693 at	NUMB	L40393	numb homolog (Drosophila)	numb homolog
				ob15e02.s1 NCI_CGAP_Kid3 Homo	
				sapiens cDNA clone IMAGE:1323770 3'	
_				similar to SW:ROA3_HUMAN P51991	
				HETEROGENEOUS NUCLEAR	
				RIBONUCLEOPROTEIN A3;, mRNA	
1732	1732 35916_s_at	INHBC	AA877215	sequence.	
1733	1733 34169 s at	OCRL	U57627	oculocerebrorenal syndrome of Lowe	ocn11
				offactory receptor; Human offactory	
1734	1734 31921_at	OLF3	U56421	receptor (OLF3) gene, complete cds.	HsOLF3
				O-linked N-acetylglucosamine (GlcNAc)	
				transferase (UDP-N-	
				acetylglucosamine:polypeptide-N-	
1735	1735 39507 at	OGT	AL050366	acetylglucosaminyl transferase)	hypothetical protein
1736	40332 at	OGFR	AF109134	opioid growth factor receptor	09-InC
1737	1737 39745 at	OPA1	AB011139	optic atrophy 1 (autosomal dominant)	KIAA0567 protein
1738	1738 41744 at	OPTN	AF070533	optineurin	optineurin
				OR11-3; offactory receptor; Homo sapiens	
				OR7E12P pseudogene, complete	
1739	1739 34539_at	OR7E12P	AF065854	sequence.	

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_	4	В	ပ	Q	ı
T					7,8-diamino-pelargonic acid
1740	1740 AFFX-BioC-3 at bioA	bioA	J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1741	1741 AFFX-BioB-M atbioA	-	J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1742	1742 AFFX-BioDn-5 abioA	bioA	J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1743	1743 AFFX-BioDn-3 abioA	bioA	J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1744	1744 AFFX-BioC-5 at bioA	bioA	J04423	ORF 1	aminotransferase
				ORF; putative; Human ribosomal protein	
1745	1745 32412 at	RPS14	M13934 °	S14 gene, complete cds.	unknown protein; ribosomal protein S14
				ORF1; ORF 2; no start codon; Human	
				mRNA for ornithine decarboxylase	
1746	1746 1315 at	OAZ1	D78361	antizyme, ORF 1 and ORF 2.	ornithine decarboxylase antizyme 1
				Topic of the second of the sec	
				OFF-2, OFF-3, nullian retinion A receptor	adula vocantar olpha
1747	1747 32800_at	RXRA; NR2B1	N66306	aipha mHNA, 3' U I H, partial sequence.	relinoid A receptor, alpha
				origin recognition complex, subunit 5-like	ongin recognition complex suburing
1748	1748 38155_at	OHCSL	U92538	(yeast)	Sololion
				ornithine aminotransferase (gyrate	
1749	1749 36636_at	OAT	M12267	atrophy)	ornithine aminotransferase
					zojididi omizita
1750	1750 1959_at	OAZIN	U886/4	סרווווחווו מפרכמו של אינו אינו אינו אינו אינו אינו אינו אינו	
1751	1751 33367 s. at	OAZIN	D88674	omithine decarboxylase antizyme inhibitor antizyme inhibitor	antizyme inhibitor
		1	,	ornithine decarboxylase; Human ornithine	t cooperation
1752	1752 1081_at	ODC1	M33764	decarboxylase gene, complete cds.	ornithine decarboxylase i
				orphan G protein-coupled receptor; Homo	.*
1753	1753 31700 at	GPR35	AF027957	(GPR35) gene, complete cds.	G protein-coupled receptor
1754	1754 1451_s_at	OSF-2	D13666	osteoblast specific factor 2 (fasciclin I-like) osteoblast specific factor 2	osteoblast specific factor 2
175E	1766 3977/ 81	OXA1	XAO695	oxidase (cytochrome c) assembly 1-like	oxidase (cytochrome c) assembly 1-like
3	103/14 at	SAMIL	20000		

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00/-	1/56 39136_at		AB01/642		oxidative-stress responsive i
1757	1757 41438_at	L8	AL049923		oxysterol-binding protein-like protein 8
1758	1758 34329_at		N25547	p21 (CDKN1A)-activated kinase 2	
1759	1759 39710_at	P311	U30521	P311 protein	P311 HUM
1760	1760 36136_at		AF010315		Pig11
1761	40441_g_at	PAI-RBP1	AL080119	PAI-1 mRNA-binding protein	hypothetical protein
1762	1762 40440_at	PAI-RBP1	AL080119		hypothetical protein
1763	1763 32001 s at	PACE4	M80482	paired basic amino acid cleaving system 4 subtilisin-like protease	subtilisin-like protease
					paired box gene 8, isoform PAX8A; paired
					box gene 8, isoform PAX8B; paired box
					gene 8, isoform PAX8C; paired box gene 8,
					isoform PAX8D; paired box gene 8, isoform
1764	1764 121_at	PAX8	66969X	paired box gene 8	PAX8E
1765	1765 40127_at	PMX1	M95929	paired mesoderm homeo box 1	homeobox protein
1766	1766 41191_at	KIAA0992	AB023209	palladin	KIAA0992 protein
1767	1767 40504_at	PON2	AF001601	paraoxonase 2	paraoxonase
				partially supported by FGENES and	
1768	1768 36032_at	dJ167A19.1	AL031427		hypothetical protein
1769	1769 39243_s_at	PSIP2	U94319	PC4 and SFRS1 interacting protein 2	DFS70
1770	41665_at	PCF11	AB020631	PCF11p homolog	KIAA0824 protein
1771	1771 38758_at	PDAP1	R98910	PDGFA associated protein 1	
1772	1772 36937_s_at	PDLIM1	U90878	PDZ and LIM domain 1 (elfin)	carboxyl terminal LIM domain protein
				PDZ domain containing guanine	PDZ domain containing guanine nucleotide
1773	1773 32026_s_at	PDZ-GEF1	AB002311	nucleotide exchange factor(GEF)1	exchange factor(GEF)1
				PDZ domain containing guanine	
1774	1774 34745_at	PDZ-GEF1	AF070570	nucleotide exchange factor(GEF)1	
				PEDF; Human pigment epithelium-derived	
1775	1775 40856_at	SERPINF1; PEDF	EDF U29953	factor gene, complete cds.	pigment epithelium-derived factor
				pentaxin-related gene, rapidly induced by	
1776	1776 1491_at	PTX3	M31166	IL-1 beta	tumor necrosis factor
				peptidylglycine alpha-amidating	peptidylglycine alpha-amidating
=======================================	1777 38465_at	PAM	M37721	monooxygenase	monooxygenase
1778	1778 35823 at	Bidd	M63573	nentidylmM isomerase B (cyclophilin B)	secreted evelophilin-like protein
	2005 at	20.7.1	NOW!	population is completed by controlled	sociona discominante process

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1779	1779 37422_at	PPIC	S71018	peptidylprolyl isomerase C (cyclophilin C)	cyclophilin C
1780	1780 37385_at	PPIG	U40763	clophilin G)	CARS-Cyp
1781	1781 36829_at	PER1	AF022991		Rigui
1782	1782 35835_at	PDL-108	AB019409	periodontal ligament fibroblast protein	
					peripheral benzodiazapine receptor;
					peripheral benzodiazapine receptor short
1783	1783 32806_at	BZRP; MBR; PBR	PBR M36035	receptor (hpbs) mRNA, complete cds.	form
1784	1784 38653_at	PMP22	D11428	peripheral myelin protein 22	PMP-22(PAS-II/SR13/Gas-3)
1785	1785 41213_at	PRDX1	X67951	peroxiredoxin 1	peroxiredoxin 1
					Aop1_Human, MER5(Aop1_Mouse)-like
1786	1786 36631_at	PRDX3	D49396	peroxiredoxin 3	protein
1787	1787 38435_at	PRDX4	U25182	peroxiredoxin 4	antioxidant enzyme AOE37-2
1788	1788 37900_at	PEX11B	AF093670	peroxisomal biogenesis factor 11B	peroxisomal biogenesis factor
1789	1789 36864_at	PEX3	AJ001625	peroxisomal biogenesis factor 3	Pex3 protein
				peroxisomal long-chain acyl-coA	peroxisomal long-chain acyl-coA
1790	1790 36625_at	ZAP128	L40401	thioesterase	thioesterase
				peroxisomal membrane protein 3 (35kD,	
1791	1791 33265_at	PXMP3	M86852	Zellweger syndrome)	peroxisome assembly factor-1
1792	36502_at	PFTK1	AB020641	PFTAIRE protein kinase 1	KIAA0834 protein
1793	1793 37694_at	PHF3	D87685	PHD finger protein 3	PHD finger protein 3
1794	1794 39381 at	XAP135	AF055030	PHD zinc finder protein XAP135	PHU zinc finger protein XAP135, isoform a; PHD zinc finger protein XAP135, isoform b
		i		phosphatase and tensin homolog	
	1/95 1434_at	Z Z Z	092436	(mutated in mulliple advanced cancers 1)	wilder in the substitution acid phosphatase alpha-
1796	1796 34797_at	PPAP2A	AF014402	phosphatidic acid phosphatase type 2A	the control of the co
1797	1797 33862 at	PPAP2R	AF017786	phosphatidic acid phosphatase type 2B	phosphatidic acid phosphohydrolase homolog
				Inhosphatidylinositol 4-kinasa catalytic	
1798	1798 40783_s_at	PIK4CA	L36151	alpha polypeptide	phosphatidylinositol 4-kinase
1796	1799 37685 at	PICA! M	1145976	phosphatidylinositol binding clathrin	CALM
	m_00010		21222		

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				phosphatidylinositol glycan, class A	•
1800	1800 39993_at	PIGA	D11466	(paroxysmal nocturnal hemoglobinuria)	PIG-A protein
180	1801 314_at	PIGB	D42138	phosphatidylinositol glycan, class B	PIG-B
5	1000 751 04	Jula	D85418	phoenhatit Minosito I nocan class C	phosphatidylinositol-alycan-class C (PIG-C)
3 6	130 -01	200		phocabatichdinocitol ahron clase E	T. Clark
3 3	1003 / / 0_ai	ייטור		phoenhotindinositol alycan, class H	phosphaticklinositol obcan, class H
1804	40029_BI	ב	20/617	prosprieticy in control grycan, crass in	hemologies of Procepties retined decemenation
		:		inster protein,	nomologue of Drospinia remital degeneración
1805	1805 38297_at	PITPNM	X98654		B gene
				phosphatidylinositol-4-phosphate 5-	phosphatidylinositol-4-phosphate 5-kinase
1806	1806 35741_at	PIP5K2B	U85245	kinase, type II, beta	type II beta
1807	1807 37320_at	PTDSS1	D14694	phosphatidylserine synthase 1	phosphatidylserine synthase 1
				phosphodiesterase 4B, cAMP-specific	
				(phosphodiesterase E4 dunce homolog,	-
1808	1808 33705_at	PDE4B	120971	Drosophila)	phosphodiesterase
				phosphodiesterase 4D interacting protein	
1809	1809 39422_at	PDE4DIP	AB007923	(myomegalin)	KIAA0454 protein
1810	1810 37676_at	PDE8A	AF056490	phosphodiesterase 8A	cAMP-specific phosphodiesterase 8A
				phosphoenolpyruvate carboxykinase 2	
1811	1811 37188_at	PCK2	X92720	(mitochondrial)	phosphoenolpyruvate carboxykinase (GTP)
1812	39175 at	PFKP	D25328	phosphofructokinase, platelet	platelet-type phosphofructokinase
1813	32210 at	PGM1	M83088	phosphoglucomutase 1	phosphoglucomutase 1
1814	1814 36963 at	PGD	U30255	phosphogluconate dehydrogenase	phosphogluconate dehydrogenase
1815	37677_at	PGK1	V00572	phosphoglycerate kinase 1	phosphoglycerate kinase 1
1816	41221	PGAM1	J04173	phosphoglycerate/mutase 1 (brain)	phosphoglycerate mutase 2
1817	35665_at	PIK3C3	246973	phosphoinositide-3-kinase, class 3	phosphatidylinositol 3-kinase
				phosphoinositide-3-kinase, regulatory	
1818	1818 1269_at	PIK3R1	M61906	subunit, polypeptide 1 (p85 alpha)	
				phosphoinositide-3-kinase, regulatory	
1819	1819 37961_at	PIK3R3	1090907	subunit, polypeptide 3 (p55, gamma)	
1820	1820 32775_r_at	PLSCR1	AB006746	phospholipid scramblase 1	phospholipid scramblase 1
1821	1821 32260 at	PEA15	X86809	phosphoprotein enriched in astrocytes 15	
	1			phosphoribosyl pyrophosphate synthetase	phosphoribosyl pyrophosphate synthetase phosphoribosyl pyrophosphate synthetase
1822	1822 36489_at	PRPS1	D00860		subunit 1

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1823	1823 37338 at	PRPSAP1	D61391	osphate synthetase-	phosphoribosypyrophosphate synthetase- associated protein 39
				oimidazole	
					phosphoribosylaminoimida20ie carboxylase,
					prosprioribosylarini loribosylarini lorini dezore
1824	1824 39056_at	PAICS	X53793	tase	succinocarboxamide synthetase
1825	1825 37392_at	PHKB	X84908	phosphorylase kinase, beta	phosphorylase kinase
1826	1826 36667_at	PYGB	U47025	rain	glycogen phosphorylase B
				phytanoyl-CoA hydroxytase (Refsum	peroxisomal phytanoyl-CoA alpha-
1827	1827 32724_at	РНҮН	AF023462		hydroxylase
1828	1828 33543_s_at	PNN	U777718	pinin, desmosome associated protein	pinin
				pituitary tumor-transforming 1 interacting	
1829	1829 39003_at	PTTG1IP	Z50022	protein	putative surface glycoprotein
1830	1830 34793_s_at	PLS3	M22299	plastin 3 (T isoform)	T-plastin polypeptide
				platelet-activating factor acetylnydrolase,	
1831	1831 32569_at	PAFAH1B1	L13385	isoform lb, alpha subunit (45kD)	Miller-Dieker lissencephaly protein
				ceptor,	platelet-derived growth factor receptor A
1832	1832 1731 at	PDGFRA	M21574	alpha polypeptide	chain
				pleckstrin homology, Sec7 and coiled/coil	cytohesin 1, isoform 1; cytohesin 1, isoform
1833	1833 38666_at	PSCD1	M85169		2
				pleckstrin homology, Sec7 and coiled/coil	
183 4	1834 38741_at	PSCD2	U70728	domains 2 (cytohesin-2)	cytohesin-2
1835	1835 36943 r_at	PLAGL1	U81992	pleiomorphic adenoma gene-like 1	C2H2 zinc finger protein PLAGL1
1836	1836 34780_at	PLXNB2	AB002313	plexin B2	plexin B2
183	1837 32193_at	PLXNC1	AF030339	plexin C1	VESPR
1838	1838 38270_at	PARG	AF005043	poly (ADP-ribose) glycohydrolase	poly(ADP-ribose) glycohydrolase
1835	1839 31951 s at	PABPC1	Z48501	poly(A) binding protein, cytoplasmic 1	polyadenylate binding protein II
1840	1840 31950_at	PABPC1	Y00345	poly(A) binding protein, cytoplasmic 1	poly(A) binding protein, cytoplasmic 1
				poly(A)-specific ribonuclease	:
184	1841 36003_at	PARN	AJ005698	(deadenylation nuclease)	poly(A)-specific ribonuclease
184	1842 34305_at	PCBP1	Z 29505	poly(rC) binding protein 1	sub2.3
184	1843 35746_r_at	PCBP2	X78136	poly(rC) binding protein 2	hnRNP-E2
<u>184</u>	1844 35745_f_at	PCBP2	X78136	poly(rC) binding protein 2	hnRNP.E2
<u>8</u>	1845 39868_at	PCBP3	AL046394	poly(rC) binding protein 3	

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1846	1846 38120 at	PKD2	1150028	połycystic kidney disease 2 (autosomal	polyovetin 2
		INDE	020320	Colinia idility	polycysum z
1847	1847 33380_at	POLS	AB005754	polymerase (DNA directed) sigma	LAK-1
4040	1040 20702 01	60 50	A 50706 40	polymerase (DNA directed), epsilon 3	polymerase (DNA directed), epsilon 3 (p17
	30/05 al	ביים	Aro/0040	(p) / subutility	Subulity
				polymerase (RNA) II (DNA directed)	
1849	1849 40791_at	POLRZA	X63564	polypeptide A (220kD)	RNA polymerase II largest subunit
				polymerase (RNA) II (DNA directed)	
1850	1850 39746_at	POLR2B	X63563	polypeptide B (140kD)	RNA polymerase II 140 kDa subunit
				polymerase (RNA) II (DNA directed)	
1851	1851 36027_at	POLR2F	AA418779	polypeptide F	
				polymerase (RNA) II (DNA directed)	
1852	1852 35631_at	POLRZH	U37689	polypeptide H	RNA polymerase II subunit
				polymerase (RNA) II (DNA directed)	
1853	1853 1248_at	POLR2H	U37689	polypeptide H	RNA polymerase II subunit
				polymerase (RNA) II (DNA directed)	
1854	1854 503_at	POLRZL	U37690	polypeptide L (7.6kD)	RNA polymerase II subunit
				polymerase (RNA) II (DNA directed)	
1855	1855 35841_at	POLR2L	N24355	polypeptide L (7.6kD)	
		1		-	
<u>8</u>	1856 34320_at	구도	AL050224	polymerase I and transcript release factor	
1857	1857 34005_at	PIGR	X73079	polymeric immunoglobulin receptor	Polymeric immunoglobulin receptor
1858	1858 40593_at	PTBP1	X66975	polypyrimidine tract binding protein 1	nuclear ribonucleoprotein
1850	1850 31600 c at	DMC214		to di Chasastani na incressation incressationi di liba	
3	2 - S	r INDEL I	2	Common and indication	
			•	pot. ORF1 (aa 1-73); ORF2, put. cre protein (aa 1-343); Bacteriophage P1 cre	*
1860	1860 AFFX-CreX-5_at		X03453	gene for recombinase protein.	
				pot. ORF1 (aa 1-73); ORF2, put. cre	
				protein (aa 1-343); Bacteriophage P1 cre	
1861	1861 AFFX-CreX-3_at		X03453	gene for recombinase protein.	
1862	1862 315_at	PRDM2	D45132	PR domain containing 2, with ZNF domain zinc-finger DNA-binding protein	zinc-finger DNA-binding protein
					•
186	1863 32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3	homeobox protein

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				precursor; Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (PAHR) gene, exon 11. clones 6B-	
1864	1864 36666_at	P4HB	M22806		prolyl 4-hydroxylase beta-subunit
1865		GS3786	D87120	steoblast protein	GS3786
1866		PFDN4	U41816		C-1
1867	1867 38698_at	PREI3	AL080070	ation protein 3	hypothetical protein
1868	1868 40269_at	PRP18	U51990	ctor 18	hPrp18
1860	1860 38301 at	DENK	100123	preproenkephalin (; Human enkephalin	proenkenhelin
1870	1870 641 at	PSEN1	L76517	presentlin 1 (Alzheimer disease 3)	presenilin 1
1871	1871 40621_at	PAWR	U63809	PRKC, apoptosis, WT1, regulator	prostate apoptosis response protein par-4
1872	1872 41773_at	PCOLN3	U58048	procollagen (type III) N-endopeptidase	PRSM1
1873	1873 31609_s_at	PCOLCE	L33799	procollagen C-endopeptidase enhancer	procollagen C-proteinase enhancer protein
				.1	
1874	1874 34795_at	PLOD2	U84573		lysyl hydroxylase isoform 2
				procollagen-lysine, 2-oxoglutarate 5-	
				dioxygenase (lysine hydroxylase, Ehlers-	
1875	1875 36184_at	PLOD	L06419	Danlos syndrome type VI)	lysyl hydroxylase
				procollagen-proline, 2-oxoglutarate 4-	procollagen-proline, 2-oxoglutarate 4-
				dioxygenase (proline 4-hydroxylase),	dioxygenase (proline 4-hydroxylase), alpha
1876	1876 37037_at	P4HA1	M24486	alpha polypeptide I	polypeptide l
				procollagen-proline, 2-oxoglutarate 4-	
				dioxygenase (proline 4-hydroxylase),	
1877	1877 34390_at	P4HA2	U90441	alpha polypeptide II	prolyl 4-hydroxylase alpha (II) subunit
				procollagen-proline, 2-oxoglutarate 4-	procollagen-proline, 2-oxoglutarate 4-
				dioxygenase (proline 4-hydroxylase), beta	dioxygenase (proline 4-hydroxylase), beta
				bolypeptide (protein disulfide isomerase;	polypeptide (protein disulfide isomerase;
1878	691 g at	P4HB	J02783	thyroid hormone binding protein p55)	thyroid hormone binding protein p55)
1879	1879 38840 s at	PFN2	L10678	profilin 2	profilin II
1880	1880 38839_at	PFN2	AL096719	profilin 2	profilin 2 isoform b; profilin 2 isoform a
				progesterone receptor membrane	
1881	1881 38802_at	PGRMC1	Y12711	component 1	putative progesterone binding protein
1882	1882 38821 at	PGRMC2	AJ002030	progesterone receptor membrane component 2	progresterone binding protein
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1883	1883 39035_at	DDS	AF006010	progestin induced protein	progestin induced protein
1884	1884 39036_g_at	DDS	AF006010	progestin induced protein	progestin induced protein
1885	1885 35218_at	PDCD10	AF022385	programmed cell death 10	TFAR15
1886	1886 37569_at	PDCD6	AF035606	programmed cell death 6	calcium binding protein
				programmed cell death 8 (apoptosis-	
1887	1887 32212_at	PDCD8	AL049703	inducing factor)	hypothetical protein
1888	1888 36592_at	PHB	S85655	prohibitin	prohibitin
1889	1889 1884_s_at	PCNA	M15796	proliferating cell nuclear antigen	proliferating cell nuclear antigen
1890	1890 41600_at	PA2G4	U59435	proliferation-associated 2G4, 38kD	cell cycle protein p38-2G4 homolog
				proline-rich Gla (G-carboxyglutamic acid)	
1891	1891 35978_at	PRRG1	AF009242	polypeptide 1	proline-rich Gla protein 1
1892	1892 36023_at	PRH1	AI864120	proline-rich protein HaellI subfamily 1	
				pro-oncosis receptor inducing membrane	pro-oncosis receptor inducing membrane
1893	1893 40803_at	PORIMIN	AL050161	injury gene	injury gene
				propionyl Coenzyme A carboxylase, alpha	Propionyl-Coenzyme A carboxylase, alpha
1894	1894 1348_s_at	PCCA	S79219	polypeptide	polypeptide precursor
				propionyl Coenzyme A carboxylase, beta	
1895	1895 36561_at	PCCB	X73424	polypeptide	propionyl-CoA carboxylase
1000	11000	ansou	7000311	proprotein convertase subtilisir/kexin type	De inform
1836	1896 41032_at	PCSKS	U2638/	G	protease Poo Isolorm A
				prosaposin (variant Gaucher disease and	prosaposin (variant Gaucher disease and
1897	1897 36795_at	PSAP	J03077	variant metachromatic leukodystrophy)	variant metachromatic leukodystrophy)
,	1 7 00100	00010	0702001	(right Cyte) confirm of riberthese	
202	103030400_1_81	1 GD3	AICU/046	procted and in Erocenter 2 (subtana EP2)	
1899	1899 828_at	PTGER2	U19487	53kD	prostaglandin E2 receptor
1900	1890_at	PLAB	AB000584	prostate differentiation factor	TGF-beta superfamily protein
1901	32611_at	PBP	X75252	prostatic binding protein	phosphatidylethanolamine binding protein
1902	719 g at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
1903	1903 718_at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
1904	33368_at	PRSS15	X76040	protease, serine, 15	Lon protease-like protein
1905	1905 40078_at	SPUVE	AF015287	protease, serine, 23	serine protease
1906	1906 39845_at	PRSS25	AF020760	protease, serine, 25	serine protease
1907	1907 688 at	PSMC1	L02426	proteasome (prosome, macropain) 26S subunit, ATPase, 1	26S protease (S4) regulatory subunit

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400	1908 35353 at	PSMC?	D11094	proteasome (prosome, macropain) 26S subunit. ATPase. 2	MSS1 protein
3	13-0000	7		ma macronain) 26S	professome (prosome, macropain) 26S
1909	1909 Fa2 at	PSMC3	M34079		subunit, ATPase, 3
	15.7			me, macropain) 26S	
1910	1910 37766 s at	PSMC5	AF035309	subunit, ATPase, 5	
				proteasome (prosome, macropain) 26S	
1911	1911 949 s at	PSMC6	D78275	subunit, ATPase, 6	proteasome subunit p42
				proteasome (prosome, macropain) 26S	
1912	1912 1314 at	PSMD1	D44466	subunit, non-ATPase, 1	proteasome subunit p112
				proteasome (prosome, macropain) 26S	
1913	1913 1192 at	PSMD12	AB003103	subunit, non-ATPase, 12	26S proteasome subunit p55
				proteasome (prosome, macropain) 26S	proteasome (prosome, macropain) 26S
1914	1914 32240_at	PSMD5	D31889	subunit, non-ATPase, 5	subunit, non-ATPase, 5
				proteasome (prosome, macropain) 26S	
1915	1915 945_at	PSMD7	D50063	subunit, non-ATPase, 7 (Mov34 homolog) proteasome subunit p40 / Mov34 protein	proteasome subunit p40 / Mov34 protein
				proteasome (prosome, macropain) 26S	
1916	1916 40276_at	PSMD7	D50063	subunit, non-Allese, / (Mov34 nomolog)	proteasome suburit p407 Mov34 protein
				proteasome (prosome, macropain) 26S	
1917	1917 32584_at	PSMD8	D38047	subunit, non-ATPase, 8	26S proteasome subunit p31
				proteasome (prosome, macropain) 26S	
1918	1918 36492_at	PSMD9	AI347155	subunit, non-ATPase, 9	
				proteasome (prosome, macropain)	
1919	41171_at	PSME2	D45248	activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
L				proteasome (prosome, macropain)	
1920	1920 1184 at	PSME2	D45248	activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
				proteasome (prosome, macropain)	
1921	1921 36974 at	PSMF1	D88378	inhibitor subunit 1 (PI31)	proteasome inhibitor hPI31 subunit
				proteasome (prosome, macropain)	
1922	1922 38371 at	PSMA1	M64992	subunit, alpha type, 1	prosomal protein P30-33K
				proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
1923	1923 1446_at	PSMA2	D00760	subunit, alpha type, 2	alpha type, 2
				proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
1924	1924 1448 at	PSMA3	D00762	subunit, alpha type, 3	alpha type, 3



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				, macropain)	proteasome (prosome, macropain) subunit,
1925	1925 1450_g_at	PSMA4	D00763	subunit, alpha type, 4	alpha type, 4
				proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
1926	1926 1449_at	PSMA4	D00763	subunit, alpha type, 4	alpha type, 4
				, macropain)	
1927	1927 37046_at	PSMA5	AI246726	subunit, alpha type, 5	
				e, macropain)	
1928	1928 36122_at	PSMA6	X59417	subunit, alpha type, 6	prosomal P27K protein
				e, macropain)	proteasome (prosome, macropain) subunit,
1929	1929 1447_at	PSMB1	D00761	subunit, beta type, 1	beta type, 1
				me, macropain)	
1930	1930 1310_at	PSMB2	D26599	subunit, beta type, 2	proteasome subunit HsC7-I
				proteasome (prosome, macropain)	
1931	33154_at	PSMB4	D26600	subunit, beta type, 4	proteasome subunit HsN3
				proteasome (prosome, macropain)	
1932	1932 1311_at	PSMB4	D26600	subunit, beta type, 4	proteasome subunit HsN3
				proteasome (prosome, macropain)	
1933	933 37666_at	PSMB5	D29011	subunit, beta type, 5	proteasome subunit X
L				proteasome (prosome, macropain)	
1934	1934 941_at	PSMB6	D29012	subunit, beta type, 6	proteasome subunit Y
				proteasome (prosome, macropain)	
1935	1935 39060_at	PSMB7	D38048	subunit, beta type, 7	proteasome subunit z
				proteasome (prosome, macropain)	
1936	1936 1313_at	PSMB7	D38048	subunit, beta type, 7	proteasome subunit z
				proteasome (prosome, macropain)	
				subunit, beta type, 9 (large multifunctional	
1937	1937 38287_at	PSMB9	AA808961	protease 2)	
	000	i C	0000	SO nominal mindered by common of this will be in the	of the second
Š	141/30_BI	73	U43463	אוויםוטון מוצחווות וואסווווים ואסוווים איים שוויים איים איים איים איים איים איים איים	יותוומוו ר
1935	1939 32558_at	PIAS3	AB021868	protein inhibitor of activated STAT3	protein inhibitor of activatied STAT3
				protein kinase (cAMP-dependent,	
194C	1940 34376_at	PKIG	AB019517	catalytic) inhibitor gamma	protein kinase inhibitor gamma
1941	1941 36957_at	PRKCBP1	W22296	protein kinase C binding protein 1	
1942	1942 1602_at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
1940	1943 1603_g_at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
1944	1944 36835_at	PRKCL2	U33052	protein kinase C-like 2	PRK2

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				cAMP-dependent, I, alpha (tissue specific	cAMP-dependent protein kinase type I-alpha
1945 4	1945 41768_at	PRKAR1A	M33336		subunit
				cAMP-dependent, 1, alpha (tissue specific	cAMP-dependent protein kinase type I-alpha
1 <u>946 2</u>	1946 227_g_at	PRKAR1A	M33336		subunit
				protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific	cAMP-dependent protein kinase type I-alpha
1947 226_at	26_at	PRKAR1A	M33336		subunit
	·			protein kinase, interferon-inducible double protein activator of the interferon-induced	protein activator of the interferon-induced
1948	1948 32205_at	PRKRA	AF072860	stranded RNA dependent activator	protein kinase
				bunit,	serine /threonine specific protein
1949	1949 37725_at	PPP1CC	X74008	gamma isoform	phosphatase
				tase 1, regulatory	
1950	1950 40438_at	PPP1R12A	D87930		myosin phosphatase target subunit 1
	*			protein phosphatase 1, regulatory	
1951	1951 39366_at	PPP1R3C	N36638	(inhibitor) subunit 3C	
				protein phosphatase 1, regulatory subunit	
1952	1952 41540_at	PPP1R7	Z50749	7	yeast sds22.homolog
		*		protein phosphatase 1A (formerly 2C),	
1953	1953 857_at	PPM1A	S87759	magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
				protein phosphatase 1A (formerly 2C),	
1954	1954 36501_at	PPM1A	S87759	magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
				protein phosphatase 1D magnesium-	
1955	1955 37107_at	PPM1D	U78305	dependent, delta isoform	Wip1
				protein phosphatase 2 (formerly 2A),	
1956	1956 924_s_at	PPP2CB	J03805	catalytic subunit, beta isoform	
				protein phosphatase 2 (formerly 2A),	
				regulatory subunit B (PR 52), alpha	
1957	1957 41167_at	PPP2R2A	M64929	isoform	protein phosphatase-2A subunit-alpha
				protein phosphatase 2 (formerly 2A),	•
400	105011000	Acaraga	NACA020	regulatory subdim D (1 to 24), alpina isoform	protein phosphatase-2A subunit-alpha
220	1300 at	rr cncm	MICHOES	Section 1	
1959	1959 32734 at	PPP2RSE	L76703	protein phospnatase 2, regulatory subunit B (B56), epsilon isoform	protein phosphatase B56-epsilon



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				protein phosphatase 2, regulatory subunit	protein phosphatase 2A Balpha1 regulatory
5 8 8	1960 40786_at	PPP2R5C	U37352	B (B56), gamma isoform	subunit
				protein phosphatase 2, regulatory subunit	protein phosphatase 2A B'alpha1 regulatory
1961 176	176_at	PPP2R5C	U37352	B (B56), gamma isoform	subunit
				protein phosphatase 2A, regulatory	
1962	1962 39127_f_at	PPP2R4	X73478	subunit B' (PR 53)	phosphotyrosyl phosphatase activator
				protein phosphatase 3 (formerly 2B),	protein phosphatase 3 (formerly 2B),
				catalytic subunit, beta isoform (calcineurin	catalytic subunit, beta isoform (calcineurin catalytic subunit, beta isoform (calcineurin A
1963	1963 38277_at	PPP3CB	M29550	A beta)	beta)
				protein phosphatase 3 (formerly 2B),	
				catalytic subunit, gamma isoform	
1964	1964 32541_at	PPP3CC	S46622	(calcineurin A gamma)	calcineurin A catalytic subunit
				protein phosphatase 4, regulatory subunit	
1965	1965 34371_at	PPP4R1	U79267		
1066	1066 37581 at	DPDEC	62b6bX	protein phosphatase 6. catalytic subunit	protein phosphatase 6
3	מילים ביי	2000	145000	Fiction (Columnia Columnia Col	protoin C (olinho)
1967	1967 35752 s at	PROSI	MISUSE	protein 3 (alpina)	protein 3 (alpira)
1968	1968 32564_at	SEC61B	AA083129	protein translocation complex beta	
1969	1969 1064_at	PTK9	U02680	protein tyrosine kinase 9	protein tyrosine kinase
				protein tyrosine phosphatase type IVA,	
1970	1970 843_at	PTP4A1	U48296	member 1	protein tyrosine phosphatase PTPCAAX1
				protein tyrosine phosphatase type IVA,	
1971	1971 38415_at	PTP4A2	U14603	member 2	protein-tyrosine phosphatase
				protein tyrosine phosphatase type IVA,	
1972	1972 1241_at	PTP4A2	U14603	member 2	protein-tyrosine phosphatase
				protein tyrosine phosphatase, non-	protein tyrosine phosphatase, non-receptor
1973	1973 40137_at	PTPN1	M31724	receptor type 1	type 1
				protein tyrosine phosphatase, non-	
1974	1974 1463_at	PTPN12	M93425	receptor type 12	protein tyrosine phosphatase
L				protein tyrosine phosphatase, non-	
	0			receptor type 13 (APO-1/CD35 (Fas)-	
1975	34198_at	P1PN13	012128	associated phosphatase)	protein tyrosine phosphatase 1E
					protein tyrosine phosphatase, receptor type,
				rotacoca oratodanoda oriona de riotora	A, isolotti i procuisor, protein (yrosine
1076	107E 149E at	PTPBA	Madees	protein tyrosine priospiratase, receptor	prospiratase, receptor type, A, isolonin z
	1 120 at	\$11.1	DOCUMENT OF THE PROPERTY OF TH	13pc; c	

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ŀ	10000	100 H	Vocate	tyrosine phosphatase, receptor	(1881 of 81- AA) nietongerg AA 1919
	1977 36204_at	FIFRE	100813		pur. Du praprovent (po - 10 to 1001)
				protein tyrosine phosphatase, receptor	
				type, f polypeptide (PTPRF), interacting	
1978	1978 41780_at	PPFIA1	U22816	protein (liprin), alpha 1	LAR-interacting protein 1b
				protein tyrosine phosphatase, receptor	
1979	1979 1488 at	PTPRK	L77886	type, K	protein tyrosine phosphatase
Γ				protein tyrosine phosphatase, receptor	
1980	1980 995_g_at	PTPRM	X58288	уре, М	protein-tyrosine phosphatase
				protein tyrosine phosphatase, receptor	
1981	1981 31892 at	PTPRM	X58288	уре, М	protein-tyrosine phosphatase
				protein-kinase, interferon-inducible double	
				stranded RNA dependent inhibitor,	
1982	1982 41141_at	PRKRIR	AL049970	repressor of (P58 repressor)	hypothetical protein
				protein-L-isoaspartate (D-aspartate) O-	
1983	1983 37737_at	PCMT1	D25547	methyttransferase	PIMT isozyme I
				protein-L-isoaspartate (D-aspartate) O-	
1984	1984 37736_at	PCMT1	D13892	methyttransferase	carboxyi methyltransferase
1985	1985 32227_at	PRG1	X17042	proteoglycan 1, secretory granule	proteoglycan 1, secretory granule
1986	1986 38590 r_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1987	1987 38589 i_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1988	1988 37936_at	HPRP4P	Al184802	PRP4/STK/WD splicing factor	
				pseudoterriin H protein; Human terriin H	
1989	1989 31697_s_at	FTHP1	J04755	processed pseudogene, complete cds.	
1990	1990 36117_at	PTK2	L13616	PTK2 protein tyrosine kinase 2	focal adhesion kinase
1991	1991 40048_at	PUM1	D43951	pumilio homolog 1 (Drosophila)	KIAA0099 protein
1992	1992 35359_at	PUM2	D87078	pumilio homolog 2 (Drosophila)	KIAA0235 protein
1993	1993 35221_at	PURA	X91648	purine-rich element binding protein A	
				put. ORFX (AA 1-75); beta subunit (AA 1-	
				340); Human liver mRNA for beta-subunit	
			-	signal transducing proteins Gs/Gi (beta-	guanine nucleotide-binding protein, beta-1
1994	1994 33341_at	GNB1	X04526	(G).	subunit
1995	1995 33720_at	LOC56902	L48692	putatative 28 kDa protein	
900	1006 30363 21	BC 3	AE042384	putative breast adenocarcinoma marker	BC-2 protein
1330	Joseph al	200	A 012301	(Joens)	

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1997	39884	HSA9761	AF091078	putative dimethyladenosine transferase	putative dimethyladenosine transferase
3	17 17000		10,000,14	٠	putative glialblastoma cell differentiation-
8881	1998 3884 1_Bt	HADA	AFU68195		related protein
1999	1999 41188_at	LC27	W28186	putative integral membrane transporter	
				putative L-type neutral amino acid	
2000	2000 38984_at	KIAA0436	AB007896	transporter	
2001	2001 39116_at	LOC54499	AF070626	putative membrane protein	
2002	2002 35286_r_at	RY1	X76302	putative nucleic acid binding protein RY-1	nucleic acid binding protein
				Putative prostate cancer tumor	
2003	2003 36852_at	N33	U42349	suppressor	
				putative protein similar to nessy	
2004	2004 33710_at	C3F	U72515		C3f
2005	40203_at	SUI1	AJ012375	or	putative translation initiation factor
2006	37678_at	NMA	U23070	putative transmembrane protein	putative transmembrane protein
				putative transmembrane protein; homolog	
				of yeast Golgi membrane protein Yif1p	
2002	2007 35326_at	54TM	AF004876	(Yip1p-interacting factor)	54TMp
				putative; Homo sapiens PTS gene,	
2008	2008 35697_at	PTS	L76259	complete cds.	6-pyruvoyltetrahydropterin synthase
				putative; originaly identified as an	
				'oncogene', product renamed by NCBI	
				staff; Homo sapiens longation factor 1-	
2009	2009 40887_g_at	PTI-1	L41498	cds.	longation factor 1-alpha 1
				putative; originaly identified as an	
				oncogene, product renamed by NCBI	
				staff; Homo sapiens longation factor 1-	
2010	2010 40886_at	PTI-1	L41498	alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
				pVHL-interacting deubiquitinating enzyme	
2011	2011 33219_at	VDU1	AB029020		KIAA1097 protein
				Pyruvate dehydrogenase complex, lipoyl-	
				containing component X; E3-binding	pyruvate dehydrogenase complex protein X
2012	2012 36164_at	PDX1	U82328	protein	subunit precursor
2013	2013 32378_at	PKM2	M26252	pyruvate kinase, muscle	pyruvate kinase, muscle
2014	2014 260_at	QDPR	M16447	quinoid dihydropteridine reductase	quinoid dihydropteridine reductase

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				R3H domain (binds single-stranded	
2015	2015 36610_at	R3HDM	D21852	nucleic acids) containing	KIAA0029 protein
2016	2016 39030_at	RABAC1	AJ133534	Rab acceptor 1 (prenylated)	prenylated Rab acceptor 1 (PRA1)
				Rab geranylgeranyltransferase, beta	
2017	2017 37703 at	RABGGTB	Y08201	subunit	rab geranylgeranyi transferase
2018	2018 38264_at	RABIF	U74324	RAB interacting factor	guanine nucleotide exchange factor mss4
2019	2019]36660_at	RAB11A	AF000231	RAB11A, member RAS oncogene family	rab11a
2020	2020 35325_at	RAB14	AF052113	RAB14, member RAS oncogene family	
2021	34393_r_at		AL050268	RAB1A, member RAS oncogene family	hypothetical protein
2022	2022 34392_s_at		AL050268	RAB1A, member RAS oncogene family	hypothetical protein
2023	2023 33326_at	RAB21	D42087	RAB21, member RAS oncogene family	RAB21, member RAS oncogene family
,		420040	, 0000	ATOUR DAY	0.1.0
2024 BUS	₌	HABZ/A	05/094	HABZ/A, member has oncogene ranny	nabz/a
2025	2025 33371_s_at	RAB31	U59877	RAB31, member RAS oncogene family	low-Mr GTP-binding protein Rab31
2026	2026 36110_at	RABSA	M28215	RAB5A, member RAS oncogene family	GTP-binding protein
			,	rab6 GTPase activating protein (GAP and	
2027	2027 35289_at	GAPCENA	AJ011679	centrosome-associated)	Rab6 GTPase activating protein, GAPCenA
2028	2028 35304_at	RAB6A	AF052130	RAB6A, member RAS oncogene family	
2029	2029 39628_at	RAB9A	AI671547	RAB9A, member RAS oncogene family	
2030	2030 41716_at	RC3	AB020663	rabconnectin-3	KIAA0856 protein
				Rac/Cdc42 guanine nucleotide exchange	
2031	2031 37543_at	ARHGEF6	D25304	factor (GEF) 6	
2032	2032]36857_at	RAD1	AF084513	RAD1 homolog (S. pombe)	DNA repair exonuclease
2033	2033 38114_at	RAD21	D38551	RAD21 homolog (S. pombe)	RAD21 homolog
2034	2034 1874 at	RAD23B	D21090	RAD23 homolog B (S. cerevisiae)	XP-C repair complementing protein (p58/HHR23B)
2035	2035 32757_at	RAE1	U84720	RAE1 RNA export 1 homolog (S. pombe)	mKINA export protein
		. –		RAGE-4 ORF2; one of 2 possible coding	
				coding regions: Himan repalce!	
				coming regions, manual remarks	
2036	2036 1524 at		1146104	complete nitrative cds	
2037	2037 36628 at	RAI RP1	1 42542	ralA binding profein 1	RI IP76 profein
2000	2038 37539 at	- 12 E	AB023176	RaignS-like dene	KIAA0959 protein
3	31 333 at	וופר	ACC20110	Liando-lino gollo	וווייסים ססססייויו

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2039		RANBP1		RAN binding protein 1	Ran-BP1(Ran-binding protein 1)
2040	2040 40824_at	RANBP16	AB018288	9	KIAA0745 protein
줐		RANBP2L1	AF012086	ke 1	Ran binding protein 2
2042		RANBP7	AF098799		RanBP7/importin 7
2043	2043 32602_at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1	smg GDS
2044	2044 1848_at	RAP1A	M22995	RAP1A, member of RAS oncogene family ras-related protein	ras-related protein
2045	2045 40146 at	RAP1B	AL080212	RAP1B, member of RAS oncogene family hypothetical protein	hypothetical protein
2046	2046 39601 at	BASSE1	A F061836	Ras association (RaIGDS/AF-6) domain	putative fumor suppressor protein
				Ras association (RaIGDS/AF-6) domain	Ras association (RaIGDS/AF-6) domain
2047	2047 37598_at	RASSF2	D79990	family 2	family 2
2048	2048 1659_s_at	RHEB2	D78132	Ras homolog enriched in brain 2	ras-related GTP-binding protein
2049	2049 37309_at	ARHA	L09159	ras homolog gene family, member A	multidrug resistance protein
2050	2050 1394_at	AHHA	L25080	ras homolog gene family, member A	GTP-binding protein
2051	2051 35803_at	ARHE	S82240	ras homolog gene family, member E	RhoE
				RAS p21 protein activator (GTPase	
2052	2052 36935_at	RASA1	M23379	activating protein) 1	GTPase-activating protein
				RAS p21 protein activator (GTPase	
2053	2053 1675_at	RASA1	M23379	activating protein) 1	GTPase-activating protein
				Ras-GTPase activating protein SH3	
2054	2054 35793_at	G3BP2	AB014560	domain-binding protein 2	KIAA0660 protein
				ras-related C3 bottulinum toxin substrate 1	
				(rho family, small GTP binding protein	
2055	2055 40864_at	RAC1	D25274	(Rac1)	
				ras-related C3 botulinum toxin substrate 1	ras-related C3 botulinum toxin substrate 1
				(rho family, small GTP binding protein	isoform Rac1; ras-related C3 botulinum toxin
2056	2056 2050_s_at	PAC1	M29870	Rac1)	substrate 1 isoform Rac1b
2057	2057 35316_at	RAGA	U41654	Ras-related GTP-binding protein	adenovirus E3-14.7K interacting protein 1
2058	2058 33234_at	BCAA	AA887480	RBP1-like protein	
2059	2059 41407_at	RDBP	L03411	RD RNA-binding protein	RD protein
2060	2060 34684_at	RECOL	L36140	RecQ protein-like (DNA helicase Q1-like) DNA helicase	DNA helicase

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2061	2061 34685_at	RECOL	AI685944	RecQ protein-like (DNA helicase Q1-like)	
				regulated at the translational level; contains I-mfa domain; untilizes unique	
				GTG start codon; Homo sapiens HIC	- Moratain isotorm Ado: HIC protein isotorm
2062	2062 37842 at	달	AF054589	isoform p32 mRNAs, complete cds.	p32
				regulator of G-protein signalling 19	
2063	2063 35756_at	RGS19IP1	AF089816		RGS-GAIP interacting protein GIPC
2064	37701_at	RGS2	L13463	24KD	heix-loop-heix phosphoprotein
2065	35722_at	RENT2	AL080198		hypothetical protein
				related RAS viral (r-ras) oncogene	
2066	2066 32827_at	RRAS2	Al365215	homolog 2	
				remainder of gene in clone 549K18	
2067	2067 34845_at	dJ796117.4	AL035398	(AL023654)	CGI-51 protein
2068	2068 1055 g at	RFC4	M87339	replication factor C (activator 1) 4 (37kD)	replication factor C, 37-kDa subunit
2069	2069 38481 at	RPA1	M63488	replication protein A1 (70kD)	replication protein A, 70-kDa subunit
2070	2070 652 g_at	RPA3	L07493	replication protein A3 (14kD)	replication protein A 14kDa subunit
2071	2071 37651_at	RCOR	D31888	REST corepressor	REST corepressor
				restin (Reed-Steinberg cell-expressed	
2072	2072 34350_at	HSN	X64838	ent-associated protein)	restin
2073	2073 31851_at	RFP2	AJ224819	ret finger protein 2	tumor suppressor
				reticulocalbin 1, EF-hand calcium binding	
2074	2074 40556_at	RCN1	D42073	domain	reticulocalbin
				reticulocalbin 2, EF-hand calcium binding	i i
2075	2075 37727_i_at	RCN2	X78669	domain	Er-hand protein
				reticulocalbin 2, EF-hand calcium binding	
2076	2076 37728_r_at	RCN2	X78669	domain	EF-hand protein
2077	2077 31536_at	RTN4	AB020693	reticulon 4	KIAA0886 protein
2078	2078 39964 at	RP2	AJ007590	retinitis pigmentosa 2 (X-linked recessive) XRP2 protein	XRP2 protein
2079	2079 38164_at	RPGR	U57629	retinitis pigmentosa GTPase regulator	retinitis pigmentosa GTPase regulator
	2044 0. 00	DB4	M15400	retinoblastoma 1 (including	retinoblastoma 1 (including osteosarcoma)
3	2000 2044_S_BI	lan	NI O+CC	Colection	



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2081	35227_at	RBBP8	U72066		CtBP interacting protein CtIP
2082	2082 33860_at	RBAF600	AB007931	retinoblastoma-associated factor 600	KIAA0462 protein
2083	2083 32597_at	RBL2	X76061	retinoblastoma-like 2 (p130)	130K protein
2084	2084 35848_at	RAI17	AL049432	retinoic acid induced 17	
				retropseudogene; Human	
				retropseudogene MSSP-1 DNA, complete	
2085	2085 31672_g_at	RBMS1P; MSSP1 D82351	D82351	cds.	MSSP-1
	Ξ			REV3-like, catalytic subunit of DNA	
2086	2086 38908_s_at	REV3L	AL096744	polymerase zeta (yeast)	hypothetical protein
				reversion-inducing-cysteine-rich protein	
2087	2087 35236_g_at	RECK	AA099265	with kazal motifs	
				reversion-inducing-cysteine-rich protein	
2088	2088 35235_at	RECK	AA099265	with kazal motifs	
				reversion-inducing-cysteine-rich protein	
2089	2089 35234_at	RECK	D50406	with kazal motifs	RECK protein precursor
2090	2090 553_g_at	ARHGAP1	U02570	Rho GTPase activating protein 1	CDC42 GTPase-activating protein
2091	2091 39700_at	ARHGAP1	Al961929	Rho GTPase activating protein 1	
				Rho guanine nucleotide exchange factor	
2092	2092 34180_at	ARHGEF10	AB002292	(GEF) 10	Rho guanine nucleotide exchange factor 10
				Rho guanine nucleotide exchange factor	
2093	2093 40828_at	ARHGEF7	D63476	(GEF) 7	PAK-interacting exchange factor beta
				rho/rac guanine nucleotide exchange	
2094	2094 40100_at	ARHGEF2	U72206	factor (GEF) 2	guanine nucleotide regulatory factor
				Rho-specific guanine nucleotide exchange	
2095	2095 36537_at	P114-RHO-GEF	AB011093	factor p114	_
2096	2096 41040_at	RPP38	U77664	ribonuclease P (38kD)	RNaseP protein P38
2097	2097 32664_at	RNASE4	D37931	ribonuclease, RNase A family, 4	RNase 4
2098	2098 36187_at	RNH	X13973	ribonuclease/angiogenin inhibitor	ribonuclease/angiogenin inhibitor
2099	2099 34314_at	RRM1	X59543	ribonucleotide reductase M1 polypeptide	M1 subunit of ribonucleotide reductase
2100	2100 2016_s_at	RPL10	M64241	ribosomal protein L10	Wilm's tumor-related protein
2101	2101 41178_at	RPL11	X79234	ribosomal protein L11	ribosomal protein L11
2102	2102 33668_at	RPL12	AF037643	ribosomal protein L12	
2103	2103 31509_at	RPL13	X64707	ribosomal protein L13	ribosomal protein L13
2104	2104 35119_at	RPL13A	X56932	ribosomal protein L13a	23 kD highly basic protein
2105	2105 31907_at	RPL14	D87735	ribosomal protein L14	ribosomal protein L14

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ribosomal protein L18
ribosomal protein L19
ribosomal protein L21
ribosomal protein L23
ribosomal protein L23
ribosomal protein L23a
ribosomal protein L24
ribosomal protein L26
ribosomal protein L27
ribosomai protein L2/a
nbosomal protein L30
ribosomal protein L31
ribosomal protein L32
ribosomal protein L34
ribosomal protein L35
ribosomal protein L36a
ribosomal protein L37
ribosomal protein L37a
ribosomal protein L38
ribosomal protein L4
ı,
ribosomal protein L41
ribosomal protein L5
ribosomal protein L6
ribosomal protein L7
ribosomal protein L8
ribosomal protein S10
ribosomal protein S11
ribosomal protein S12
ribosomal protein S13
ribosomal protein S15a
ribosomal protein S16

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2141	2141 34593 g at	RPS17	M13932	ribosomal protein S17	ribosomal protein S17
2142	2142 34592_at	RPS17	M13932	ribosomal protein S17	ribosomal protein S17
2143	2143 31330_at	RPS19	M81757	ribosomal protein S19	S19 ribosomal protein
2144	2144 31527_at	RPS2	X17206		ribosomal protein S2
2145	2145 32438_at	RPS20	L06498	0	ribosomal protein S20
2146	2146 347_s_at	RPS23	D14530	ribosomal protein S23	ribosomal protein
2147	2147 32315_at	RPS24	M31520	ribosomal protein S24	ribosomal protein S24
2148	2148 31573_at	RPS25	M64716	ribosomal protein S25	ribosomal protein
				ribosomal protein S27 (metallopanstimulin	
2149	2149 32748_at	RPS27	AI557852	1)	
2150	2150 34570_at	RPS27A	S79522	ribosomal protein S27a	ubiquitin carboxyl extension protein
2151	2151 39798_at	RPS28	R87876	ribosomal protein S28	
2152	2152 34645_at	RPS3	X55715	ribosomal protein S3	ribosomal protein S3
2153	1653_at	RPS3A	M84711	ribosomal protein S3A	v-fos transformation effector protein
2154	2154]34643_at	RPS4X	M58458	ribosomal protein S4, X-linked	ribosomal protein S4X isoform
2155	32437_at	RPS5	U14970	ribosomal protein S5	ribosomal protein S5
2156	31511_at	RPS9	U14971	ribosomal protein S9	ribosomal protein S9
2157	2157 31538_at	RPLP0	M17885	ribosomal protein, large, Po	ribosomal protein P0
2158	31956_(_at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
2159	31957_r_at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
				ribosome binding protein 1 homolog	
2160	2160 33213_g_at	RRBP1	AF006751	180kD (dog)	ES/130
				Ric-like, expressed in many tissues	
2161	2161 38331_at	RIT	Y07566	(Drosophila)	Ric-like, expressed in many tissues
2162	2162]35656_at	RNF6	AJ010346	ring finger protein (C3H2C3 type) 6	RING-H2
2163		RNF11	U69559	ring finger protein 11	
2164	2164 35811_at	RNF13	AF037204	ring finger protein 13	RING zinc finger protein
2165		RNF14	AB022663	ring finger protein 14	ring finger protein 14
2166	2166 33484_at	RNF2	Y10571	ring finger protein 2	ring finger protein 2
2167	2167 37964_at	RNF3	W25793	ring finger protein 3	
2168	2168 35777_at	RNF4	AB000468	ring finger protein 4	zinc finger protein
		·		ring zinc-finger protein; escapes X chromosome inactivation; Human ring zinc	
2169	37650 at	ZNF127-Xp	U41315	Inger protein (ZNF12/-Xp) gene and 5 flanking sequence.	ZNF127-Xp
2170	2170 37732_at	RYBP	AL049940	RING1 and YY1 binding protein	

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2171 38073	38073_at	RNMT	AB007858	RNA (guanine-7-) methyttransferase	RNA (guanine-7-) methyltransferase
21724	2172 41460_at	RBM14	AF080561	RNA binding motif protein 14	SYT interacting protein SIP
21734	2173 41741_at	RBM3	U28686		RNPL
2174		RBM4	U89505		Hlark
2175		RBM5	AF091263		RNA binding motif protein 5
2176	at	RBM6	AF069517		RNA binding protein DEF-3
2177	2177 40260_g_at	RBM9	AL009266		hypothetical protein
2178	2178 39731 at	RBMX	223064	RNA binding motif protein, X chromosome hnRNP G protein	hnRNP G protein
2179	2179 33867 s. at	BRMS1	X77494	RNA binding motif, single stranded interacting protein 1	RNA binding motif, single stranded interacting protein 1. isoform a
				RNA binding protein S1, serine-rich	
2180	2180 36186_at	RNPS1 (~ L37368	domain	RNA-binding protein
				RNA guanylytransferase and 5'-	
2181	2181 35202_at	RNGTT	AF025654	phosphatase	mRNA capping enzyme
2182	2182 33237_at	KIAA0801	AB018344	RNA helicase	KIAA0801 protein
2183	2183 36045_at	RNAH	AJ223948	RNA helicase family	RNA helicase
2184	2184 38762_at	RNAHP	AF083255	RNA helicase-related protein	RNA helicase-related protein
				RNA-binding protein gene with multiple	
2185	2185 38049_g_at	RBPMS	D84110	splicing	RBP-MS/type 4
				RNA-binding protein gene with multiple	
2186	2186 38047_at	RBPMS	D84109	splicing	RBP-MS/type 3
2187	2187 38974_at	DJ-1	AF021819	RNA-binding protein regulatory subunit	RNA-binding protein regulatory subunit
				RNA-binding region (RNP1, RRM)	
2188	2188 39725_at	RNPC2	L10910	containing 2	splicing factor
2189	2189 38011_at	RMP	AB006572	RPB5-mediating protein	RPB5 meidating protein
2190	2190 35195_at	RTCD1	Y11651	RTC domain containing 1	phosphate cyclase
				runt-related transcription factor 1 (acute	
2191	943_at	RUNX1	D43968	myeloid leukemia 1; aml1 oncogene)	AML1b protein
2192	40124 at	RUVBL1	Y18418	RuvB-like 1 (E. coli)	erythrocyte cytosolic protein of 54 kDa, ECP- 54
2193	2193 35758_at	RUVBL2	AB024301	RuvB-like 2 (E. coli)	RuvB-like DNA helicase TIP49b
				S100 calcium binding protein A10 (annexin II ligand, calpactin I, light	
2194	2194 39338_at	S100A10	AI201310	polypeptide (p11))	

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				ntaining inositol	
2195	36089_at	SAC2	AB023183		KIAA0966 protein
				Sac domain-containing inositol	
196	2196 41101_at	SAC3	D87464	\neg	KIAA0274 gene product
Γ				SAC1 suppressor of actin mutations 1-like	
197	2197 36511_at	SACM1L	AB020658		KIAA0851 protein
8	24702 24	+ IX O T V	A1 0400E4	S-adenoevhomorvetaina hydrolasa-lika 1	hypothetical protein
2	04136_all	71014			
199	2199 41302 at	AHCYL 1	R59606	S-adenosylhomocysteine hydrolase-like 1	
8	2200 36685 at	AMD1		S-adenosylmethionine decarboxylase 1	
					S-adenosylmethionine decarboxylase 1
201	2201 263 g at	AMD1	M21154	S-adenosylmethionine decarboxylase 1	precursor
202	2202 41449 at	SGCE	AJ000534	sarcoglycan, epsilon	epsilon-sarcoglycan
203	2203 36083_at	SAS	U01160	sarcoma amplified sequence	SAS
204	36536_at	SCHIP1	AF070614	schwannomin interacting protein 1	schwannomin interacting protein 1
2205	2205 33423 g_at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
2206	2206 33422 at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
2207	2207 36207_at	SEC14L1	D67029	SEC14-like 1 (S. cerevisiae)	SEC14 (S. cerevisiae)-like 1
2208	2208 39099 at	SEC23A	X97064	Sec23 homolog A (S. cerevisiae)	Sec23 protein
				SEC24 related gene family, member A (S.	
2209	2209 34199 at	SEC24A	AJ131244	cerevisiae)	Sec24A protein
	1			SEC24 related gene family, member B (S.	
2210	2210 35845_at	SEC24B	AJ131245	cerevisiae)	Sec24B protein
				SEC24 related gene family, member D (S.	
2211	2211 32770 at	SEC24D	AB018298	cerevisiae)	KIAA0755 protein
2212	2212 34349 at	SECESI	AJ011779	SEC63 protein	SEC63 protein
2213	2213 32521_at	SFRP1	AF056087	secreted frizzled-related protein 1	secreted frizzled related protein
				secreted phosphoprotein 1 (osteopontin,	
-				bone sialoprotein I, early T-lymphocyte	
2214	2214 34342_s_at	SPP1	AF052124	activation 1)	osteopontin
				secreted protein, acidic, cysteine-rich	secreted protein, acidic, cysteine-rich
2215	671_at	SPARC	J03040	(osteonectin)	(osteonectin)
2216	2216 34265 at	SGNE1	Y00757	secretory granule, neuroendocrine protein 1 (782 protein)	secretory granule, neuroendocrine protein 1 (7B2 protein)
2217	2217 37405 at	SELENBP1	U29091	selenium binding protein 1	selenium-binding protein
	- SS. 10				

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2218			U43286	se 2	selenophosphate synthetase 2
2219		-	Z11793		selenoprotein P
Γ				bulin domain	
				(Ig), short basic domain, secreted,	
2220	2220 377_g_at	SEMA3C	AB000220	(semaphorin) 3C	semaphorin E
				sema domain, immunoglobulin domain	
				(Ig), short basic domain, secreted,	
2221	2221 376_at	SEMA3C	AB000220	(semaphorin) 3C	semaphorin E
Γ				sema domain, immunoglobulin domain	
				(Ig), short basic domain, secreted,	
2222	2222 35666_at	SEMA3F	U38276		semaphorin III family homolog
2223	2223 38826 at	ŀ	2-Sep D50918		septin 2
					phosphotyrosine independent ligand for the
2224	2224 40898_at	SOSTM1	U46751	sequestosome 1	Lck SH2 domain p62
				serine (or cysteine) proteinase inhibitor,	
2225	2225 34789_at	SERPINB6	S69272	clade B (ovalbumin), member 6	cytoplasmic antiproteinase
				serine (or cysteine) proteinase inhibitor,	serine (or cysteine) proteinase inhibitor,
	*	-		clade E (nexin, plasminogen activator	clade E (nexin, plasminogen activator
2226	2226 38125_at	SERPINE1	M14083	inhibitor type 1), member 1	inhibitor type 1), member 1
				serine (or cysteine) proteinase inhibitor,	
				clade H (heat shock protein 47), member	
2227	2227 39167_r_at	SERPINH2	D83174	2	collagen binding protein 2
				serine palmitoyttransferase, long chain	
2228	2228 38818_at	SPTLC1	Y08685	base subunit 1	serine palmitoyltransferase, subunit I
				serine threonine kinase 39 (STE20/SPS1	
2229	2229 40966_at	STK39	AF099989	homolog, yeast)	Ste-20 related kinase SPAK
2230	2230 41737 at	SRRM1	AF048977	serine/arginine repetitive matrix 1	Ser/Arg-related nuclear matrix protein
2231	2231 36019 at	STK19	126260	serine/threonine kinase 19	RP protein
				serine/threonine kinase 24 (STE20	
2232	2232 40473_at	STK24	AF024636	homolog, yeast)	STE20-like kinase 3
				serine/threonine kinase 3 (STE20	
2233	2233 32142_at	STK3	U26424	homolog, yeast)	MST2
				serine/threonine-protein kinase PRP4	
2234	2234 32784 at	PRP4	AB011108	homolog	KIAA0536 protein

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				serum response factor (c-fos serum	serum response factor (c-fos serum
				response element-binding transcription	response element-binding transcription
2235	2235 40109_at	SRF	J03161	factor)	factor)
				serum response factor (c-fos serum	serum response factor (c-fos serum
-				response element-binding transcription	response element-binding transcription
2236	2236 1409_at	SRF	J03161	factor)	factor)
2237	2237 41544 at	SNK	AF059617	serum-inducible kinase	serum-inducible kinase
2238	2238 34849_at	SARS	X91257	seryl-tRNA synthetase	seryl-tRNA synthetase
Γ				SET translocation (myeloid leukemia-	SET translocation (myeloid leukemia-
2239	2239 40189_at	SET	M93651	associated)	associated)
2240	2240 32160 at	SIAH1	U76247	sentia homolog 1 (Drosophila)	hSIAH1
2241	2241 33799_at	SIAH2	U76248	seven in absentia homolog 2 (Drosophila) hSIAH2	hSIAH2
2242	2242 39088_at	NIFIE14	Y18007	seven transmembrane domain protein	seven transmembrane domain protein
			·	seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7)	
2243	2243 39747 at	rpb-7	U52427	gene, complete cds.	RNA polymerase II seventh subunit
2244	2244 38518 at	SCM12	Y18004	sex comb on midleg-like 2 (Drosophila)	SCML2 protein
				SH3 domain binding glutamic acid-rich	
2245	2245 36040_at	SH3BGR	Al337192	protein	
0,00	77100	000	**************************************	SH3 domain binding glutamic acid-rich	SH3 domain binding glutamic acid-rich-like
2240	2240 397 14_BI	SUSBURL	ALOAKOOI	PIOUGHI IING	Piocelli
2247	2247 38968 at	SH3BP5	AB005047	Sh3-domain binding protein 3 (b) N- associated)	SH3 binding protein
2248	2248 39691 at	SH3GLB1	AB007960	SH3-domain GRB2-like endophilin B1	SH3-containing protein SH3GLB1
				SHC (Src homology 2 domain containing)	
2249	2249 38118_at	SHC1	U73377	transforming protein 1	p66shc
				sialytransferase 9 (CMP-	
				NeuAc:lactosylceramide alpha-2,3-	
2250	2250 34256_at	SIAT9	AB018356	sialytransferase; GM3 synthase)	GM3 synthase
2251	2251 39139_at	SPC18	Al357653	signal peptidase complex (18kD)	
				signal recognition particle 14kD	
2252	2252 41194_at	SRP14	AI525652	(homologous Alu RNA binding protein)	
2253	2253 35231_at	SRP19	X12791	signal recognition particle 19kD	signal recognition particle 19kD
2254	2254 36060_at	SRP54	U51920	signal recognition particle 54kD	signal recognition particle

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SRP72 AF069765 \$ SRP9 AF070649 \$ MISGE STAT1 M97935 \$ at STAT1 M97935 \$ STAT1 M97935 \$ STAT1 M97935 \$ STAT1 M97935 \$ STAT1 M97936 \$ STAT1 M97936 \$ STAT1 M97935 \$ ASH2L AB022785 AW044624 AFR1 AW044624 AW044624 AFR1 AW044624 AW044624 AFR1 AF023612 AJ224335 AWIRE U90911 AJ224335 WIRE U90911 AJ224335 UPF3A AW021542 AJ224335 SAP18 AW021542 AJ265993 at SAP18 AF055993	•		
AF0706499 8 X06272 6 M97935 6 M97935 7 M97935 7 M97935 7 M97935 7 M97936 7 M74089 7 M74089 7 M74089 7 M74089 7 M74089 8		signal recognition particle 72kD	signal recognition particle 72
X06272 8 1 1 1 1 1 1 1 1 1			
M97935 M97935 M97935 M97935 M97935 M97936 L29277 AW044624 AW044624 AW044624 AW044624 AW044624 AW044624 AW044624 AW044624 AW044624 AW021542 A J224335 A J26915 M74089		ptor	signal recognition particle receptor ('docking
M97935 6 M97935 6 M97935 7 M97935 7 M97936 7 M97936 7 M97936 7 M97936 7 M97936 7 M97936 7 M74624 AW044624 AW044624 AW044624 AW044624 AW044624 AW044624 AW021542 A JUS6915 M74089 M74089 M74089 M74089 M74089 M74089 M74089 M74089	-		protein')
M97935 M97935 M97935 M97936 M979911 M979911 M979911 M9791670 M74089 M74089 M74089 M9790815 M9790815		signal transducer and activator of	
M97935 M97935 M97935 M97936 LAB022785 AW044624 AW044624 AW044624 AW044624 AW044624 AW044624 AW044624 AW044624 AW021542 AL031670 M74089 M74089 M74089 M74089 M74089 M74089 M74089 M74089 M74089			transcription factor ISGF-3
STAT1 M97935 STAT1 M97935 STAT1 M97936 STAT1 M97936 STAT3 L29277 STAM U43899 ASH2L AB022785 RER1 AW044624 RER1 AW044624 RER1 AW044624 ASH2L AB022785 ASH2L AB022785 ASH2L AB022785 ASH2L AB022785 ASH2L AW044624 ABET3 AJ031670 WIRE U90911 WIRE U90911 WIRE U90911 WIRE U90911 WIRE AJ024335 WIRE U96915 WIRE SAP18 U96915 WIRE SAP18 U96915 WIRE U96915 WIRE SAP18 U96915 WIRE WIRE U96915 WI		d activator of	
STAT1 M97935 STAT1 M97935 STAT1 M97936 STAT3 L29277 STAM U43899 ASH2L AB022785 AN044624 AN044624 AN044624 AL031670 A			transcription factor ISGF-3
STAT1 M97935 STAT1 M97936 STAT3 L29277 STAM U43899 ASH2L AB022785 AN044624 AN06911 AN06915 AN06915 AN06915 AN06915 AN065993		signal transducer and activator of	
STAT1 M97936 STAT3 L29277 STAM U43899 ASH2L AB022785 AN044624 AN06911 AN06915 AN061164 AN0621542 AN061164 AN0621542 AN061164 AN0621542		transcription 1, 91kD	transcription factor ISGF-3
39708_at STAT1 M97936 39708_at STAT3 L29277 160_at STAM U43899 35804_at ASH2L AB022785 41552_g_at RER1 AW044624 41551_at RER1 AW044624 35632_g_at DIM1 AF023612 35632_at DIM1 AF023612 35683_at G1L AL031670 37178_at na M74089 40787_at WIRE U90911 34705_at BET3 AJ224335 39131_at UPF3A N36842 41277_at SAP18 AW021542 33859_at SAP18 U96915 40992_s_at SAP30 AF055993		signal transducer and activator of	
STAT3 L29277 STAM U43899 ASH2L AB022785 at RER1 AW044624 AW044624 AW044624 AW044624 AW044624 AW044624 AW044624 AW04624 AW04624 AU31670		transcription 1, 91kD	
STAT3 L29277 STAM U43899 ASH2L AB022785 at RER1 AW044624 AW044624 AW044624 AW044624 AW044624 AW044624 AW044624 AW04624 AWW021670 AWMRE U90911 WIRE U90911 WIRE U90911 SAP18 AW021542 SAP18 AW021542 at SAP18 U96915		signal transducer and activator of	
STAT3 L29277 STAM U43899 ASH2L AB022785 at RER1 AW044624 BER1 AW044624 AW044624 AW044624 AW044624 AW044624 AW04624 AWMRE U90911 WIRE U90911 WIRE U90911 WIRE U90911 SAP18 AW021542 SAP18 AW021542 at SAP18 U96515		transcription 3 (acute-phase response	
STAM 043899 ASH2L AB022785 at RER1 AW044624 at RER1 AW044624 at DIM1 AF023612 G1L AL031670 na M74089 WIRE U90911 WIRE U90911 WIRE U90911 SAP18 AW021542 SAP18 AW021542 at SAP30 AF055993		factor)	DNA-binding protein
STAM 043899 ASH2L AB022785 at RER1 AW044624 at PER1 AW044624 at DIM1 AF023612 at DIM1 AF023612 at M74089 WIRE U90911 WIRE U90911 BET3 AJ224335 UPF3A N36842 SAP18 AW021542 at SAP18 U96515 at SAP30 AF055993		signal transducing adaptor molecule (SH3	
at RER1 AB022785 at RER1 AW044624 at RER1 AW044624 at DIM1 AF023612 G1L AL031670 na M74089 WIRE U90911 WIRE U90911 SAP18 AW021542 SAP18 AW021542 at SAP30 AF055993	U43899	domain and ITAM motif) 1	STAM
at RER1 AW044624 at RER1 AW044624 at DIM1 AF023612 at DIM1 AF023612 at DIM1 AF023612 at WIRE U90911 WIRE U90911 WIRE U90911 SAP18 AW021542 SAP18 AW021542 at SAP30 AF055993		similar to Drosophila ash2 gene; Homo	
at ASH2L AB022785 at RER1 AW044624 at DIM1 AW044624 at DIM1 AF023612 na AL031670 na M74089 WIRE U90911 WIRE U90911 BET3 AJ224335 UPF3A N36842 SAP18 AW021542 SAP18 U96915 at SAP30 AF055993	_	sapiens ASH2L gene, complete cds,	
at RER1 AW044624 at DIM1 AW044624 at DIM1 AF023612 G1L AL031670 na M74089 WIRE U90911 UPF3A AJ224335 UPF3A N36842 SAP18 AW021542 SAP18 U96915 at SAP30 AF055993	AB022785	similar to Drosophila ash2 gene.	
RER1 AW044624 at DIM1 AF023612 G1L AL031670 na M74089 WIRE U90911 WIRE AJ224335 UPF3A N36842 SAP18 AW021542 SAP18 U96915 at SAP30 AF055993	AW044624	similar to S. cerevisiae RER1	
at DIM1 AF023612 G1L AL031670 na M74089 WIRE U90911 WIRE U90911 SAP18 AJ224335 UPF3A N36842 SAP18 AW021542 SAP18 U96915 at SAP30 AF055993	AW044624	similar to S. cerevisiae RER1	
G1L AL031670 na M74089 WIRE U90911 BET3 AJ224335 UPF3A N36842 SAP18 AW021542 SAP18 U96915	AF023612	similar to S. pombe dim1+	Dim1p homolog
35083_at G1L AL031670 37178_at na M74089 40787_at WIRE U90911 34705_at BET3 AJ224335 39131_at UPF3A N36842 41277_at SAP18 AW021542 33859_at SAP18 U96915 40992_s_at SAP30 AF055993		similar to SW:GOLI_DROME Q06003	•
37178_at na M74089 40787_at WIRE U90911 34705_at BET3 AJ224335 39131_at UPF3A N36842 41277_at SAP18 AW021542 33859_at SAP18 U96915 40992_s_at SAP30 AF055993	AL031670	GOLIATH PROTEIN	ring finger protein 24
40787_at WIRE U90911 34705_at BET3 AJ224335 39131_at UPF3A N36842 41277_at SAP18 AW021542 33859_at SAP18 U96915 40992_s_at SAP30 AF055993	M74089	similar to TB1	
40787_at WIRE U90911 34705_at BET3 AJ224335 39131_at UPF3A N36842 41277_at SAP18 AW021542 33859_at SAP18 U96915 40992_s_at SAP30 AF055993		similar to Wiskott-Aldrich syndrome	
34705_at BET3 AJ224335 39131_at UPF3A N36842 41277_at SAP18 AW021542 33859_at SAP18 U96915 40992_s_at SAP30 AF055993	119091	protein interacting protein	
39131_at UPF3A N36842 41277_at SAP18 AW021542 33859_at SAP18 U96915 40992_s_at SAP30 AF055993	AJ224335	similar to yeast BET3 (S. cerevisiae)	hBET3 protein
41277_at SAP18 AW021542 33859_at SAP18 U96915 40992_s_at SAP30 AF055993	N36842	similar to yeast Upf3, variant A	
33859_at SAP18 U96915 40992_s_at SAP30 AF055993	AW021542	sin3-associated polypeptide, 18kD	
s_at SAP30 AF055993	U96915	sin3-associated polypeptide, 18kD	sin3 associated polypeptide p18
	AF055993	sin3-associated polypeptide, 30kD	mSin3A associated polypeptide p30
		sine oculis homeobox homolog 1	sine oculis homeobox (Drosophila) homolog
2276 40004_at SIX1 X91868 (Drosophila)	X91868	(Drosophila)	1

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				singed-like (fascin homolog, sea urchin)	
2277	2277 39070_at	SNL	U03057	(Drosophila)	actin bundling protein
2278	2278 39086_g_at	SSBP1	AA768912	single-stranded DNA binding protein	
2279	2279 32668_at	SSBP2	AL080076	single-stranded DNA binding protein 2	hypothetical protein
				Sjogren syndrome antigen A2 (60kD,	
8 %	2280 35294_at	SSA2	M25077	ribonucleoprotein autoantigen SS-A/Ro)	60kD Ro/SSA autoantigen
2001	2005 4 25	CAOO	Mosory	Sjogren syndrome antigen A2 (60kD,	60K7 Ro/SSA artrantinen
	2532_9_ai	2006	1100211	Cinate and and anima D (automition	Coaron chadromo antigon D (enfoantigon
2282	38450 at	SSB	X69804	Sjogren syndrome anngen o (adloannigen) [La]	Sjogren syndronie armyen o (adroannyen La)
2283	2283 37715_at	SNW1	AF045184	SKI-interacting protein	nuclear receptor coactivator NCoA-62
2284	2284 37389_at	IMAGE145052	Al346580	small acidic protein	
				small nuclear ribonucleoprotein 70kD	
2285	2285 40875_s_at	SNRP70	X06815	polypeptide (RNP antigen)	hU1-70K-like protein (216 AA)
				small nuclear ribonucleoprotein	
2286	2286 38679_g_at	SNRPE	AA733050	polypeptide E	
				small nuclear ribonucleoprotein	-
2287	2287 37337_at	SNRPG	AI803447	polypeptide G	
				small nuclear ribonucleoprotein	
2288	2288 34842_at	SNRPN	U41303	polypeptide N	small nuclear ribonuleoprotein particle N
. 6	17 04 0	-04110		small nuclear RNA activating complex,	
2289	2289 35247_at	SNAPCS	AI557062	polypeptide 5, 19KD	
				SMART/HDAC1 associated repressor	
2290	2290 32172_at	SHARP	AL096858	protein	hypothetical protein
				SMC1 structural maintenance of	
2291	2291 32849_at	SMC1L1	D80000	chromosomes 1-like 1 (yeast)	-
				SMT3 suppressor of mif two 3 homolog 1	
2292	2292 38738_at	SMT3H1	X99584	(yeast)	SMT3A protein
				SMT3 suppressor of mif two 3 homolog 2	
2293	2293 41185_f_at	SMT3H2	Al971724	(yeast)	
2294	2294 38288_at	SNA12	U69196	snail homolog 2 (Drosophila)	
L				soc-2 suppressor of clear homolog (C.	
2295	2295 38659_at	SHOC2	AB020669	elegans)	KIAA0862 protein
2296	2296 40928 at	WSB1	WORAGE	SOCS box-containing WD protein SWIP-1	
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2297	2297 36609_at	SLC1A3	D26443	solute carrier family 1 (glial high affinity glutamate transporter), member 3	glutamate transporter
2298	2298 35320_at	SLC11A2	AB004857	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 NRAMP2	NRAMP2
2299	2299 33143_s_at	SLC16A3	U81800	solute carrier family 16 (monocarboxylic acid transporters), member 3	monocarboxylate transporter
2300	2300 39260_at	SLC16A4	U59185	solute carrier family 16 (monocarboxylic acid transporters), member 4	solute carrier family 16 (monocarboxylic acid transporters), member 4
2301	2301 36979_at	SLC2A3	M20681	solute carrier family 2 (facilitated glucose transporter), member 3	solute carrier family 2 (facilitated glucose transporter), member 3
2302	2302 32084_at	SLC22A5	AF057164	solute carrier family 22 (organic cation transporter), member 5	organic cation transporter OCTN2
2303	2303 38122_at	SLC23A1	D87075	solute carrier family 23 (nucleobase transporters), member 1	
				solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator),	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator).
2304	2304 32822_at	SLC25A4	J02966	member 4 solute carrier family 25 (mitochondrial	member 4 solute carrier family 25 (mitochondrial
2305	2305 37740_r_at	SLC25A5	J02683	carrier; adenine nucleotide translocator), member 5	carrier; adenine nucleotide translocator), member 5
2306	2306 40436 g at	SLC25A6	J03592	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	
2307	2307 40435 at	SLC25A6	103592	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	
2308	2308 37675 at	SLC25A3	X60036	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	phosphate carrier protein
7309	2309 33901_at	SLC29A1	U81375	solute carrier family 29 (nucleoside transporters), member 1	equilibrative nucleoside transporter 1
2310	2310 40364_at	SLC31A1	U83460	solute carrier family 31 (copper transporters), member 1	high-affinity copper uptake protein

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201	24740 04	CI C2182	100464	copper	nutative copper uptake protein
3	2311 34/49_at	SLC31AZ	U83461	7	pulative copper aprane protein
				solute carrier family 35 (CMP-sialic acid	
2312	2312 37895_at	SLC35A1	D87969		CMP-sialic acid transporter
				solute carrier family 35 (UDP-N-	
				acety/glucosamine (UDP-GlcNAc)	
2313	2313 38208_at	SLC35A3	AB021981	transporter), member 3	UDP-N-acetylglucosamine transporter
				solute carrier family 4, sodium bicarbonate	
2314	2314 34936_at	SLC4A7	AB012130	cotransporter, member 7	sodium bicarbonate cotransporter2
				solute carrier family 6 (neurotransmitter	
2315	2315 34166_at	SLC6A7	S80071	transporter, L-proline), member 7	brain-specific L-proline transporter
				solute carrier family 7 (cationic amino acid solute carrier family 7 (cationic amino acid	solute carrier family 7 (cationic amino acid
2316	2316 32186_at	SLC7A5	M80244	transporter, y+ system), member 5	transporter, y+ system), member 5
L					
				solute carrier family 7 (cationic amino acid solute carrier family 7 (cationic amino acid	solute carrier family 7 (cationic amino acid
2317	2317 39533 at	SLC7A6	D87432	transporter, y+ system), member 6	transporter, y+ system), member 6
				solute carrier family 9 (sodium/hydrogen	
				exchanger), isoform 1 (antiporter, Na+/H+,	
2318	2318 32681_at	SLC9A1	S68616	amiloride sensitive)	Na+/H+ exchanger NHE-1 isoform
				solute carrier family 9 (sodium/hydrogen	
2315	2319 36542_at	SLC9A6	AF030409	exchanger), isoform 6	sodium-hydrogen exchanger 6
2320	2320 39097_at	SON	X63753	SON DNA binding protein	SON DNA-binding protein
	1	8000	0	(clidacoca) e polomod coolacido de sec	aniania anialo avehana factor
3 8	2321 32037 - at	2002	A FOOT 400	soli ol sorollos nomos E (crosopina)	
725	2322 41462_BI	SINAZ	AFU05482	SOUTHING THEY IN C	Solilling Havill &
232;	2323 39360_at	SNX3	AF034546	sorting nexin 3	sorting nextin 3
232	2324 40605_at	SNX4	AA524345	sorting nexin 4	
232	2325 37808_at	SNX7	AL049989	sorting nexin 7	hypothetical protein
		Y		Source: H.sapiens genes for histones	
232	2326 33352_at	H2A	X57985	H2B.1 and H2A.	histone H2A
232	2327 36112_r_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2
2328	2328 36111 s at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2



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				Source: Homo sapiens chromosome 10	
2329	2329 1173 g at		HG172-HT3924	clone HP11-96B5, WOHKING DHAFT SEQUENCE, 8 unordered pieces.	
				Source: Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete	
2330	2330 40617 at	44M2.1	AC004381	sequence.	hypothetical protein FLJ20274
				Source: Homo sapiens clk2 kinase	
			-	(CLK2), propin1, cote1,	
				glucocerebrosidase (GBA), and metaxin	*
				genes, complete cds; metaxin	
				pseudogene and glucocerebrosidase	
				pseudogene; and thrombosponding	
2331	2331 33740_at	COTE1	AF023268	(THBS3) gene, partial cds.	chromosome 1 open reading frame 2
				Source: Homo sapiens hJTB gene,	
2332	2332 41834 g at	HJTB PAR	AB016492	complete cds.	jumping transfocation breakpoint
				Source: Homo sapiens hJTB gene,	
2333	2333 41833_at	HJTB PAR	AB016492	complete cds.	jumping translocation breakpoint
			`	Source: Homo sapiens mRNA for	
2334	2334 32335_r_at	Ubc2	AB009010	polyubiquitin UbC, complete cds.	polyubiquitin UbC
				Source: Homo sapiens mRNA for	
2335	2335 32334_f_at	UbC2	AB009010	polyubiquitin UbC, complete cds.	polyubiquitin UbC
				Source: Human CCAAT-box-binding	
2336	2336 32194_at	CBF	M37197	factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
				Source: Human CCAAT-box-binding	
2337	2337 229_at	CBF	M37197	factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
L				Source: Human Chromosome 16 BAC	
				clone CIT987SK-A-101F10, complete	
2338	2338 41791 at	101F10.3	AC002550	sequence.	hypothetical protein
				Source: Human Chromosome 16 BAC	
				clone CIT987SK-A-211C6, complete	
2339	2339 41488 at	A-211C6.1	AC002394	sequence.	hypothetical protein A-211C6.1
				Source: Human Chromosome 16 BAC	
				clone CIT987SK-A-362G6, complete	
2340	2340 35742_at	A-362G6.1	U95740	sequence.	hypothetical protein A-362G6.1

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				Source: Human Chromosome 16 BAC	
				cione CiT987SK-A-61E3, complete	
2341,	2341,41733_at	61E3.1	AC003007	sequence.	Unknown gene product (partial)
				Source: Human DNA sequence from	
				clone RP4-742C19 on chromosome 22,	
2342	2342 36894_at		AL031846	complete sequence.	
				Source: Human mRNA for HLA class I	
2343	2343 37383_f_at	HLA class I - locus	locus X58536	locus C heavy chain.	HLA class I heavy chain
				Source: Human N-	
				srase I (GlcNAc-	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-
2344	2344 39778_at	T1 GLCN	AC-1M55621		N-acetylglucosaminyltransferase
2345	2345 41573_at	SP3	X68560	Sp3 transcription factor	
				spastic ataxia of Charlevoix-Saguenay	
2346	2346 32102_at	SACS	AB018273	(sacsin)	KIAA0730 protein
				spastic paraplegia 4 (autosomal dominant;	
2347	2347 35171_at	SPG4	AB029006	spastin)	KIAA1083 protein
2348	at	SPOP	AJ000644	-type POZ protein	SPOP
2349	at	SSH3BP1	AF001628		interactor protein AbIBP4
2350		SSH3BP1	AF006516		e3B1
2351		SPTBN1	M96803	spectrin, beta, non-erythrocytic 1	beta-spectrin
2352	2352 34304 s at	SAT	AL050290	spermidine/spermine N1-acetyttransferase	
				sphingomyelin phosphodiesterase 1, acid	
2353	2353 32574_at	SMPD1	X29960	lysosomal (acid sphingomyelinase)	sphingomyelin phosphodiesterase
				spinocerebellar ataxia 1	
				(olivopontocerebellar ataxia 1, autosomal	
2354	2354 36142_at	SCA1	X79204	dominant, ataxin 1)	ataxin-1
				spinocerebellar ataxia 2	
	•			(olivopontocerebellar ataxia 2, autosomal	
2355	2355 36998_s_at	SCA2	Y08262	dominant, ataxin 2)	ataxin 2
0		L		splicing factor 30, survival of motor neuron	
2356	2356 38040_at	SPF30	AF107463	related	splicing factor
2357	2357 36973_at	SF3B2	U41371	splicing factor 3b, subunit 2, 145kD	spliceosome associated protein



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2358	2358 36224_g_at		Al827895	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	
2359	2359 40638_at	SFPQ	X70944	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	PTB-associated splicing factor
2360	2360 36098_at	SFRS1	M72709	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
2361	2361 140_s_at	SFRS10	U68063	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	transformer-2 beta
2362	2362 32183_at		M74002	splicing factor, arginine/serine-rich 11	arginine-rich nuclear protein
2363	2363 35258_f_at	SFRS2IP	AF030234	splicing factor, arginine/serine-rich 2, interacting protein	splicing factor Sip1
2364	2364 40457_at	SFRS3	AF038250	splicing factor, arginine/serine-rich 3	
2365	2365 36991_at	SFRS4	L14076		pre-mRNA splicing factor
2366	2366 40453_s_at	SFRS5	U30826	splicing factor, arginine/serine-rich 5	SRp40-1
2367	2367 40262_at	SRP46	AF031166	Splicing factor, arginine/serine-rich, 46kD	SRp46 splicing factor
2368	2368 35839_at	SOLE	D78130	squalene epoxidase	squalene epoxidase
2369	2369 39047 at	SART3	AB020880	squamous cell carcinoma antigen recognised by T cells 3	squamous cell carcinoma antigen SART-3
2370	2370 41784_at	DKFZp564B0769	AL080186	SR rich protein	hypothetical protein
2371	2371 36091_at	SCAP2	AF051323	src family associated phosphoprotein 2	Src-associated adaptor protein
2372	2372 41354_at	STC1	U25997	stanniocalcin 1	stanniocalcin precursor
2373	2373 32043_at	STC2	AF098462	stanniocalcin 2	stanniocalcin-related protein
2374	2374 41295_at	STARD7	AL041780	START domain containing 7	
2375	2375 38800_at	STMN2	D45352	stathmin-like 2	
2376	2376 41823_at	STAU	AJ132258	staufen, RNA binding protein (Drosophila) staufen protein	staufen protein
2377	2377 38669_at	SLK	D86959	Ste20-related serine/threonine kinase	KIAA0204 protein
2378	2378 37147_at	SCGF	AF020044	stem cell growth factor, lymphocyte secreted C-type lectin	lymphocyte secreted C-type lectin precursor
2379	2379 36913_at	SLBP	U75679	stem-loop (histone) binding protein	histone stem-loop binding protein
2380	2380 38034_at	STS	M16505	steroid sulfatase (microsomal), arylsulfatase C, isozyme S	steroid suffatase (microsomal), arylsuffatase C, isozyme S



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				_	steroid-5-alpha-reductase, alpha polypeptide
				polypeptide 1 (3-oxo-5 alpha-steroid delta	1 (3-oxo-5 alpha-steroid delta 4-
2381	2381 589_at	SRD5A1	M32313		dehydrogenase alpha 1)
2382	33369 at	SC4MOL	AI535653	sterol-C4-methyl oxidase-like	
				sterol-C5-desaturase (ERG3 delta-5-	
2383	2383 33421_s_at	SCSDL	AB016247	desaturase homolog, fungal)-like	sterol-C5-desaturase
2384	2384 40419 at	EPB72	X85116	stomatin; H.sapiens epb72 gene exon 1.	band 7 integral membrane protein
2385	2385 33322 i at	SFN	X57348		stratifin
				stress-associated endoplasmic reticulum protein 1: ribosome associated membrane	
2386	2386 37035 at	SERP1	AI557272	protein 4	
					stromal cell derived factor receptor 1 isoform
					b; stromal cell derived factor receptor 1
2387	2387 35747_at	SDFR1	AF035287	stromal cell derived factor receptor 1	isoform a
2388	2388 32666_at	SDF1	U19495	stromal cell-derived factor 1	intercrine-alpha
2389	2389 33834_at	SDF1	L36033	stromal cell-derived factor 1	pre-B cell stimulating factor homologue
2390	2390 41627 at	SDF2	D50645	stromal cell-derived factor 2	SDF2
				succinate dehydrogenase complex,	succinate dehydrogenase flavoprotein
2391	2391 34826_at	SDHA	L21936	subunit A, flavoprotein (Fp)	subunit
L				succinate dehydrogenase complex,	
				subunit C, integral membrane protein,	
2392	2392 34385_at	SDHC	U57877	15kD	integral membrane protein CII-3
L				succinate dehydrogenase complex,	
2393	2393 40467_at	SDHD	AB006202	subunit D, integral membrane protein	cytochrome b small subunit of complex II
				succinate-CoA ligase, ADP-forming, beta	ATP-specific succinyl-CoA synthetase beta
2394	2394 40893_at	SUCLA2	AF058953	subunit	subunit
2395	2395 35832_at	KIAA1077	AB029000	sulfatase FP	KIAA1077 protein
2396	33712 at	SULT4A1	N63574	sulfotransferase family 4A, member 1	
2397	2397 34814 at	UBA2	AL041443	SUMO-1 activating enzyme subunit 2	
				superkiller viralicidic activity 2-like (S.	
2398	2398 37998 at	SKIV2L	U09877	cerevisiae)	helicase-like protein
				superoxide dismutase 1, soluble	superoxide dismutase 1, soluble
2395	2399 36620_at	SOD1	X02317	(amyotrophic lateral sclerosis 1 (adult))	(amyotrophic lateral sclerosis 1 (adult))
248	2400 40069 at	SVIL	AF051850	supervillin	supervillin
2401	2401 36676 at	GHRF GRF	AL031659	supported by FGENESH	growth hormone releasing hormone

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CBF-B HAP2 NF- AL031778 supported by GENEWISE, GENSCAN TTRAP AL031775 supported by GENSCAN ST13 U17714 carcinoma) (Hsp70 interacting protein) ST13 U17714 carcinoma) (Hsp70 interacting protein) STPUL AF080567 sushi-repeat protein STPUL AF080567 sushi-repeat protein STPUL AF080567 sushi-repeat containing protein, X STPUL AF080567 sushi-repeat ordining protein, X STPUL AF080567 sushi-repeat ordining protein, X STPUL AF080567 sushi-repeat ordining protein, X SWARCA1 M88163 subfamily a, member 1 SWARCA2 X72889 subfamily a, member 2 SWARCA3 AB010882 subfamily a, member 4 SWARCA4 U29175 subfamily a, member 5 SWARCA5 AB010882 subfamily a, member 5 SYBL1 X92396 synaptobrevin-like 1 SYRL1 AB020717 synaptobrevin-like 1 SYRL1 AB020717 synaptobrevin-like 1 SYRL2 X68194 synaptobrevin-like 1 SNAPC3 AB028952 synaptobrevin-like 1 SNAPC3 AB028952 synaptobrevin-like 1 SDC2 J04621 1.cell surface-associated, fibroglycan SDC3 AB007937 syndecan 2 (heparan sulfate proteoglycan SDC3 AB007937 syndecan 3 (N-syndecan) STXAA L32315 syndecan 3 (N-syndecan) STXAA L32315 syndecan binding protein (syntenin) and syndecan binding protein (syntenin) STXAA L32315 syndecan 5		A	B	ပ	۵	ш
TTRAP	2402	33297_at		AL031778	supported by GENEWISE, GENSCAN and FGENES	nuclear transcription factor Y, alpha, isoform 1
TTRAP						
ST13 U17714 suppression of fumorigenicity 13 (colon ST15 ST5 U15780 sushi-repeat protein) protein) protein SRPUL AF060567 sushi-repeat protein SRPUL AF060567 sushi-repeat protein KIAA0640 AB014540 SWAP-70 protein KIAA0640 AB014540 SWAP-70 protein SWARCA1 AB014540 SWAP-70 protein SWARCA2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, authority a, member 1 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, authority a, member 2 SWARCA2 X72889 subfamily a, member 4 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, authority and matrix associated, actin dependent regulator of chromatin, authority and authority and actin dependent regulator of chromatin, authority and authority and actin dependent regulator of chromatin, authority and authority and actin dependent regulator of chromatin, authority and authority and actin dependent regulator of chromatin, authority and authority and actin dependent regulator of chromatin, authority and authority and authority and actin dependent regulator of chromatin, authority and authori	2403	34825_at	TTRAP	AL031775	supported by GENSCAN	TRAF and TNF receptor-associated protein
ST13 U17714 carcinoma) (Hsp70 interacting protein) protein ST15 STF U15780 suppression of tumorigenicity 5 procession of tumorigenicity 5 SRPUL AF060567 sushi-repeat protein SRPX U61374 chromosome KIAA0640 AB014540 SWAP-70 protein SWAPCA1 M88163 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, authamily a, member 1 SWARCA2 X72889 subfamily a, member 1 SWARCA2 X72889 subfamily a, member 2 SWAISNF related, matrix associated, actin dependent regulator of chromatin, authamily a, member 4 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, authamily a, member 5 SWAISNF related, matrix associated, actin dependent regulator of chromatin, authamily a, member 5 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, authamily a, member 5 SYBL X92236 synaptobrown-like 1 SYPL X88194 synaptobrown-like 1 SYPL X88194 synaptobrown-like protein SYPL X802396 synaptobrown-like protein SYPL X802395 synaptobrown-like protein					suppression of tumorigenicity 13 (colon	
ST5 U15780 suppression of tumorigenicity 5 procession of tumorigenicity 5 procession of tumorigenicity 5 procession of sushi-repeat protein procession of sushi-repeat protein procession of sushi-repeat protein procession of sushi-repeat ocutaining protein, X procession ocutaining actin dependent regulator of chromatin, and x procession occurrence occurren	2404	1640_at	ST13	U17714	carcinoma) (Hsp70 interacting protein)	putative tumor suppressor ST13
SRPUL AF060567 sushi-repeat protein 8 SRPX U61374 chromosome Incompassion KIAA0640 AB014540 SWAP-TO protein Incompassion KIAA0640 AB014540 SWAPP-TO protein Incompassion SMARCA1 M88163 SWAPP-TO protein Incompassion SMARCA2 X72889 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, authorising a member 2 Incompassion SMARCA2 X72889 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, authorising authorising authorising a member 2 Incompassion SMARCA4 U29175 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, authorising authorising authorising authorising a synaptobrevin-like 1 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, authorising a synaptobrevin-like 1 SYNL1 AB020717 Synaptobrevin-like 1 Synaptobrevin-like 1 SYNL1 AB028952 Synaptobrevin-like 1 Synaptopodin SNAP23 AJ011915 Synaptopodin Synaptopodin SDC2 JO4621 1, cell surface-associated proteon, 23MD SDC3 AB007937	2405	37745_s_at	ST5	U15780	suppression of tumorigenicity 5	p82
SRPX U61374 Chromosome KIAA0640 AB014540 SWAP-70 protein SWAP-70 protein SWAP-70 protein SWAPCA1 M88163 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 SYRU1 SWARCA5 AB010882 SYMI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 SYRU1 SYPL SYPL SYPL SYRU1 SYRU1 SYRU1 SYRU1 SYRU2 SYRU1 S	2406	37805_at	SRPUL	AF060567	sushi-repeat protein	sushi-repeat protein
SRPX U61374 chromosome KIAA0640 AB014540 SWAP-70 protein SWAP-70 protein SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 1 SMARCA2 X72889 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 SMARCA2 X72889 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 SWAPCA4 U29175 Subfamily a, member 4 SWAI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 SWAI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 SYNU X82396 Synaptobrevin-like 1 SYNU X68194 synaptopodin synaptopodin Synaptopodin synaptopodin 1, cell surface-associated protein, 23kD SDC2 J04621 1, cell surface-associated, fibroglycan SDC3 AB007937 <t< td=""><td></td><td></td><td></td><td></td><td>sushi-repeat-containing protein, X</td><td></td></t<>					sushi-repeat-containing protein, X	
KIAA0640 AB014540 SWAP-70 protein Italy	2407	31855_at	SRPX	U61374	chromosome	
SMARCA1 M88163 subfamily a, member 1 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 SYBL1 X92396 synaptobrevin-like 1 SYPL X68194 synaptobrevin-like 1 SYPL X68194 synaptobrevin-like 1 SNAP23 AJ011915 synaptosomal-associated protein, 23kD SDC2 J04621 1, cell surface-associated, fibroglycan) SDC3 AB007937 syndecan 2 (heparan sulfate proteoglycan syndecan) 3 (N-syndecan) SDC3 AB007937 syndecan binding protein (syntenin) 3 STX12 AL035315 syndaxin 12	2408	31869_at	KIAA0640	AB014540	SWAP-70 protein	KIAA0640 protein
SMARCA1 M88163 subfamily a, member 1 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 SYBL1 X92396 synaptobrevin-like 1 SYBL1 X88194 synaptobrevin-like 1 SYBL2 AB007937 synaptosomal-associated protein, 23kD SDC3 AB007937 syndecan 2 (heparan sulfate proteoglycan) syndecan 2 (heparan sulfate proteoglycan) syndecan 3 (N-syndecan) syndecan 2 (syntenin) syndecan 3 (N-syndecan) syndecan 2 (syntenin) syndecan 3 (N-syndecan) syndecan 2 (syntenin) syndecan 3 (N-syndecan) syndecan 3 (syntenin) syntenin syntenin syntenin syntenin) syntenin synt					SWI/SNF related, matrix associated, actin	
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SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 SYNJ1 AB010882 subfamily a, member 5 SYBL1 X92396 synaptobrevin-like 1 SYPL X68194 synaptobrevin-like 1 SYPL X68194 synaptopodin KIAA1029 AB028952 synaptopodin SDC2 AJ011915 synaptosomal-associated protein, 23kD SDC2 J04621 1, cell surface-associated, fibroglycan 1, cell surface-associated, fibroglycan 5, syndecan 3 (N-syndecan) SDC3 AB007937 syndecan 3 (N-syndecan) SDC3 SYNdecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX34 U32315 syntaxin 3A	2409	40213_at	SMARCA1	M88163	subfamily a, member 1	transcription activator
SMARCA2 X72889 subfamily a, member 2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 SWARCA4 U29175 subfamily a, member 4 SWARCA5 AB010882 subfamily a, member 5 SYNJ1 AB020717 synaptobrevin-like 1 SYPL X92396 synaptobrevin-like 1 SYPL X68194 synaptobrevin-like protein, 23kD KIAA1029 AB028952 synaptosomal-associated protein, 23kD synaptosomal-associated protein, 23kD synaptosomal-associated protein, 23kD synaptosomal-associated fibroglycan 1, cell surface-associated, fibroglycan 5 SDC2 J04621 1, cell surface-associated fibroglycan 5 SDC3 AB007937 syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan 2, syndecan 3 (N-syndecan) syndecan 3 (N-syndecan) syndecan 3 (N-syndecan) syndecan 5 STX12 AL035306 syntaxin 12 STX34 U32315 syntaxin 34					SWI/SNF related, matrix associated, actin	
SMARCA2 X72889 subfamily a, member 2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 SMARCA4 U29175 subfamily a, member 4 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 SYBL1 X92396 synaptobrevin-like 1 SYPL X92396 synaptobrevin-like 1 SYPL X68194 synaptopodin KIAA1029 AB020717 synaptophysin-like protein, 23kD syndecan 2 (heparan sulfate proteoglycan syndecan 3 (N-syndecan) SDC2 J04621 1, cell surface-associated, fibroglycan syndecan 3 (N-syndecan) SDC3 AB007937 syndecan 3 (N-syndecan) SDCB AF000652 syndaxin 12 STX12 AL035306 syntaxin 12 STX3A U32315 syntaxin 3A					dependent regulator of chromatin,	
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SMARCA4 U29175 subfamily a, member 4 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, SWI/SNF related, matrix associated, actin dependent regulator of chromatin, SYBL1 X92396 synaptobrevin-like 1 SYBL1 X92396 synaptobrevin-like 1 SYRL1 X88194 synaptobrevin-like protein SYPL X68194 synaptobrevin-like protein SYPL X68194 synaptopodin SYPL X68194 synaptopodin SYPL X68194 synaptopodin syndecan 2 (heparan sulfate proteoglycan syndecan 3 (N-syndecan) SDC2 J04621 1, cell surface-associated, fibroglycan syndecan 3 (N-syndecan) SDC3 AB007937 syndecan 3 (N-syndecan) SDC3 AF000652 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX34 U32315 syntaxin 3A					SWI/SNF related, matrix associated, actin	
SMARCA4 U29175 subfamily a, member 4 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, SWI/SNF related, matrix associated, actin dependent regulator of chromatin, SMARCA5 AB010882 subfamily a, member 5 SYBL1 X92396 synaptobrevin-like 1 SYNJ1 AB020717 synaptobrevin-like 1 SYPL X68194 synaptophysin-like protein KIAA1029 AB028952 synaptopodin AD011915 synaptosomal-associated protein, 23kD SDC2 J04621 1, cell surface-associated, fibroglycan SDC3 AB007937 syndecan 2 (heparan sulfate proteoglycan SDC3 AB007937 syndecan 3 (N-syndecan) STX12 AL035306 syntaxin 12 STX3A LJ32315 syntaxin 12					dependent regulator of chromatin,	
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 SYBL1 X92396 subfamily a, member 5 SYBL1 X92396 synaptobrevin-like 1 SYNJ1 AB020717 synaptobrevin-like 1 SYNJ1 AB020717 synaptophysin-like protein KIAA1029 AB028952 synaptophysin-like protein SYNJ1 AB028952 synaptophysin-like protein SYNJ1 AB028952 synaptophysin-like protein SYNJ1 AND01915 synaptopodin SDC2 AJ011915 synaptosomal-associated protein, 23kD SDC3 AB007937 syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan 3, syndecan 3 (N-syndecan) SDC3 AB007937 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX3A LJ32315 syntaxin 3A	2411	32579_at	SMARCA4	U29175	subfamily a, member 4	transcriptional activator
SMARCA5 AB010882 subfamily a, member 5 SYBL1 X92396 synaptobrevin-like 1 SYNJ1 AB020717 synaptobrevin-like 1 SYNJ1 AB020717 synaptophysin-like protein KIAA1029 AB028952 synaptopodin KIAA1029 AB028952 synaptopodin SDC2 AJ011915 synaptosomal-associated protein, 23kD SDC2 J04621 1, cell surface-associated, fibroglycan SDC3 AB007937 syndecan 3 (N-syndecan) SDC3 AF000652 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX3A LJ32315 syntaxin 3A					SWI/SNF related, matrix associated, actin	
SMARCA5 AB010882 subfamily a, member 5 SYBL1 X92396 synaptobrevin-like 1 SYNJ1 AB020717 synaptophysin-like protein SYPL X68194 synaptophysin-like protein KIAA1029 AB028952 synaptopodin KIAA1029 AB028952 synaptopodin synaptosomal-associated protein, 23kD syndecan 2 (heparan sulfate proteoglycan SDC2 J04621 1, cell surface-associated, fibroglycan SDC3 AB007937 syndecan 3 (N-syndecan) SDCBP AF000652 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX3A LJ32315 syntaxin 3A					dependent regulator of chromatin,	
SYBL1 X92396 synaptobrevin-like 1 SYNJ1 AB020717 synaptophysin-like protein SYPL X68194 synaptophysin-like protein KIAA1029 AB028952 synaptopodin AJ011915 synaptosomal-associated protein, 23kD SDC2 J04621 1, cell surface-associated, fibroglycan SDC3 AB007937 syndecan 3 (N-syndecan) SDC3 AF000652 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX3A LJ32315 syntaxin 3A	2412	39132_at	SMARCA5	AB010882	subfamily a, member 5	hSNF2H
SYNJ1 AB020717 synaptojanin 1 SYPL X68194 synaptophysin-like protein KIAA1029 AB028952 synaptopodin t SNAP23 AJ011915 synaptosomal-associated protein, 23kD SDC2 J04621 1, cell surface-associated, fibroglycan SDC3 AB007937 syndecan 3 (N-syndecan) SDC3 AF000652 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX3A LJ32315 syntaxin 3A	2413	34753_at	SYBL1	X92396	synaptobrevin-like 1	synaptobrevin-like 1
SYPL X68194 synaptophysin-like protein KIAA1029 AB028952 synaptopodin t SNAP23 AJ011915 synaptosomal-associated protein, 23kD SDC2 J04621 1, cell surface-associated, fibroglycan SDC3 AB007937 syndecan 3 (N-syndecan) SDC3 AF000652 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX3A LJ32315 syntaxin 3A	2414	41692_at	SYNJ1	AB020717	synaptojanin 1	KIAA0910 protein
KIAA1029 AB028952 synaptopodin t SNAP23 AJ011915 synaptosomal-associated protein, 23kD SDC2 J04621 1, cell surface-associated, fibroglycan SDC3 AB007937 syndecan 3 (N-syndecan) SDCBP AF000652 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX3A LJ32315 syntaxin 3A	2415	38075_at	SYPL	X68194	synaptophysin-like protein	synaptophysin-like protein
SNAP23 AJ011915 synaptosomal-associated protein, 23kD syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan 2 (beparan sulfate proteoglycan 1, cell surface-associated, fibroglycan 2 (beparan sulfate proteoglycan 1, cell surface-associated, fibroglycan 2 (beparan 2 (bepa	2416	36452_at	KIAA1029	AB028952	synaptopodin	KIAA1029 protein
SDC2 J04621 1, cell surface-associated, fibroglycan SDC3 AB007937 syndecan 3 (N-syndecan) SDCBP AF000652 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX3A U32315 syntaxin 3A	[5	30178 r at	SMAD23	A 1011915	Cynantocomal-accociated protein 23kD	synaptosome associated protein of 23 kilodations isoform A
SDC2 J04621 1, cell surface-associated, fibroglycan SDC3 AB007937 syndecan 3 (N-syndecan) SDC3 AB007937 syndecan 3 (N-syndecan) SDCBP AF000652 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX3A U32315 syntaxin 3A		32110_1_at	2724	200	synaphysical accounted process, comp	
SDC2 J04621 1, cell surface-associated, fibroglycan) SDC3 AB007937 syndecan 3 (N-syndecan) SDCBP AF000652 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX3A U32315 syntaxin 3A					syndecan 2 (heparan sulfate proteoglycan	
SDC3 AB007937 syndecan 3 (N-syndecan) SDCBP AF000652 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX3A U32315 syntaxin 3A	2418	3 39757_at	SDC2	J04621	1, cell surface-associated, fibroglycan)	
SDCBP AF000652 syndecan binding protein (syntenin) STX12 AL035306 syntaxin 12 STX3A U32315 syntaxin 3A	2418	32092_at	SDC3	AB007937	syndecan 3 (N-syndecan)	KIAA0468 protein
STX12 AL035306 syntaxin 12 STX3A U32315 syntaxin 3A	2420)38110_at	SDCBP	AF000652	syndecan binding protein (syntenin)	syntenin
STX3A U32315 Svntaxin 3A	242	38685_at	STX12	AL035306	syntaxin 12	hypothetical protein
	242	38381_at	STX3A	U32315	syntaxin 3A	syntaxin 3

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2423	2423 38774_at	STX7	U77942	syntaxin 7	syntaxin 7
2424	2424 37510_at	STX8	AF036715	syntaxin 8	syntaxin 8
2425	2425 33942_s_at	7.	AF004563	Inding protein 1	hUNC18b
2426	2426 37962_r_at	STXBP3	D63506	syntaxin binding protein 3	unc-18homologue
				Synthetic construct chimeric DNA-binding	
2427	2427 33315_at		M29204		chimeric DNA-binding factor
				TAF7 RNA polymerase II, TATA box	
				g protein (TBP)-associated factor,	
2428	2428 192_at	TAF7	U18062		TFIID subunit TAFI155
				TAF9 RNA polymerase II, TATA box	j
				binding protein (TBP)-associated factor,	
2429	2429 193_at	TAF9	U21858		TAFII32 precursor
				TAFII20; contains homology to histone	
			0	H2B; TFIID subunit; TAFII15; contains	
				homology to histone H2B; TFIID subunit;	
				Human TFIID subunits TAF20 and TAF15	
2430	2430 37620_at	TAF12; TAF2J; TAU57693	U57693	mRNA, complete cds.	TAF20; TAF15
2431	2431 32166_at	TLN1	AB028950	talin 1	KIAA1027 protein
2432	2432 39765_at	TLN2	AB002318	talin 2	
2433	2433 41168_at	TAPBP	AF029750	TAP binding protein (tapasin)	tapasin
2434	2434 39779_at	TARBP1	U38847	TAR (HIV) RNA binding protein 1	TAR RNA loop binding protein
2435	32241_at	TARDBP	AL050265	TAR DNA binding protein	hypothetical protein
2436	39416_at	TIP-1	U90913	Tax interaction protein 1	Tax interaction protein 1
				Tex1 (human T-cell leukemia virus type I)	
2437	2437 498_at	TAX1BP1	U33821	binding protein 1	tax1-binding protein TXBP151
				Tax1 (human T-cell leukemia virus type I)	
2438	2438 35279_at	TAX1BP1	U33821	binding protein 1	tax1-binding protein TXBP151
2439	2439 36702_at	TBX19	AJ010277	T-box 19	TBX19 protein
2440	2440 32196_at	TIP120A	AB020636	TBP-interacting protein	KIAA0829 protein
2441	2441 34791_at	TCP1	X52882	t-complex 1	t-complex 1
				t-complex-associated-testis-expressed 1-	
2442	2442 36921_at	TCTE1L	U02556	like	t-complex-associated-testis-expressed 1-like
Ŀ				t-complex-associated-testis-expressed 1-	t-complex-associated-testis-expressed 1- t-complex-associated-testis-expressed 1-like
2443	2443 946_at	TCTEL1	D50663	like 1	•

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				TEIG; EGRa; Homo sapiens TGFb inducible earth protein and earth growth	
			-		TGFb inducible early protein; early growth
2444	2444 38374_at	TIEG; EGRA; KLF	KLF AF050110	一	response protein alpha
				enomenic reneat hinding factor (NIMA.	telomeric repeat binding factor 1. isoform 2:
2445	2445 32255_i_at	TERF1	U40705		telomeric repeat binding factor 1, isoform 1
2446	2446 32134 at	TES	AL050162	testis derived transcript (3 LIM domains)	hypothetical protein
				testis enhanced gene transcript (BAX	testis enhanced gene transcript (BAX
2447	2447 33988_at	TEGT	X75861	inhibitor 1)	inhibitor 1)
2448	2448 32080_at	TETRAN	L11669	tetracycline transporter-like protein	tetracycline transporter-like protein
2449	38612_at	TSPAN-3	M69023	tetraspan 3	
2450	37321 at	TTC1	U46570	tetratricopeptide repeat domain 1	tetratricopeptide repeat protein
2451	39065 s at	TTC3	D83077	tetratricopeptide repeat domain 3	TPRD
2452	2452 224_at	TIEG	S81439	TGFB inducible early growth response	zinc finger transcription factor
				TGFB-induced factor (TALE family	
2453	2453 38805_at	TGIF	X89750	homeobox)	TGIF protein
				The AAs encoded by bases 5728-5736	
				and 5917-5926 may be ASN-linked	
				glycosylation sites; insulin-like precursor;	
				Homo sapiens growth factor-binding	
				protein-3 precursor (IGFBP3) gene,	
2454	2454 37319_at	IGFBP3	M35878	complete cds.	growth factor-binding protein-3 precursor
			-	The AAs encoded by bases 5728-5736	-
				and 5917-5926 may be ASN-linked	
	-			glycosylation sites; insulin-like precursor;	
				Homo sapiens growth factor-binding	
				protein-3 precursor (IGFBP3) gene,	
2455	2455 1586_at	IGFBP3	M35878	complete cds.	growth factor-binding protein-3 precursor

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				The first in-frame ATG codon is located at nucleotides 17-19, followed by a second ATG codon Sownstream. And the second ATG codon is potential initiation point for translation of NPPase; Human mRNA for nucleotide	O O O
2457	2457 36992 at	Z -	1; NHU12485 Al653621	pyrophospiladase, complete cas.	מים ביים ביים ביים ביים ביים ביים ביים ב
2458	2458 34768 at	DC	AL080080	thioredoxin domain-containing	hypothetical protein
2459	2459 31508_at	TXNIP	S73591	thioredoxin interacting protein	brain-expressed HHCPA78 homolog VDUP1
2460	2460 39425_at	TXNRD1	X91247	thioredoxin reductase 1	thioredoxin reductase (NADPH)
2461	2461 32214_at	TXNL	AF003938	thioredoxin-like, 32kD	thioredoxin-like protein
2462	2462 38473_at	TARS	M63180	threonyl-tRNA synthetase	threonyl-tRNA synthetase
2463	2463 659_g_at	THBS2	L12350	thrombospondin 2	thrombospondin 2
2464	2464 658_at	THBS2	L12350	thrombospondin 2	thrombospondin 2
7070	10004	O CH	104401	the Ald California	G/T mismatch-specific thymine DNA
2455	2465 31557 at	TMSB4X	M17733	thymosin beta 4. X chromosome	thymosin beta 4
				thyroid hormone receptor coactivating	
2467	2467 32654_g_at	SMAP	AW020536	protein	
2468	2468 39699_at	TRIP12	D28476	thyroid hormone receptor interactor 12	thyroid hormone receptor interactor 12
2469	2469 41251_at	TRIP3	L40410	thyroid hormone receptor interactor 3	thyroid receptor interactor
2470	39341_at	TRIP6	AJ001902	thyroid hormone receptor interactor 6	TRIP6
2471	2471 37348_s_at	TRIP7	AA845349	thyroid hormone receptor interactor 7	
				thyroid hormone receptor-associated	
2472	2472 41625 at	TRAP240	AB011165	protein, 240 kDa subunit	KIAA0593 protein
2473	2473 34323_at	TRIP15	AF084260	thyroid receptor interacting protein 15	signalosome subunit 2
				TIA1 cytotoxic granule-associated RNA	TIA1 protein, isoform 1; TIA1 protein,
2474	2474 33852_at	TIA1	M77142	binding protein	Isotorm 2
2475	2475 41763 g_at	TIAL1	D64015	TIA1 cytotoxic granule-associated RNA binding protein-like 1	T-cluster binding protein
2476	2476 36655_at	TJP2	L27476	tight junction protein 2 (zona occludens 2)	tight junction protein 2 (zona occludens 2) tight junction protein 2 (zona occludens 2)
2477	2477 37801_at	T.J6	AF112972	TJ6 protein	TJ6

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2478	35238_at	TRAF5	AB000509	TNF receptor-associated factor 5	TRAF5
2479	2479 33243_at	GG2-1	AF099935	TNF-induced protein	MDC-3.13 isoform 2
2480	2480 40310_at	TLR2	AF051152	toll-like receptor 2	Toll/interleukin-1 receptor-like protein 4
2481	1030_s_at	TOP1	U07806	topoisomerase (DNA) I	DNA topoisomerase I
2482	2482 36571_at	TOP2B	X68060	topoisomerase (DNA) II beta (180kD)	DNA topoisomerase II
2483	32233_at	TOR1B	AF007872	torsin family 1, member B (torsin B)	torsinB
2484	2484 32219_at	TLK1	D50927	tousled-like kinase 1	KIAA0137 protein
2485	2485 35321_at	TLK2	AB004884	tousled-like kinase 2	PKU-alpha
				TRAF family member-associated NFKB	
2486	39742_at	TANK	U59863	activator	I-TRAF
2487	2487 40051_at	KIAA0057	D31762	TRAM-like protein	TRAM-like protein
2488	2488 1073_at	TCEA1	M81601	transcription elongation factor A (SII), 1	transcription elongation factor SII
				transcription elongation factor A (SII)-like	
2489	2489 38317_at	TCEAL1	M99701		transcription elongation factor A (SII)-like 1
				transcription elongation factor B (SIII),	RNA polymerase II elongation factor SIII,
2490	2490 1399_at	TCEB1	L34587	polypeptide 1 (15kD, elongin C)	p15 subunit
				transcription elongation factor B (SIII),	RNA polymerase II elongation factor-like
2491	2491 41759_at	TCEB1L	247087	polypeptide 1-like	protein
				transcription elongation regulator 1	
2492	2492 39426_at	TCERG1	AF017789	(CA150)	putative transcription factor CA150
				transcription factor 12 (HTF4, helix-loop-	
2493	2493 33348_at	TCF12	M80627	helix transcription factors 4)	helix-loop-helix protein
				ilindolooniaani VESA imministrationilin	
2494	2494 1373 at	TCES	M31523	enhancer binding factors E12/E47)	
				transcription factor 8 (represses	
2495	2495 33440_at	TCF8	U19969	interleukin 2 expression)	2EB
				transcription factor AP-4 (activating	
2496	2496 39638_at	TFAP4	S73885	enhancer binding protein 4)	AP-4
2497	2497 37757_at	TFDP1	L23959	transcription factor Dp-1	E2F-related transcription factor
2498	32578_at	TCFL4	AW005997	transcription factor-like 4	
				transcription factor-like 5 (basic helix-loop-	
2499	2499 35614_at	TCFL5	AB012124	(helix)	transcription factor-like 5
2500	2500 35749_at	TADA3L	AF069733	transcriptional adaptor 3-like	ADA3-like protein

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					KIAA1080 protein; Golgi-associated, gamma- adaptin ear containing, ARF-binding protein
2501	2501 35297_at	GGA2 VEAR	AC002400	Transcriptional coactivator P15 like	2
2502	2502 33876 et	TA7	AI 050107	transcriptional co-activator with PDZ-	hypothetical protein
3	n - 0 1000			transcriptional co-repressor: Human	
				silencing mediator of retinoid and thyroid	
				Θ	silencing mediator of retinoid and thyroid
2503	2503 39358_at	SMRT	U37146	cds.	hormone action
				transcriptional regulator interacting with	
2504	2504 37312_at	TRIP-Br2	D50917	the PHS-bromodomain 2	KIAA0127 gene product
2505	2505 40631_at	TOB1	D38305	transducer of ERBB2, 1	Tob
2506	2506 32554_s_at	TBL1	Y12781	transducin (beta)-like 1	transducin (beta) like 1 protein
2507	2507 37324_at	TFRC	X01060	transferrin receptor (p90, CD71)	transferrin receptor (p90, CD71)
2508	2508 39344_at	HSU53209	U53209	transformer-2 alpha (htra-2 alpha)	transformer-2 alpha
				transforming growth factor beta-stimulated	
2509	2509 39032_at	TSC22	AJ222700	protein TSC-22	TSC-22
				transforming growth factor, beta 1	transforming growth factor, beta 1 (Camurati-
2510	2510 41445_at	TGFB1	X02812	(Camurati-Engelmann disease)	Engelmann disease)
				transforming growth factor, beta receptor	
2511	2511 1815_g_at	TGFBR2	D50683	II (70-80kD)	TGF-betallR alpha
				transforming growth factor, beta receptor	
2512	2512 1814_at	TGFBR2	D50683	II (70-80kD)	TGF-betallR alpha
				transforming growth factor, beta-induced,	
2513	2513 1385_at	TGFBI	M77349	68kD	transforming growth factor induced protein
				transforming, acidic coiled-coil containing	
2514	2514 40841_at	TACCI	AF049910	protein 1	TACC1
				transforming, acidic coiled-coil containing	
2515	2515 38816_at	TACC2	AF095791	protein 2	TACC2 protein
2516	2516 36931_at	TAGLN	M95787	transgelin	smooth muscle protein
2517	2517 36678_at	TAGLN2	D21261	transgelin 2	transgelin 2
2518	2518 31829_r_at	TGOLN2	AF027515	trans-golgi network protein 2	hTGN48
				transient receptor potential cation channel	
2519	2519 39124_r_at	TRPC1	X89066	subfamily C, member 1	TRPC1 protein
2520	2520 39123 s at	TRPC1	X89066	transient receptor potential cation channel, subfamily C, member 1	TRPC1 protein

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2525	41051_		X95073	translin-associated factor X	Translin associated protein X
2526	2526 32831_at	TIMM17A	AA453183	translocase of inner mitochondrial membrane 17 homolog A (yeast)	
2527	2527 36198_at	TOMM20-PENDIN	NDIN D13641	translocase of outer mitochondrial membrane 20 (yeast) homolog	mitochondrial outer membrane protein 19
2528	2528 37050 r at	TOMM34	A1130910	translocase of outer mitochondrial membrane 34	-
2529	2529 32853_at	TOMM70A	AB018262	translocase of outer mitochondrial membrane 70 homolog A (yeast)	KIAA0719 protein
2530	2530 34796 at	TRAM	X63679	translocating chain-associating membrane protein	TRAM protein
2531	2531 38100_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2532	2532 950_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2533	2533 41531_at	TM4SF1	A1445461	transmembrane 4 superfamily member 1	
2534	2534 39362_r_at	TM4SF6	AF043906	transmembrane 4 superfamily member 6	T245 protein
2535	2535 32083_at	TM7SF1	AF027826	transmembrane 7 superfamily member 1 (upregulated in kidney)	putative seven pass transmembrane protein
2536	38835_at	TM9SF1	U94831	transmembrane 9 superfamily member 1	multispanning membrane protein
2537	2537 34307_at	TM9SF2	U81006	transmembrane 9 superfamily member 2	p76
2538	2538 37955_at	TMEM4	AB015631	transmembrane protein 4	type II membrane protein
2539	2539 37445_at	TMEMS	AB015633	transmembrane protein 5	type II membrane protein
2540	2540 36128_at	TMP21	L40397	transmembrane trafficking protein	
2541	2541 38982_at	RAP1	W28865	TRF2-interacting telomeric RAP1 protein	
2542	2542 39382_at	TRIM2	AB011089	tripartite motif-containing 2	KIAA0517 protein
2543	2543 36825_at	TRIM22	X82200	tripartite motif-containing 22	gpStaf50
2544	2544 38537_at	TRIM32	U18543	tripartite motif-containing 32	zinc-finger protein
2545	2545 32635_at	TRIM33	AB029036	tripartite motif-containing 33	KIAA1113 protein
2546	2546 33107_at	TRIM37	AB020705	tripartite motif-containing 37	KIAA0898 protein
2547	2547 40461_at	TIX1	AB007855	triple homeobox 1	
2548	2548 36791_g_at	TPM1	M19267	(tropomyosin 1 (alpha)	
2548	2549 36790_at	TPM1	M19267	(tropomyosin 1 (alpha)	tropomyosin 1 (alpha)

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				RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VALOSIN CONTAINING PROTEIN) (VALOSIN CONTAINING PROTEIN) (VOL): Human homolog of spil001853ITERA_MOUSE TRANSITIONAL ENDONALSMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) pirIl525197 transitional endoplasmic reticulum ATPase - mouse gil55217 (214044) murine valosin- containing protein; 99% identical to mouse, rat, and gib homologs; Array cross- complementing gene 9; Putative DNA repair protein; Hypothetical 96.6 kDa putative membrane protein; Most similar to hypothetical proteins in fission and budding yeast, and C. elegans: (ABO04530 PR YLL031c [Schizosaccharomyces pombe] producing hypothetical protein (AL021766) [Schizosaccharomyces cerevisiae) gial[P101e245463 (Z73136) ORF YLL031c [Saccharomyces cerevisiae] grotein; Most similar to hypothetical protein; Most similar to hypothetical proteins; P101e2756130 (Z81072) F30A10.5 TERA_HUMAN; XRCC9; P1.11659_3;	TERA_HUMAN; XRCC9; P1.11659_3;
2521	2521 34380_at	XRCC9	AC004472	720201102077	F1.1 1639_4, F1.1 1639_3
2522	2522 33351_at	GC20	AF064607	6	GC20 protein
2523	2523 40537_at	IF2	AB018284	translation initiation factor IF2	KIAA0741 protein
2524	2524 32173_at	UK114	X95384	translational inhibitor protein p14.5	14.5 kDa translational inhibitor protein, p14.5
2524	32173_at	UK114	X95384		14.3 AUA II AII SIANOI IAI II III II

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2550	2550 36792_at	TPM1	224727	tropomyosin 1 (alpha)	tropomyosin isoform
2551	2551 32313_at	TPM2	M12125	tropomyosin 2 (beta)	tropomyosin 2 (beta)
2552	2552 32777_at	WRB	Y12478	tryptophan rich basic protein	congenital heart disease 5 protein
2553	2553 38121_at	WARS	X59892	tryptophanyl-tRNA synthetase	471 aa polypeptide (gamma2)
				Tu translation elongation factor,	
2554	2554 39867_at	TUFM	S75463	mitochondrial	P43
2555	2555 31944_at	TULP3	Al028290	tubby like protein 3	
2556	2556 32272_at	K-ALPHA-1	K00558	tubulin, alpha, ubiquitous	tubulin, alpha, ubiquitous
2557	39332_at	TUBB	AF035316	tubulin, beta polypeptide	
2558	39331_at	TUBB	X79535	tubulin, beta polypeptide	beta tubulin
2559	33346_r_at	TUBG1	M61764	tubulin, gamma 1	gamma-tubulin
2560	36176_at	TBCC	U61234	tubulin-specific chaperone c	cofactor C
2561	35159_at	TBCE	U61232	tubulin-specific chaperone e	cofactor E
2562	2562 37007_at	TDE1	U49188	tumor differentially expressed 1	tumor differentially expressed 1
				tumor necrosis factor receptor	
2563	2563 34892_at	TNFRSF10B	AF016266	superfamily, member 10b	TRAIL receptor 2
				tumor necrosis factor receptor	
				superfamily, member 12 (translocating	
2564	2564 41190_at	TNFRSF12	U83598	chain-association membrane protein)	death domain receptor 3 soluble form
				tumor necrosis factor receptor	
2565	2565 1563_s_at	TNFRSF1A	M58286	superfamily, member 1A	tumor necrosis factor receptor
			-	tumor necrosis factor receptor	
2566	2566 35150_at	TNFRSF5	X60592	superfamily, member 5	CDw40
				tumor necrosis factor receptor	
2567	2567 37643_at	TNFRSF6	X63717	superfamily, member 6	APO-1 cell surface antigen precursor
			-	tumor necrosis factor, alpha-induced	
2568	2568 36988_at	TNFAIP1	M80783	protein 1 (endothelial)	B12 protein
				tumor necrosis factor, alpha-induced	
2569	2569 38631_at	TNFAIP2	M92357	protein 2	B94 protein
			,	turnor necrosis factor, alpha-induced	
2570	2570 595_at	TNFAIP3	M59465	protein 3	A20
2571	2571 40076_at	TPD52L2	AF004430	turnor protein D52-like 2	hD54+ins2 isoform
2572	2572 1711_at	TP53BP1	U09477	turnor protein p53 binding protein, 1	p53-binding protein
2573	2573 34822_at	TP53BP2	U58334	tumor protein p53 binding protein, 2	Bbp/53BP2
2574	2574 38568_at	TP53BPL	U82939	tumor protein p53-binding protein	p53 binding protein

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	A	В	ပ	Q	Ę
2575	2575 31584_at	TPT1	X16064	tumor protein, translationally-controlled 1	tumor protein, translationally-controlled 1
2576	2576 31888_s_at	TSSC3	AF001294	tumor suppressing subtransferable candidate 3	IPL
2577	2577 147_at	TSG101	U82130	sptibility gene 101	tumor susceptibility protein
06.70	40000	FOLKE			rietora scibrid NNA Li IJ O
0/07	40320_al	TVBOS	A39200	i Osobi iliaj	PITCH DIA DIRGING PROBILI
2580	25/9 2066_5_81 2580 35246_8t	TYRO3	U18934	TYRO3 protein tyrosine kinase	receptor tyrosine kinase
				tyrosine 3-monooxygenase/tryptophan 5-	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta
2581	2581 32324_at	YWHAB	X57346	polypeptide	polypeptide
				tyrosine 3-monooxygenase/tryptophan 5-	
2582	2582 409_at	YWHAQ	X56468	monooxygenase activation protein, trieta polypeptide	14.3.3 protein
				tyrosine 3-monooxygenase/tryptophan 5-	
2583	2583 32530_at	YWHAQ	X56468	nohooxygenase acuvation protein, meta polypeptide	14.3.3 protein
				tyrosine 3-monooxygenase/tryptophan 5- monooxygenase activation protein, zeta	
2584	2584 1235_at	YWHAZ	M86400	polypeptide	phospholipase A2
2585	2585 32718_at	TPST1	AF038009	tyrosylprotein sulfotransferase 1	tyrosylprotein sulfotransferase-1
2586	2586 35172_at	TPST2	AF049891	tyrosylprotein sulfotransferase 2	tyrosylprotein sulfotransferase-2
2587	2587 38977_at	YARS	U89436	tyrosyl-tRNA synthetase	tyrosyl-tRNA synthetase
2588	2588 36517 at	U2AF1	M96982	U2(RNU2) small nuclear RNA auxillary factor t	U2 snRNP auxiliary factor small subunit
2589	2589 32858_at	UBN1	Al341565	ubinuclein 1	
2590	2590 34824_at	UBQLN2	AB015344	ubiquilin 2	ubiquilin 2
2591	2591 38451_at	UQCR	T58471	ubiquinol-cytochrome c reductase (6.4kD) subunit	
2592	2592 39427_at	UQCRB	779616	ubiquinol-cytochrome c reductase binding protein	
2593	2593 40854_at	UQCRC2	J04973	ubiquinol-cytochrome c reductase core protein II	ubiquinol-cytochrome c reductase core protein II

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1	C			ubiguinol-cytochrome c reductase hinge	
2594	2594 36104 at	UQCRH	AA526497	protein	
2595	2595 1366_i_at	UBC		лС	ubiquitin C
2596	2596 1367 f at	UBC	M26880		ubiquitin C
				arboxyl-terminal esterase L1	ubiquitin carboxyl-terminal esterase L1
2597	2597 36990_at	UCHL1	X04741		(ubiquitin thiolesterase)
2598	2598 811_at	UFD1L	U6444	ation 1-like	ubiquitin fusion-degradation 1 like protein
2599	2599 40623_at	UBE3B	AI749193	ubiquitin protein ligase	
				ubiquitin protein ligase E3A (human	
				papilloma virus E6-associated protein,	E6-associated protein E6-AP/ubiquitin-
2600	2600 41205_at	UBE3A	U84404	Angelman syndrome)	protein ligase
2601	2601 34383_at	USP1	AB014458	ubiquitin specific protease 1	ubiquitin specific protease
2602	2602 37683_at	USP10	D80012	ubiquitin specific protease 10	
2603	2603 162_at	USP11	U44839	ubiquitin specific protease 11	UHX1 protein
				ubiquitin specific protease 14 (tRNA-	
2604	2604 36982_at	USP14	U30888	guanine transglycosylase)	tRNA-Guanine Transglycosylase
2605	2605 39866_at	USP22	AB028986	ubiquitin specific protease 22	KIAA1063 protein
2606	2606 35847_at	USP24	AB028980	ubiquitin specific protease 24	KIAA1057 protein
				ubiquitin specific protease 4 (proto-	
2607	2607 1357_at	USP4	U20657	oncogene)	ubiquitin protease
				ubiquitin specific protease 5 (isopeptidase	
2608	2608 34405_at	USP5	U47927	Ţ	isopeptidase T
L				ubiquitin specific protease 7 (herpes virus- herpesvirus associated ubiquitin-specific	herpesvirus associated ubiquitin-specific
2609	2609 37672_at	USP7	Z72499	associated)	protease (HAUSP)
2610	2610 39794_at	USP8	D29956	ubiquitin specific protease 8	ubiquitin specific protease 8
				ubiquitin specific protease 9, X	
2611	32572_at	USP9X	X98296	chromosome (fat facets-like Drosophila)	ubiquitin hydrolase
				ubiquitin-activating enzyme E1C (UBA3	
2612	2612 40066_at	UBE1C	AF046024	homolog, yeast)	UBA3
				ubiquitination factor E4A (UFD2 homolog,	ubiquitination factor E4A (UFD2 homolog,
2613	2613 36579_at	UBE4A ·	D50916	yeast)	yeast)
L				ubiquitination factor E4B (UFD2 homolog,	:
2614	2614 41339_at	UBE4B	AF043117	yeast)	ubiquitin-fusion degradation protein 2
2615	2615 36959 at	UBE2V1	U49278	ubiquitin-conjugating enzyme E2 variant 1 UEV-1	UEV-1
			3 := 3:		

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				conjugating enzyme E2A (RAD6	ubiquitin-conjugating enzyme E2A (RAD6
2616	2616 890_at	UBEZA	M74524		homolog)
				ubiquitin-conjugating enzyme E2D 1	
2617	2617 37826_at	UBE2D1	AF020761	(UBC4/5 homolog, yeast)	
				ubiquitin-conjugating enzyme E2D 2	
2618	2618 38705_at	UBE2D2	Al310002	(UBC4/5 homolog, yeast)	
				ubiquitin-conjugating enzyme E2D 2	
2619	2619 832 at	UBE2D2	U39317	(UBC4/5 homolog, yeast)	UbcH5B
				ubiquitin-conjugating enzyme E2D 3	
2620	2620 39083_at	UBE2D3	U39318	(UBC4/5 homolog, yeast)	UbcH5C
				ubiquitin-conjugating enzyme E2D 3	
2621	2621 504_at	UBE2D3	U39318	(UBC4/5 homolog, yeast)	UbcH5C
L				ubiquitin-conjugating enzyme E2E 3	
2622	2622 34850_at	UBE2E3	AB017644	(UBC4/5 homolog, yeast)	ubiquitin-conjugating enzyme E2
L				ubiquitin-conjugating enzyme E2G 2	
2623	2623 32236_at	UBE2G2	AF032456	(UBC7 homolog, yeast)	ubiquitin conjugating enzyme G2
L				ubiquitin-conjugating enzyme E2I (UBC9	
2624	2624 38480_s_at	UBEZI	U66867	homolog, yeast)	ubiquitin conjugating enzyme 9
				ubiquitin-conjugating enzyme E2I (UBC9	
2625	2625 838_s_at	UBEZI	U45328	homolog, yeast)	ubiquitin-conjugating enzyme
2626	2626 223_at	UBE2L3	S81003	ubiquitin-conjugating enzyme E2L 3	L-UBC
2627	2627 40505 at	UBE2L6	AA883502	ubiquitin-conjugating enzyme E2L 6	
				ubiquitin-conjugating enzyme E2N	
2628	2628 36604_at	UBEZN	D83004	(UBC13 homolog, yeast)	ubiquitin-conjugating enzyme E2 UbcH-ben
2629	2629 457_s_at	UBL1	U67122	ubiquitin-like 1 (sentrin)	SUMO-1
883	2630 155_s_at	UBL1	U61397	ubiquitin-like 1 (sehtrin)	ubiquitin-homology domain protein PIC1
263	2631 40839_at	UBL3	AL080177	ubiquitin-like 3	hypothetical protein
2632	2 37336_at	UBXD2	D87684	UBX domain-containing 2	KIAA0242 protein
				UDP-Gal:betaGlcNAc beta 1,4-	
263	2633 40960_at	B4GALT1	D29805	galactosyltransferase, polypeptide 1	beta-1,4-galactosyltransferase
				UDP-Gal:betaGlcNAc beta 1,4-	
263	2634 34177_at	B4GALT2	AF038660	galactosyftransferase, polypeptide 2	beta-1,4-galactosyltransferase
				UDP-Gal:betaGlcNAc beta 1,4-	
263	2635 39445_at	B4GALT3	AF038661	galactosyftransferase, polypeptide 3	beta-1,4-galactosyttransferase
2636	2636 A0215 et	ยบยา	D50840	UDP-glucose ceramide	ceramide alucosytransferase
3	0140212_at	0000	20000	(grace) manicipated	

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2637	2637 35214_at	ОGDH	AF061016	UDP-glucose denydrogenase	UDP-glucose denyarogenase
	I		-		nridine diphosphoglucose
888	2638 37373_at	UGP2	U27460	UDP-glucose pyrophosphorylase 2	pyrophosphorylase
				UDP-N-acetyi-alpha-D-	
				galactosamine:polypeptide N-	-
				acetylgalactosaminyltransferase 1	UDP-GalNAc:polypeptide N-
2639	2639 38041_at	GALNT1	U41514	(GalNAc-T1)	acetylgalactosaminyftransferase
				UDP-N-aceMdIucosamine-2-epimerase/N-	UDP-N-aceMglucosamine-2-epimerase/N-UDP-N-acetMglucosamine-2-epimerase / N-
2640	2640 36515_at	GNE	AJ238764	acetylmannosamine kinase	acetylmannosamine kinase
				UDP-N-acteylglucosamine	UDP-N-acetylglucosamine
2641	2641 41242_at	UAP1	AB011004	pyrophosphorylase 1	pyrophosphorylase
2642	2642 34827_at	ULK1	AF045458	unc-51-like kinase 1 (C. elegans)	serine/threonine kinase ULK1
				uncharacterized bone marrow protein	
2643	2643 37315_f_at	BM036	A1057607	ВМозе	
				uncharacterized hypothalamus protein	
2644	2644 35750_at	HT010	AL049948	HT010	
				uncharacterized hypothalamus protein	
2645	2645 41058 g_at	HT012	AI760162	HT012	
				uncharacterized hypothalamus protein	
2646	2646 41057_at	HT012	AI760162	HT012	
				unnamed protein product; Human gene	
2647	2647 38610_s_at	KRT10; KPP	X14487	for acidic (type I) cytokeratin 10.	keratin 10
2648	2648 34402_at	UNRIP	AB024327	unr-interacting protein	WD-40 repeat protein
				upstream regulatory element binding	upstream regulatory element binding protein
2649	34372_at	UREBI	AB002310	protein 1	
2650	2650 37686_s_at	UNG	Y09008	uracil-DNA glycosylase	uracil-DNA glycosylase
				uridine monophosphate synthetase	uridine monophosphate synthetase (orotate
				(orotate phosphoribosyl transferase and	phosphoribosyl transferase and orotidine-5'-
2651	2651 33815_at	UMPS	J03626	orotidine-5'-decarboxylase)	decarboxylase)
					dermatan/chondroitin sulfate 2-
2652	2652 41859_at	UST	AB020316	uronyl-2-suffotransferase	sulfotransferase
				UV Radiation Resistance Associated Gene: Hisabiens mRNA: UV Badiation	
2653	2653 39429_at	UVRAG	X99050	Resistance Associated Gene.	p63 (processed form)

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Γ					v-abl Abelson murine leukemia viral
					oncogene homolog 1 isoform a; v-abl
				v-abi Abelson murine leukemia viral	Abelson murine leukemia viral oncogene
2654	2654 39730_at		X16416		homolog 1 isoform b
2655		VPS45A	AJ133421	vacuolar protein sorting 45A (yeast)	vacuolar protein sorting
				VAMP (vesicle-associated membrane	
2656	2656 38801_at	VAPA	AI742846	protein)-associated protein A (33kD)	
					vascular cell adhesion molecule 1, isoform a
					precursor; vascular cell adhesion molecule
2657	583_s_at	VCAM1	M30257	vascular cell adhesion molecule 1	1, isoform b precursor
2658	2658 1953_at	VEGF	AF024710	vascular endothelial growth factor	vascular endothelial growth factor
2659	2659 36100 at	VEGF	AF022375	vascular endothelial growth factor	vascular endothelial growth factor
					VEGF related factor isoform VRF186
2660	2660 37268_at	VEGFB	U43368	vascular endothelial growth factor B	precursor
					vascular endothelial growth factor related
2661	2661 159_at	VEGFC	U43142	vascular endothelial growth factor C	protein
	-			VDAC protein; similar to mouse VDAC 3;	
				Homo sapiens voltage dependent anion	
2662	2662 36102 at	VDAC3; HD-VDA	DA0AF038962	channel protein mRNA, complete cds.	voltage dependent anion channel protein
2663	2663 40147 at		U18009	vesicle amine transport protein 1	vesicle amine transport protein 1
2664	2664 33930 at	RA410	AB020724	vesicle transport-related protein	KIAA0917 protein
				vesicle-associated membrane protein 2	
2665	2665 32254_at	VAMP2	AL050223	(synaptobrevin 2)	
				vesicle-associated membrane protein 3	
2666	2666 35783_at	VAMP3	H93123	(cellubrevin)	
2667	2667 40103_at	VILZ	X51521	villin 2 (ezrin)	villin 2
2668	2668 34091_s_at	VIM	Z19554	vimentin	vimentin
			٠		vinculin isoform VCL; VCL isoform meta-
2669	2669 36601_at	VCL	M33308	vinculin	VCL
2670	2670 39091 at	δWI.	AE070523	viamin A responsive: cytoskeleton related JWA protein	JWA protein
				vitamin D (1.25- dihydroxyvitamin D3)	vitamin D (1.25- dihydroxyvitamin D3)
2671	2671 1388_g_at	VDR	J03258	receptor	receptor
				v-Ki-ras2 Kirsten rat sarcoma 2 virat	
2672	2672 1940_at	KRAS2	M54968	oncogene homolog	K-ras oncogene protein

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				fibrosarcoma	
2673	2673 41504_s_at	MAF	AF055376		short form transcription factor C-MAF
				v-maf musculoaponeurotic fibrosarcoma	
2674	2674 32835_at	MAFF	AA725102	oncogene homolog F (avian)	
2675	2675 40198_at	VDAC1	L06132	voltage-dependent anion channel 1	voltage-dependent anion channel
2676	2676 37696 at	VDAC2	L06328	voltage-dependent anion channel 2	voltage-dependent anion channel
2677	2677 171 at	VBP1	USEB33		VHL binding protein-1
				v-raf-1 murine leukemia viral oncogene	
2678	2678 38743_f_at	RAF1	X06409	homolog 1	
				v-ral simian leukemia viral oncogene	
				homolog B (ras related; GTP binding	v-ral simian leukemia viral oncogene
2679	2679 32776_at	RALB	M35416	protein)	homolog B
				v-rel reticuloendotheliosis viral oncogene	
		-		homolog A, nuclear factor of kappa light	
				polypeptide gene enhancer in B-cells 3,	
2680	2680 36645_at	RELA	L19067	p65 (avian)	NF-kappa-B transcription factor subunit
				v-rel reticuloendotheliosis viral oncogene	
				homolog A, nuclear factor of kappa light	
				polypeptide gene enhancer in B-cells 3,	
2681	2681 1295_at	RELA	L19067	p65 (avian)	NF-kappa-B transcription factor subunit
				v-yes-1 Yamaguchi sarcoma viral	v-yes-1 Yamaguchi sarcoma viral oncogene
2682	2682 1674_at	YES1	M15990	oncogene homolog 1	homolog 1
				v-yes-1 Yamaguchi sarcoma viral related	v-yes-1 Yamaguchi sarcoma viral related
2683	2683 1402_at	LYN	M16038	oncogene homolog	oncogene homolog
2684	2684 1058_at	WASF3	S69790	WAS protein family, member 3	
2685	2685 38736_at	WDR1	AL050108	WD repeat domain 1	hypothetical protein
2686	2686 41430_at	WDR7	AB011113	WD repeat domain 7	KIAA0541 protein
7897	2687 36009_at	CLESS	AFOSTOSZ	Weakly similar to giutathione peroxidase 2	_
2688	2688 36909_at	WEE1	X62048	WEE1+ homolog (S. pombe)	wee1 tyrosine kinase
				1	eukaryotic translation initiation factor 4H,
	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	10000	00000	Williams-beuren syndrome chromosome	Solom 1; eukaryone translanon initiation
2007	2003 4 12 12 I BI	Woody	חלסתסס	i initial	ומכוטו אווי ואסוטוווו ב
2690	2690 41635_at	WTAP	D14661	Wilms' tumour 1-associating protein	Wilms' tumour 1-associating protein
2691	2691 31862 at	WNT5A	120861	wingless-type MMTV integration site family, member 5A	wingless-type MMTV integration site family, member 5A precursor

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					Wolf-Hirschhorn syndrome candidate 2
2692	2692 34225_at	WHSC2	AF101434	ndidate 2	protein
2693	2693 33438_at	WBP2	AL049981	WW domain binding protein 2	
	-			WW domain binding protein 4 (formin	
2694	2694 35213_at	WBP4	AF071185	binding protein 21)	formin binding protein 21
2695	2695 39995_s_at	WWOX	U13395	WW domain containing oxidoreductase	oxidoreductase
				WW domain-containing adapter with a	=
2696	2696 36822_at	WAG	U51334	coiled-coil region	putative RNA binding protein RBP56
Γ				xeroderma pigmentosum,	
2697	2697 1307_at	XPA	D14533	complementation group A	XPAC protein
				xeroderma pigmentosum,	
2698	2698 1873_at	XPC	D21089	complementation group C	XP-C repair complementing protein (p125)
				XPA binding protein 1; putative ATP(GTP)	
2699	2699 41756_at	NTPBP	AJ010842	binding protein	ATP(GTP)-binding protein
				X-ray repair complementing defective	٠
				repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	
2700	2700 38733_at	XRCC5	M30938	80kD)	ATP-dependant DNA helicase II
				X-ray repair complementing defective	
				repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	
2701	2701 585_at	XRCC5	M30938	80kD)	ATP-dependant DNA helicase II
				X-ray repair complementing defective	
			-	repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	
2702	2093_s_at	XRCC5	J04977	80kD)	ATP-dependant DNA helicase II
2703	2703 35827_at	KIAA0905	AB020712	yeast Sec31p homolog	KIAA0905 protein
2704	2704 40988_at	YME1L1	AJ132637	YME1-like 1 (S. cerevisiae)	ATP-dependent metalloprotease YME1L
2705 891	891_at	1771	M77698	YY1 transcription factor	GLI-Krupple related protein
				zb29g04.s1	
	.,			Soares_parathyroid_tumor_NbHPA Homo	
	-			sapiens cDNA clone IMAGE:305046 3',	
2706	2706 34887_at		N92548	mRNA sequence.	
.		•		Zic family member 1 (odd-paired homolog,	
2/0/	2707 36308_at	ZIC1	076435	Urosophila)	Zic protein
2708	2708 35681_r_at	ZFHX1B	AB011141	zinc finger homeobox 1b	KIAA0569 protein

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2709	34786	TSGA	AB018285	zinc finger protein	KIAA0742 protein
2710	2710 39977_at	ZNF-U69274	U69274	zinc finger protein	zinc finger protein
2711	2711 40140_at	ZFP103	D76444	zinc finger protein 103 nomolog (mouse)	Zinc linger protein 103 nomotog
2712	2712 36295_at	ZNF134		zinc finger protein 134 (clone pHZ-15)	zinc finger protein ZNF134
2713	2713 32192 g at	ZNF144	D13969	zinc finger protein 144 (Mel-18)	Mel-18 protein
2714	2714 36928_at	ZNF146	X70394	zinc finger protein 146	zinc finger protein
2715	2715 41532_at	ZNF151	Y09723	zinc finger protein 151 (pHZ-67)	Miz-1 protein
2716	2716 32628_at	ZNF161	D28118	zinc finger protein 161	DB1
2717	2717 41436_at	ZNF198	AJ224901	zinc finger protein 198	ZNF198 protein
2718	2718 40724_at	ZNF200	Y14443	zinc finger protein 200	zinc finger protein
2719	2719 35368_at	ZNF207	AF046001	zinc finger protein 207	zinc finger protein 207
2720	2720 41542_at	ZNF216	AF062346	zinc finger protein 216	zinc finger protein 216 splice variant 1
2721	2721 840_at	ZNF220	U47742	zinc finger protein 220	monocytic leukaemia zinc finger protein
2722	2722 39762_at	ZNF262	AB007885	zinc finger protein 262	zinc finger protein 262
2723	2723 34299_at	ZNF278	AL096880	zinc finger protein 278	hypothetical protein
2724	2724 39005_s_at	ZNF294	AB018257	zinc finger protein 294	KIAA0714 protein
2725	2725 37860_at	ZNF337	AL049942	zinc finger protein 337	hypothetical protein
				zinc finger protein 36, C3H type, homolog	
2726	2726 40448_at	ZFP36	M92843	(esnow)	zinc finger transcriptional regulator
2727	2727 38740_at	ZFP36L1	X79067	zinc finger protein 36, C3H type-like 1	butyrate response factor 1
2728	2728 36046 at	ZNF363	AL050144	zinc finger protein 363	hypothetical protein
					hypothetical protein, similar to (U06944)
2729	2729 32129_at	ZNF364	AL079314	zinc finger protein 364	PRAJA1 [Mus musculus]
2730	2730 41033_at	ZNF84	M27878	zinc finger protein 84 (HPF2)	DNA binding protein
2731	2731 40610_at	ZFR	AI743507	zinc finger RNA binding protein	
2732	2732 39751_at	ZDHHC3	AF052182	zinc finger, DHHC domain containing 3	
				zinc metalloproteinase (STE24 homolog,	
2733	2733 33912_at	ZMPSTE24	Y13834	yeast)	farnesylated-proteins converting enzyme 1
2734	2734 36521_at	DZIP1	AB023213	zinc-finger protein DZIP1	KIAA0996 protein
2735	2735 35995_at	ZWINT	AF067656	ZW10 interactor	ZW10 interactor Zwint
2736	2736 706_at		HG4582-HT4987		
2737	2737 960_g_at		HG2463-HT2559		
2738	2738 956_at		HG1980-HT2023		
2739	2739 955_at		HG1862-HT1897		
2740	2740 324_f_at		HG1515-HT1515		

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4															guanine nucleotide binding protein (G	protein), beta polypeptide 1	guanine nucleotide binding protein (G	protein), beta polypeptide 1
0																		
0	HG1800-HT1823	HG2639-HT2735	HG1112-HT1112	HG3543-HT3739	HG2036-HT2090	HG162-HT3165	HG2855-HT2995	HG2855-HT2995	AL038340	HG3044-HT3742	HG4322-HT4592	HG4322-HT4592	HG1112-HT1112	HG1322-HT5143		AL031282		AL031282
8																dJ283E3.1		dJ283E3.1
A	2741 327_t_at	2742 333_s_at	2743 1840_g_at	2744 1664_at	2745 1624_at	2746 1278_at	2747 1179_at	2748 1180_g_at	2749 32243_g_at	2750 311_s_at	2751 297_g_at	2752 296_at	2753 1839_at	2754 723_s_at		2755 33300_at		2756 41249_at
	2741	2742	2743	2744	2745	2746	274,	2748	2749	275(275	275,	275;	275		275	ĺ	275

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T	X .				Product
-	Systematic	Common	Genbank	Description	Sapor
				ALU WARNING: Human Alu-Sq	
7	AFFX-hum_alu_at		U14573	subfamily consensus sequence.	
က	38820 at		15-Sep AF051894	15 kDa selenoprotein	15 kDa selenoprotein
	I			26S proteasome-associated pad1	
4	33247_at	POH1	U86782	homolog	26S proteasome-associated pad1 homolog
				35 kDa protein; Homo sapiens splicing	
				factor, arginine/serine-rich 7 (SFRS7)	
2	32165_at	SFRS7	L41887	gene, complete cds.	splicing factor, arginine/serine-rich 7
				39 kDa protein; Human N33 protein form	
9	36851 g at	N33	U42360	2 (N33) gene, exon 11 and complete cds.	N33 protein form 2
				3-hydroxy-3-methylglutaryl-Coenzyme A	3-hydroxy-3-methylglutaryl-Coenzyme A
7	39328_at	HMGCR	M11058	reductase	reductase
					succinyl CoA:3-oxoacid CoA transferase
80	41142 at	ОХСТ	U62961	3-oxoacid CoA transferase	precursor
				3-phosphoadenosine 5-phosphosulfate	
6	34411_at	PAPSS1	Y10387	synthase 1	PAPS sunthetase
2	738_at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase
Ξ	31794 at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase
				5-aminoimidazole-4-carboxamide	
				ribonucleotide formyltransferase/IMP	5-aminoimidazole-4-carboxamide-1-beta-D-
12	38811_at	ATIC	D82348	cyclohydrolase	ribonucl eotide transformylase/inosinicase
				5-methyltetrahydrofolate-homocysteine	
1 3	38383_at	MTR	U73338	methyltransferase	methionine synthase
4	39025_at	LOC54543	AI557912	6.2 kd protein	

_		_					$\overline{}$		7
ш	divolent cation tolerant protein Cl ITA	delta7-sterol reductase	ADAM10		metalloprotease/disintegrin/cysteine-rich protein precursor	gravin		KIAA0629 protein KIAA0920 protein	הייטול הייטול הייטול הייטול הייטול
<u>Q</u>	60S Ribosomal Protein L35A LIKE pseudogene match: proteins P04646 P02434 P18077 P05744 P41056 CE04362 match: cDNAs Y16430 X52966 X03475 V01440 X55030 J00995 match: ESTs AA554649 AA747384 AA572868 AA329139 AA745138 AA330809 AA483371 AA507788 AA483213 D55111 N90267 N91909 AA662153 AA720551 AA608598 AA649846 AA654164 match: genomic DNAs Z32550 X05705 X05706	7-dehydrocholesterol reductase	a disintegrin and metalloproteinase domain 10	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	A kinase (PRKA) anchor protein (gravin) 12	A kinase (PRKA) anchor protein 10	A kinase (PRKA) anchor protein 11	A Milase (F nice) allonor protein &
ပ		ALU21366 AF034544	AF009615	AA142964	U41766	U81607	AA114830	AB014529	ADUZS 137
B		GICK0/21Q.1	ADAM10	ADAM17	ADAM9	AKAP12	AKAP10	AKAP11	ANAFZ
A		40446_at	40797 at	41601 at	34761_r_at	37680_at		34657_at	35985_at
		15	2 2	18	19	20	21	22	3

Fig 21

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				ABL is the cellular homolog proto- oncogene of Abelson's murine leukemia virus and is associated with the 19:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using alternative first exon 1b; ABL is the cellular homolog proto- oncogene of Abelson's murine leukemia virus and is associated with the 19:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using exon 1a; Human proto- oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete	
	1636_g_at	ABL	U07563	cds.	proto-oncogene tyrosine-protein Kinase
25	41724_at	DXS1357E	X81817	accessory proteins BAP31/BAP29	accessory proteins BAP31/BAP29
				acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A	
56	41530_at	ACAA2	D16294	thiolase)	mitochondrial 3-oxoacyl-CoA thiolase
	34668_at	ACATN	D88152	acetyl-Coenzyme A transporter	acetyl-coenzyme A transporter
28	36553_at	ASMTL	AA669799	acetylserotonin O-methyltransferase-like	
29	37034 at	ANP32A	U73477	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	acidic nuclear phosphoprotein pp32
	38479 at	ANP32B	Y07969	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	APRIL
	34397_at	OA48-18	AF069250	acid-inducible phosphoprotein	okadaic acid-inducible phosphoprotein
32	39168_at	ALTE	AB018328	Ac-like transposable element	KIAA0785 protein
ဗ္ဗ	40077_at	ACO1	211559	aconitase 1, soluble	iron regulatory factor
34	37578_at	AFAP	D25248	actin filament associated protein	actin filament associated protein
35	1718_at	ARPC2	U50523	actin related protein 2/3 complex, subunit 2 (34 kD)	actin related protein 2/3 complex, subunit 2 (34 kD)

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	<	۵	c	C	Ш
T	C			complex, subunit	
36	34692_r_at	ARPC4	AF006087		p20-Arc
_				actin related protein 2/3 complex, subunit	
37	38392_at	ARPCS	AF006088	5 (16 kD)	p16-Arc
38	32755_at	ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	alpha 2 actin
ī	AFFX-HSAC07/XACTB		X00351	actin, beta	beta actin
9	AFFX-HSAC07/YACTB		X00351	actin, beta	beta actin
4	32318 s at		X63432	actin, beta	mutant beta-actin (beta'-actin)
42		ACTG1	X04098	actin, gamma 1	gamma-actin
Т		ACTN1	X15804	actinin, alpha 1	actinin, alpha 1
	at	ACTN4	U48734	actinin, alpha 4	alpha actinin
45	38642 at	ALCAM	Y10183	activated leucocyte cell adhesion molecule MEMD protein	MEMD protein
				activated RNA polymerase II transcription	
46	36171_at	PC4	AI521453	cofactor 4	
47	39764_at	ACVR1	Z22534	activin A receptor, type I	ALK-2
48	35162_s_at	ACVR2	D31770	activin A receptor, type II	activin typell A receptor precursor
49	34394_at	ADNP	AB018327	activity-dependent neuroprotector	KIAA0784 protein
	_			acyl-Coenzyme A dehydrogenase,	-
20	40673_at	ACADSB	U12778	short/branched chain	acyl-CoA dehydrogenase
21	40459_at	ACOX1	Se9189	acyl-Coenzyme A oxidase 1, palmitoyl	peroxisomal acyl-coenzyme A oxidase
				adaptor-related protein complex 1, beta 1	
52	40745_at	AP1B1	L13939	subunit	beta-prime-adaptin
				adaptor-related protein complex 1,	
23	35275_at	AP1G1	AL050025	gamma 1 subunit	hypothetical protein
				adaptor-related protein complex 2, mu 1	adaptor-related protein complex 2, mu 1
54	39795_at	AP2M1	D63475	subunit	subunit
				adaptor-related protein complex 2, sigma	
22	39347_at	AP2S1	X97074	1 subunit	clathrin-associated protein
				adaptor-related protein complex 3, beta 1	
26	32039_at	AP3B1	U81504	subunit	beta-3A-adaptin subunit of the AP-3 complex
L				adaptor-related protein complex 3, delta 1	
57	36172_s_at	AP3D1	AF002163	subunit	delta-adaptin
		4000 A	104000	adaptor-related protein complex 3, sigma	AP-3 complex signaga subunit
ဂ္ဂ	_	AFSSI	091932	- Administration (manage)	adding like protein
29	33102_at	AUU3	D6/031	adducin 3 (garnina)	adducii Fiike proteii i

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	¥	8	د	0	J
	*				adenosine deaminase, RNA-specific,
					isoform ADAR-a; adenosine deaminase,
			-		RNA-specific, isoform ADAR-b; adenosine
9	38014 at	ADAR	X79448	adenosine deaminase, RNA-specific	deaminase, RNA-specific, isoform ADAR-c
\mathbf{T}				adenosine deaminase, RNA-specific, B1	
61	38748 at	ADARB1	U76421	(RED1 homolog rat)	dsRNA adenosine deaminase DRADA2b
29	168 at	ADK	U50196	adenosine kinase	adenosine kinase
Ţ	55 at	BS69	AA127624	adenovirus 5 E1A binding protein	
Г		ADCY3	AB011083	adenylate cyclase 3	KIAA0511 protein
_		ADCY7	D25538	adenylate cyclase 7	adenylate cyclase 7
Т	33800_at	ADCY9	AF036927	adenylate cyclase 9	adenylyl cyclase type IX
67	40788 at	AK2	U84371	adenylate kinase 2	adenylate kinase 2A
89	36639 at	ADSL	AF067853	adenylosuccinate lyase	adenylosuccinate lyase
1	935_at	CAP	L12168	adenylyl cyclase-associated protein	adenylyl cyclase-associated protein
2	33405_at	CAP2	N90755	adenylyl cyclase-associated protein 2	
7	34378 at	ADFP	X97324	adipose differentiation-related protein	adipophilin
72	36861_at	DKFZp56411922	AL049946	adlican	hypothetical protein
73	33987_at	ARF1	M36340	ADP-ribosylation factor 1	ADP-ribosylation factor 1
74	39336_at	ARF3	M74491	ADP-ribosylation factor 3	ADP-ribosylation factor 3
75	36585_at	ARF4	M36341	ADP-ribosylation factor 4	ADP-ribosylation factor 4
				ADP-ribosylation factor domain protein 1,	
92	37537_at	ARFD1	L04510	64kD	nucleotide binding protein
				ADP-ribosylation factor GTPase activating	
77	39905_i_at	ARFGAP1	AA402332	protein 1	
78	37296_at	ARL1	L28997	ADP-ribosylation factor-like 1	ADP-ribosylation factor-like 1
L	_			ADP-ribosylation factor-like 6 interacting	
.79	36572_r_at	ARL6IP	D31885	protein	
				ADP-ribosyltransferase (NAD+; poly (ADP	
8	41146_at	ADPRT	J03473	ribose) polymerase)	poly(ADP-ribosyl)transferase
L				ADP-ribosyltransferase (NAD+; poly (ADP	-
8	1287_at	ADPRT	J03473	ribose) polymerase)	poly(ADP-ribosyl)transferase
85	34777_at	ADM	D14874	adrenomedullin	adrenomedullin precursor
·				AF034176 Human mRNA (Tripodis and	
- 8			7	Ragoussis) Homo sapiens cUNA clone	
3	32218_at		AF034176	media contig.	-

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AFG3L2 Y18314 AFG3 ATPase family gene 3-like 2 (yeast) pagrin AGRN AF016903 agrin AHNAK M80899 AHNAK nucleoprotein (desmoyokin) alanyl-tRNA synthetase ALDH1A3 U07919 member A3 aldehyde dehydrogenase 1 family, member A3 aldehyde dehydrogenase 2 family aldehyde dehydrogenase 3 family, member A1 ALDH2 X05409 (mitochondrial) aldehyde dehydrogenase 3 family, member A1 aldehyde dehydrogenase 3 family, member A1 ALDH3A2 U46689 member A1 aldehyde dehydrogenase 3 family, member A1 ALDH3A1 U34256 aldehyde dehydrogenase 9 family, member A1 ALDH9A1 U34252 aldehyde dehydrogenase 9 family, member A1 AKR1B1 X15414 (aldehyde reductase family 1, member B1 AKR1B1 X15414 (aldehyde reductase family 1, member C3 AKR1C3 D17793 type II) AKR1C3 D17793 type II) AKR7A2 AF026947 (alteroxin aldehyde reductase family 1, member C3 AGPS Y09443 althydilycerone phosphate synthase AGAPS AB0223234 alpha integrin		A	В	O	Ω	ш
33434_at AGRN AFO16903 agrin 37027_at AHNAK M80899 AHNAK nucleoprotein (desmoyokin) 36186_at AARS D32050 alanyi-IRNA synthelase 36686_at ALDH1A3 U07919 aldehyde dehydrogenase 1 family. 32747_at ALDH3A2 U46689 member A3 40409_at ALDH3A2 U46689 member A1 36132_at ALDH3A1 U24266 member A1 36132_at ALDH3A1 U34265 member A1 38780_at ALDH9A1 U34266 member A1 38780_at ALDH9A1 U34266 member A1 38780_at ALDH9A1 U34266 member A1 38780_at AKR181 X15414 (aldehyde dehydrogenase 9 family. 38780_at AKR162 AC52694	24	34315 at	AFG31.2	Y18314	AFG3 ATPase family gene 3-like 2 (veast)	paraplegin-like protein
AFINAK M80899 AFINAK nucleoprotein (desmoyokin) 36185_at AARS D32050 alanyl-HRNA synthetase aldehydrogenase 1 family, aldehydrogenase 2 family aldehydrogenase 3 family aldehydrogenase 3 family aldehydrogenase 3 family aldehydrogenase 4 family aldehydrogenase 5 family aldehydrogenase 6 family 1, member A1 aldehydrogenase 6 family 1, member A2 aldehydrogenase 6 family 1, member A2 aldehydrogenase 6 family 1, member A3 aldehydrog			AGEN	AF016903	agrin	agrin precursor
36686_at			AHNAK	MRORGO	AK nucleoprofein (desmovokin)	
36686_at ALDH1A3 U07919 member A3 aldehyde dehydrogenase 2 family, aldehyde dehydrogenase 2 family, aldehyde dehydrogenase 2 family, aldehyde dehydrogenase 3 family, aldehyde dehydrogenase 3 family, aldehyde dehydrogenase 3 family, aldehyde dehydrogenase 3 family, aldehyde dehydrogenase 4 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 9 family, aldehyde reductase family 1, member R1 aldehyde reductase family 1, member R2 aldo-keto reductase family 1, member R2 aldo-keto reductase family 7, member R2 aldo-keto reductase family 7, member R2 aldo-keto reductase family 7, member R3 aldo-keto reductase family			AARS	D32050		alanyl-tRNA synthetase
ALDH1A3 U07919 member A3 ALDH2 X05409 (mitochondrial) ALDH2 X05409 (mitochondrial) ALDH3A2 U46689 member A2 ALDH3A1 U24266 aldehyde dehydrogenase 4 family. ALDH7A1 S74728 member A1 ALDH9A1 U34252 member A1 AKR1A1 J04794 (aldehyde dehydrogenase 9 family. AKR1B1 X15414 (aldehyde dehydrogenase 9 family. AKR1B1 X15414 (aldehyde reductase family 1, member A1 AKR1B1 X15414 (aldehyde reductase family 1, member R1 AKR1C3 D17793 type II) AKR1C3 D17793 type II) AKR7A2 AF026947 (alfatoxin aldehyde reductase) AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha phydroxysteroid dehydrogenase) ARBO23234 alkylglycerone phosphate synthase ATRX AB022324 alkylglycerone phosphate synthase ATRX AB022324 alpha integrin binding protein 63					e 1 family,	
ALDH2 X05409 (mitochondrial) ALDH3A2 U46689 member A2 ALDH3A2 U46689 member A2 ALDH4A1 U24266 member A1 ALDH4A1 U24266 member A1 ALDH9A1 U34252 aldehyde dehydrogenase 7 family. ALDH9A1 U34252 member A1 AKR1A1 J04794 (aldehyde dehydrogenase 9 family. AKR1B1 X15414 (alde-keto reductase) AKR1B1 X15414 (alde-keto reductase) AKR1C3 D17793 type II) AKR1C3 D17793 type II) AGPS AFO26947 (aflatoxin aldehyde reductase) AGPS AGPS AGPS AGPS AGPS AGPS AGPS AGPS AGPS AGPS AGPS AGPS AGPS	88	36686_at	ALDH1A3	U07919	member A3	aldehyde dehydrogenase 6
ALDH2 X05409 (mitochondrial) ALDH3A2 U46689 member A2 ALDH4A1 U24266 member A1 ALDH7A1 S74728 member A1 ALDH9A1 U34252 member A1 AKR1A1 J04794 aldehyde dehydrogenase 7 family. AKR1B1 X15414 alde-keto reductase 1 family 1, member A1 AKR1B1 X15414 (aldehyde reductase 1 family 1, member R1 AKR1C3 D17793 ype II) AKR7A2 AFO26947 (aldehyde reductase 1 family 1, member A2 AKR7A2 AFO26947 (aldeo-keto reductase family 1, member C3 G2AN Jype II) aldo-keto reductase family 1, member C3 AKR7A2 AFO26947 (aldehyde reductase family 1, member C3 G2AN Jype II) aldo-keto reductase family 1, member C3 AGPS Y09443 aldo-keto reductase family 1, member C3 AFIQ AFO26947 (aldose reductase family 1, member C3 AGPS Y09443 alkylglycerone phosphate synthase AFIQ U16954 ALL1-tused gene from chromosome 1q <td></td> <td></td> <td></td> <td></td> <td></td> <td>aldehyde dehydrogenase 2 family</td>						aldehyde dehydrogenase 2 family
ALDH3A2 U46689 member A2 aldehyde dehydrogenase 3 family, aldehyde dehydrogenase 4 family, ALDH4A1 U24266 member A1 aldehyde dehydrogenase 7 family, member A1 ALDH3A1 U34252 member A1 AKR1A1 J04794 (aldehyde reductase) AKR1B1 X15414 (aldehyde reductase) AKR1B1 X15414 (alde-keto reductase) AKR1C3 D17793 lype II) AKR7A2 AFO26947 (alfatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AGPS Y09443 alkylglycerone phosphate synthase AFIQ U16954 ALL1-fused gene from chromosome 1q GZÁN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 ATRX I172936 spha thalassemia/mental retardation ATRX I172936	89	32747_at	ALDH2	X05409	(mitochondrial)	(mitochondrial)
ALDH3A2 U46689 member A2 ALDH4A1 U24266 member A1 ALDH7A1 S74728 aldehyde dehydrogenase 7 family, member A1 ALDH9A1 U34252 member A1 AKR1A1 J04794 (aldehyde dehydrogenase 9 family, member A1 AKR1B1 X15414 (aldehyde reductase family 1, member R1 AKR1B1 X15414 (aldo-keto reductase family 1, member R1 AKR1C3 D17793 lype II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AGPS Y09443 alpha glucosidase II alpha subunit					aldehyde dehydrogenase 3 family,	
ALDH4A1 U24266 member A1 ALDH7A1 S74728 member A1 ALDH7A1 S74728 member A1 ALDH9A1 U34252 member A1 AKR1A1 J04794 aldehyde dehydrogenase 9 family, member A1 AKR1B1 X15414 aldo-keto reductase family 1, member B1 AKR1B1 X15414 (aldebyde reductase) AKR1C3 D17793 lype II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha inlegrin binding protein 63 ATRX ATR	90	40409_at	ALDH3A2	U46689	member A2	aldehyde dehydrogenase
ALDH4A1 U24266 member A1 ALDH7A1 S74728 member A1 ALDH9A1 S74728 member A1 ALDH9A1 U34252 member A1 AKR1A1 J04794 (aldehyde dehydrogenase 9 family, member A1 AKR1B1 X15414 (aldehyde reductase) AKR1B1 X15414 (aldose reductase) AKR1C3 D17793 lype II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AF1Q U16954 ALL1-fused gene from chromosome 1q G22AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha inlegrin binding protein 63 ALD alpha inlegrin binding protein 63 ALD cerevisiae)					aldehyde dehydrogenase 4 family,	
ALDH7A1 S74728 aldehyde dehydrogenase 7 family, member A1 ALDH9A1 U34252 aldehyde dehydrogenase 9 family, member A1 AKR1A1 J04794 (aldehyde reductase family 1, member R1 aldo-keto reductase family 1, member R1 aldo-keto reductase family 1, member C3 aldo-keto reductase family 7, member A2 aldo-keto reductase family 1, member A2	91	37331_g_at	ALDH4A1	U24266	member A1	pyrroline-5-carboxylate dehydrogenase
ALDH7A1 S74728 member A1 ALDH9A1 U34252 member A1 AKB1A1 J04794 (aldehyde reductase family 1, member A1 AKB1B1 X15414 (aldo-keto reductase) AKR1B1 X15414 (aldo-keto reductase) AKR1C3 D17793 type II) AKR7A2 AF026947 (alfatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 ATBX L172936 cerevisiae)					aldehyde dehydrogenase 7 family,	
ALDH9A1 U34252 member A1	92	36132_at	ALDH7A1	S74728	member A1	antiquitin
ALDH9A1 U34252 member A1 AKR1A1 J04794 (aldehyde reductase) AKR1B1 X15414 (aldose reductase) AKR1B1 X15414 (aldose reductase) AKR1C3 D17793 type II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q GZAN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 ATRX L172936 cerevisiae)					aldehyde dehydrogenase 9 family,	
AKR1A1 J04794 (aldehyde reductase family 1, member A1 aldo-keto reductase) AKR1B1 X15414 (aldose reductase) AKR1B1 X15414 (aldose reductase) AKR1C3 D17793 type II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AGPS V09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q GZAN ALL1-fused gene from chromosome 1q alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 ATRX L172936 cerevisiae)	93	33899_at	ALDH9A1	U34252	member A1	gamma-aminobutyraldehyde dehydrogenase
AKR1A1 J04794 (aldehyde reductase) AKR1B1 X15414 (aldose reductase family 1, member B1 aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) AKR1C3 D17793 type II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q GZAN ALL1-fused gene from chromosome 1q GZAN ALL1-fused gene from chromosome 1q GZAN alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 ATRX L172936 cerevisiae)					aldo-keto reductase family 1, member A1	aldo-keto reductase family 1, member A1
AKR1B1 X15414 (aldose reductase) aldo-keto reductase) AKR1B1 X15414 (aldose reductase) aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) aldo-keto reductase family 7, member A2 A2AN aldo-keto gallo-keto reductase family 7, member A2 A2AN aldo-keto reductase family 7, member A2 A2AN aldo-keto reductase family 7, member A2AN aldo-keto reductase family 8, member A2AN aldo-keto reductase family 8, member A2AN aldo-keto reductase family 8,	94	38780_at	AKR1A1	J04794	(aldehyde reductase)	(aldehyde reductase)
AKR1B1 X15414 (aldose reductase) aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q GZAN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 ATBX I172936 cerevisiae)					aldo-keto reductase family 1, member B1	aldo-keto reductase family 1, member B1
AKR1C3 D17793 Salpha hydroxysteroid dehydrogenase, (3-alpha hydroxysteroid dehydrogenase, type II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX 172936 Cerevisiae) Cerevisiae Ce	95	36589_at	AKR1B1	X15414	(aldose reductase)	(aldose reductase)
AKR1C3 D17793 type II) aldo-keto reductase family 7, member A2 aldo-keto reductase family 7, member A2 aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. Cerevisiae) Cerevisiae)					aldo-keto reductase family 1, member C3	
AKR1C3 D17793 type II) AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. Cerevisiae)				••	(3-alpha hydroxysteroid dehydrogenase,	aldo-keto reductase family 1, member C3 (3-
AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.	96	37399_at	AKR1C3	D17793	type II)	alpha hydroxysteroid dehydrogenase, type II)
AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.					aldo-keto reductase family 7, member A2	
AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.	97	32510 at	AKR7A2	AF026947	(aflatoxin aldehyde reductase)	aflatoxin aldehyde reductase AFAR
AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.						alkyl-dihydroxyacetonephosphate synthase
AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.	86	39225_at	AGPS	Y09443	alkylglycerone phosphate synthase	precursor
G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX 172936 cerevisiae)	66	36941 at	AF10	U16954	ALL1-fused gene from chromosome 1q	AF1Q protein
KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.	8	37040 at	GZAN	D42041	alpha glucosidase II alpha subunit	alpha glucosidase II alpha subunit
alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.	10	35223 at	KIAA1017	AB023234	alpha integrin binding protein 63	KIAA1017 protein
Syndrome X-linked (RAD54 homolog, S. Larax 1172936 Cerevisiae)					alpha thalassemia/mental retardation	,
ATRX (172936 cerevisiae)					syndrome X-linked (RAD54 homolog, S.	putative DNA dependent ATPase and
ATTIN (01230)	102	102 39147_g_at	ATRX	U72936	cerevisiae)	helicase

	¥	8	0	a	w
				alpha thalassemia/mental retardation	
				syndrome X-linked (RAD54 homolog, S.	putative DNA dependent ATPase and
103	818_s_at	ATRX	U72936	cerevisiae)	helicase
				alternative translation initiation; H.sapiens	
				HLTF gene for helicase-like transcription	
104	34327_at	五.T.	246606	factor.	helicase-like transcription factor
				aminoadipate-semialdehyde	
				dehydrogenase-phosphopantetheinyl	
105	35761_at	AASDHPPT	AL050073	transferase	hypothetical protein
		NPEPPS	AJ132583	aminopeptidase puromycin sensitive	puromycin sensitive aminopeptidase
107	41338_at	AES	Al951946	amino-terminal enhancer of split	
108	36996_at	6-80	U41635	amplified in osteosarcoma	OS-9 precurosor
				amylo-1, 6-glucosidase, 4-alpha-	
				glucanotransferase (glycogen	
				debranching enzyme, glycogen storage	
109	38253_at	AGL	U84011	disease type III)	glycogen debranching enzyme isoform 6
				amyloid beta (A4) precursor protein	amyloid beta (A4) precursor protein
110	110 41136_s_at	APP	Y00264	(protease nexin-II, Alzheimer disease)	(protease nexin-II, Alzheimer disease)
				amyloid beta (A4) precursor protein-	
111	111 40148_at	APBB2	U62325	binding, family B, member 2 (Fe65-like)	FE65-like protein
L				amyloid beta precursor protein	
112	38471_r_at	APPBP2	D86981	(cytoplasmic tail) binding protein 2	KIAA0228 protein
				amyloid beta precursor protein	
113	38470_i_at	APPBP2	D86981	(cytoplasmic tail) binding protein 2	KIAA0228 protein
				amyloid beta precursor protein binding	
14	35364_at	APPBP1	U50939	protein 1, 59kD	amyloid precursor protein-binding protein 1
				amyotrophic lateral sclerosis 2 (juvenile)	
115	40064_at	ALS2CR3	AB011121	chromosome region, candidate 3	KIAA0549 protein
				androgen receptor (dihydrotestosterone	
_				receptor; testicular feminization; spinal	
				and bulbar muscular atrophy; Kennedy	
116		AR	M23263	disease)	androgen receptor
=	_	AMOTL2	AB023206	angiomotin like 2	angiomotin like 2
118		ANGPT1	D13628	angiopoietin 1	angiopoietin 1
119	1929_at	ANGPT1	U83508	angiopoietin 1	angiopoietin-1

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36965_at	at	ANK3	U13616	ankyrin 3, node of Ranvier (ankyrin G)	ankyrın G
37403 at	at	ANXA1	X05908	annexin A1	annexin l
122 36637 at		_	L19605	annexin A11	56K autoantigen
123 769 s at			D00017		lipocortin II
124 31684 at		ANXA2P1	M62896	annexin A2 pseudogene 1	
125 31444 s at	at		M62895	annexin A2 pseudogene 3	
1					annexin IV (placental anticoagulant protein
126 37374_at	at	ANXA4	M82809	annexin A4	(1)
127 37670 at	at	ANXA7	J04543		annexin VII isoform 1; annexin VII isoform 2
			110070	antigen identified by monoclonal	noning
128 41138 at	at	MICZ	W102/9		amycii
129 40506 s at	s at	PABPC4; APP1; A	AU75686	APP-1; Homo sapiens polyadenylate binding protein mRNA, complete cds.	polyadenylate binding protein
	at	1	X81198	archain 1	archain
				arginine-glutamic acid dipeptide (RE)	
32253_at	at	RERE	AB007927	repeats	KIAA0458 protein
132 549 at		RARS	S80343	arginyl-tRNA synthetase	arginyl-tRNA synthetase
39164	at	ARIH2	AF099149	ariadne homolog 2 (Drosophila)	TRIAD1 type I
134 41729	at	ARIH1	AJ009771	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila) putative RING finger protein	putative RING finger protein
36057	क्र	ALEX2	AB011084	armadillo repeat protein ALEX2	KIAA0512 protein
				ARP1 actin-related protein 1 homolog A,	
136 40052_at	at	ACTR1A	X82206	centractin alpha (yeast)	alpha-centractin
				ARP2 actin-related protein 2 homolog	
137 35734_at	_at	ACTR2	A1935551	(yeast)	
				ARP2 actin-related protein 2 homolog	
138 35733	at _at	ACTR2	AF006082	(yeast)	Arp2
				ARP3 actin-related protein 3 homolog	
139 35271	at at	ACTR3	AF006083	(yeast)	Arp3
140 40516	at	AHR	L19872	aryl hydrocarbon receptor	AH-receptor
141 36671	at	ASNS	M27396	asparagine synthetase	asparagine synthetase
142 41241	at	NARS	D84273	asparaginyl-tRNA synthetase	Asparaginyl tRNA Synthetase
143 38703	at	DNPEP	AF005050	aspartyl aminopeptidase	aspartyl aminopeptidase
144 34181	at	AGA	X55330	aspartylglucosaminidase	aspartylglucosaminidase

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	37229_at	ATR	U49844	ataxia telangiectasia and Rad3 related	FRAP-related protein
146	34817_s_at	A2LP	U70671	ataxin 2 related protein	ataxin-2 related protein
				ATP binding protein associated with cell	
147	379_at	APACD	AB006679	differentiation	ATP binding protein
148	40881_at	ACLY	X64330	ATP citrate lyase	ATP-citrate (pro-S-)-lyase
				ATP synthase, H+ transporting,	
				mitochondrial F0 complex, subunit b,	
149	41228_r_at	ATP5F1	X60221	isoform 1	H+-ATP synthase subunit b
				ATP synthase, H+ transporting,	
				mitochondrial F0 complex, subunit c	mitochondrial ATP synthase subunit 9
150	34811_at	ATP5G3	U09813	(subunit 9) isoform 3	precursor
				ATP synthase, H+ transporting,	
151	35760_at	ATP5H	AF087135	mitochondrial F0 complex, subunit d	F1FO-type ATPase subunit d
				ATP synthase, H+ transporting,	
152	38751_i_at	ATP5I	AA426364	mitochondrial F0 complex, subunit e	
			,	ATP synthase, H+ transporting,	
153	153 36107_at	ATP5J	AA845575	mitochondrial F0 complex, subunit F6	-
				ATP synthase, H+ transporting,	
154	154 38693_at	ATP5L	AA917672	mitochondrial F0 complex, subunit g	
				ATP synthase, H+ transporting,	
				mitochondrial F1 complex, gamma	
155	155 40115_at	ATP5C1	D16562	polypeptide 1	ATP synthase gamma-subunit
				ATPase, Ca++ transporting, cardiac	ATPase, Ca++ transporting, cardiac muscle,
156	39791_at	ATP2A2	M23114	muscle, slow twitch 2	slow twitch 2
				ATPase, Ca++ transporting, cardiac	ATPase, Ca++ transporting, cardiac muscle,
157	39790_at	ATP2A2	M23115	muscle, slow twitch 2	slow twitch 2
				ATPase, Ca++ transporting, type 2C,	
158	158 38684_at	ATP2C1	AJ010953	member 1	putative Ca2+-transporting ATPase
159	159 35831_at	ATP9A	AB014511	ATPase, Class II, type 9A	KIAA0611 protein
160	40853_at	ATP10D	A1478147	ATPase, Class V, type 10D	
161	161 36635_at	ATP11B	AB023173	ATPase, Class VI, type 11B	KIAA0956 protein
				ATPase, Cu++ transporting, alpha	
162	36523_at	ATP7A	L06133	polypeptide (Menkes syndrome)	Cu++-transporting P-type ATPase
,	1 1000	MOULY	1022204	ATPase, H+ transporting, lysosomal	
2	163 33834_at	AIFOW	AA6///95	(vacuolar proton purrip)	

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				ATPase, H+ transporting, lysosomal	
164	37395_at	ATP6S14	D49400	(vacuolar proton pump) 14kD	vacuolar ATPase
				ATPase, H+ transporting, lysosomal	
165	36994_at	ATP6L	M62762	(vacuolar proton pump) 16kD	vacuolar H+ ATPase proton channel subunit
				ATPase, H+ transporting, lysosomal	
166	36167_at	ATP6F	D89052	(vacuolar proton pump) 21kD	proton-ATPase-like protein
				ATPase, H+ transporting, lysosomal	
167	37367_at	ATP6E	X76228	(vacuolar proton pump) 31kD	vacuolar H+ ATPase E subunit
				ATPase, H+ transporting, lysosomal	
168	37948_at	ATP6C	J05682	(vacuolar proton pump) 42kD	H+ -ATPase C subunit
				ATPase, H+ transporting, lysosomal	
169	33875_at	ATP6H	AI547262	(vacuolar proton pump) 9kD	
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump) membrane sector	
170	40903_at	ATP6M8-9	AL049929	associated protein M8-9	hypothetical protein
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump), alpha	
171	34889_at	ATP6A1	AA056747	polypeptide, 70kD, isoform 1	
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump), beta polypeptide,	
172	40568_at	ATP6B2	L35249	56/58kD, isoform 2	vacuolar H+-ATPase 56,000 subunit
				ATPase, H+ transporting, lysosomal	-
173	35770_at	ATP6S1	D16469	(vacuolar proton pump), subunit 1	ORF
				ATPase, Na+/K+ transporting, beta 1	
174	37669_s_at	ATP1B1	U16799	polypeptide	Na,K-ATPase beta subunit
				ATPase, Na+/K+ transporting, beta 3	sodium/potassium-transporting ATPase beta-
175	32563_at	ATP1B3	U51478	polypeptide	3 subunit
				ATP-binding cassette, sub-family A	
176	35717_at	ABCA8	AB020629	(ABC1), member 8	KIAA0822 protein
				ATP-binding cassette, sub-family C	
177	38261_at	ABCC3	AF085692	(CFTR/MRP), member 3	multidrug resistance-associated protein 3B
178	35648_at	KIAA0442	AB007902	autism-related protein 1	autism-related protein 1
179	38068_at	AMFR	M63175	autocrine motility factor receptor	autocrine motility factor receptor
180	38433_at	AXL	M76125	AXL receptor tyrosine kinase	tyrosine kinase receptor
181	35268 at	AXOT	AL050171	axotrophin	hypothetical protein DKFZp586F1122 similar to axotrophin

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182	35350_at	GALNAC4S-6ST	AB011170	B cell RAG associated protein	KIAA0598 protein
				B lymphoma Mo-MLV insertion region	murine leukemia viral (bmi-1) oncogene
183	41562_at	BMI1	L13689	(mouse)	homolog
182		- IMa	13689	B lymphoma Mo-MLV insertion region	murine leukemia viral (bmi-1) oncogene homolog
S S	36578	BIBCo	1137547	ral IAP reneat-containing 2	MIHB
		BAF53A	AF041474		BAF53a
	33175 at	BBS4	AA156237	Bardet-Biedl syndrome 4	
				basic helix-loop-helix domain containing,	
188	40790_at	BHLHB2	AB004066	class B, 2	1-Dec
189	40108_at	BZAP45	D13630	basic leucine-zipper protein BZAP45	basic leucine-zipper protein BZAP45
				basic transcription element binding protein	
190	190 40202_at	втеві	D31716		GC box binding protein
191	35055_at	BTF3	X53281	basic transcription factor 3	general transcription factor
192	192 38364_at	BCE-1	AF068197	BCE-1 protein	BCE-1
				B-cell CLL/lymphoma 6 (zinc finger protein	
193	40091_at	BCL6	U00115	51)	zinc-finger protein
				B-cell translocation gene 1, anti-	
194	37294_at	BTG1	X61123	proliferative	B-cell translocation protein 1
				BCL2/adenovirus E1B 19kD interacting	BCL2/adenovirus E1B 19kD-interacting
195	32060_at	BNIP2	U15173	protein 2	protein 2
				BCL2/adenovirus E1B 19kD interacting	
196	38010_at	BNIP3	AF002697	protein 3	E1B 19K/Bcl-2-binding protein Nip3
				BCL2/adenovirus E1B 19kD interacting	BCL2/adenovirus E1B 19kDa-interacting
197	39436_at	BNIP3L	AF079221	protein 3-like	protein 3a
				-	glucocortoid receptor-associated protein
198	34798_at	BAG1	Z35491	BCL2-associated athanogene	RAP46
199	199 35291_at	BAG2	AL050287	BCL2-associated athanogene 2	hypothetical protein
200	200 36463 at	BAG5	AB020680	BCL2-associated athanogene 5	KIAA0873 protein
201	38050 at	BTF	D79986	Bcl-2-associated transcription factor	KIAA0164 gene product
202	38101_at	BDG-29	AB011151	BDG-29 proten	KIAA0579 protein
				beclin 1 (coiled-coil, myosin-like BCL2	
203	39378_at	BECN1	U17999	interacting protein)	
				beta subunit; Human pyruvate dehydrogenase (FC 1 2 4 1) beta subunit	
204	204 39160 at	PDHB	D90086	dene, exons 1-10.	pyruvate dehydrogenase (lipoamide) beta

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205	34644_at	B2M	AB021288	beta-2-microglobulin	beta 2-microglobulin
506	40601_at	88P	A1057115	beta-amyloid binding protein precursor	
				beta-hexosaminidase alpha chain; Human	
				beta-hexosaminidase alpha chain (HEXA)	
207	39340_at	HEXA	M16424	gene, exon 14.	hexosaminidase A preproprotein
208	38126 at	BGN	J04599		biglycan preproprotein
509	33198 at	BART1	AA206524	binder of Arl Two	
				biotin-amide amidohydrolase; Homo	
				ene, exons 2,	
210	210 37274_at	Btd	AF018631	3, and 4 and complete cds.	biotinidase
				biphenyl hydrolase-like (serine hydrolase;	
				breast epithelial mucin-associated	
211	40912 s at	BPHL	X81372	antigen)	biphenyl hydrolase-related protein
т-	35267 q at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
213	35266_at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
214	37700 at	BLMH	X92106	bleomycin hydrolase	bleomycin hydrolase
				bone morphogenetic protein receptor, type	
215	39565 at	BMPR1A	Z22535		ALK-3
216	39551 at	BHC80	N98667	BRAF35/HDAC2 complex (80 kDa)	
				brain abundant, membrane attached	
217	32607_at	BASP1	AF039656	signal protein 1	neuronal tissue-enriched acidic protein
<u> </u>				brain abundant, membrane attached	
218	32606_at	BASP1	AA135683	signal protein 1	
219	37945_at	BACH	U91316	brain acyl-CoA hydrolase	acyl-CoA thioester hydrolase
220	37958_at	BCMP1	AL049257	brain cell membrane protein 1	brain cell membrane protein 1
221	221 40023 at	BDNF	X60201	brain-derived neurotrophic factor	brain-derived neurotrophic factor
				branched chain keto acid dehydrogenase	
				E1, beta polypeptide (maple syrup urine	branched chain alpha-ketoacid
222	41683_i_at	ВСКОНВ	U50708	disease)	dehydrogenase E1 beta subunit
					breast cancer antiestrogen resistance 3
223	36812_at	BCAR3	U92715	breast cancer anti-estrogen resistance 3	protein
				brefeldin A-inhibited guanine nucleotide-	
224	38306_at	BIG1	AA477576	exchange protein 1	
225	37947_at	BRD3	D26362	bromodomain containing 3	bromodomain containing protein 3
	1	2	0000000	BTB and CNC homology 1, basic leucine	BTB and CNC homology 1, basic leucine
526	226 31895 at	BACHI	ABOUZBO3	Zipper transcription factor i	Zipper transcription ractor r

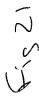
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227	36634_at	BTG2	U72649		8TG2
_	37218 at	BTG3	D64110	BTG family, member 3	ANA
229	41547_at	BUB3	AF047472	east)	spleen mitotic checkpoint BUB3
230	34783_s_at	BUB3	AF047473	benzimidazoles 3 homolog (yeast)	testis mitotic checkpoint BUB3
231	32781_f_at	BPAG1	AA058762	bullous pemphigoid antigen 1 (230/240kD)	-
232	932 32780 at	BPAG1	AB018271	byllous pemphigoid antigen 1 (230/240kD) KIAA0728 protein	KIAA0728 protein
233	233 32629 f at	BTN3A1	U90552	butyrophilin, subfamily 3, member A1	butyrophilin
234	234 39357 at	C2F	U72514	C2f protein	CZł
235	40709 at	LOC58502	W27601	C2H2 (Kruppel-type) zinc finger protein	
236	37031_at	C9orf10	D80005	C9orf10 protein	C9orf10 protein
237	33856_at	CXX1	Y13374	CAAX box 1	putative prenylated protein
920	10 35036	Conti	D01055	cadherin 11, type 2, OB-cadherin	OB-cartherin-2
3	2/200		200	cadherin 11, type 2, OB-cadherin	
239	2087_s_at	CDH11	D21254	(osteoblast)	OB-cadherin-1
5	0100	0000	Madned	cadharin 2 tina 1 N-radharin (neurona))	cadherin 2 type 1 preproprotein
2€2	2000_สเ	ארוט	INIO4004	ימתופווון בי ואף וי וי במתופווון (ווכמיפיום)	ממוימו די ז'ל מי לי
241	31670 s at	CAMK2G	U81554	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	CaM kinase II isoform
				calcium/calmodulin-dependent protein	
242	38716_at	CAMKK2	AB018330	kinase kinase 2, beta	KIAA0787 protein
243	31854 at	CASK	AF035582	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	CASK
244		CALD1	M64110	caldesmon 1	caldesmon
245	_	CALD1	M83216	caldesmon 1	caldesmon
				calmodulin 1 (phosphorylase kinase,	
246	41288_at	CALM1	AL036744	delta)	
<u> </u>				calmodulin 2 (phosphorylase kinase,	
247	911_s_at	CALM2	M19311	delta)	calmodulin 2 (phosphorylase kinase, delta)
248	40125_at	CANX	L10284	calnexin	calnexin
249	37001_at	CAPN2	M23254	calpain 2, (m/II) large subunit	neutral protease large subunit
220	36138_at	CAPNS1	X04106	calpain, small subunit 1	calpain, small subunit 1



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.251	41257_at	CAST	D16217	calpastatin	calpastatin
252	33385_g_at	CAST	U31346	calpastatin	calpastatin
253	40953	CNN3	S80562	calponin 3, acidic	acidic calponin
254	37345_at	CALU	AF013759	calumenin	calumein
				onsive element binding protein	cAMP responsive element binding protein 1, isoform A: cAMP responsive element binding
255	37535_at	CREB1	M27691		protein 1, isoform B
2	40040	on the	100500	cAMP responsive element binding protein	eranscription factor 7IP
8		2010	000000	cAMP responsive element binding protein-	ומומכוולוים ומכוכו רבו
257	39438_at	CREBL2	AF039081	like 2	Cre binding protein-like 2
		,			cyclic AMP-responsive element modulator
258	32065_at	CREM	S68134	cAMP responsive element modulator	beta isoform
259	32067_at	CREM	S68271	cAMP responsive element modulator	cyclic AMP-responsive element modulator
260	32066 d at	CBEM	S68134	cAMP responsive element modulator	cyclic AMP-responsive element modulator beta isoform
				capping protein (actin filament) muscle Z-	
261	40910_at	CAPZA1	U56637	line, alpha 1	capping protein alpha subunit isoform 1
262	36641 at	CAP7A2	U03851	capping protein (actin filament) muscle Z- line, aloha 2	capping protein alpha
				capping protein (actin filament) muscle Z-	
263	37012_at	CAPZB	U03271	line, beta	F-actin capping protein beta subunit
				carbohydrate (chondroitin 6)	
264	32094_at	CHST3	AB017915	sulfotransferase 3	chondroitin 6-sulfotransferase
592	41447_at	CHSY1	AB023207	carbohydrate (chondroitin) synthase 1	KIAA0990 protein
	•			carbohydrate (keratan sulfate Gal-6)	
266	41395_at	CHST1	AB003791	sulfotransferase 1	keratan sulfate Gal-6-sulfotransferase
				carbohydrate (N-acetylglucosamine-6-0)	N-acetylglucosamine-6-O-sulfotransferase
267	37960_at	CHST2	AB014679	sulfotransferase 2	(GlcNAc6ST)
268	268 36454_at	CA12	AF037335	carbonic anhydrase XII	carbonic anhydrase precursor
269	269 34876_at	CPD	06290	carboxypeptidase D	carboxypeptidase D
270	36606_at	CPE	X51405	carboxypeptidase E	carboxypeptidase E precursor
	_			Cas-Br-M (murine) ectropic retroviral	
27.1	35632_at	CBLB	U26710	transforming sequence b	cbl-b
272	272 40184_at	CSNK1A1	L37042	casein kinase 1, alpha 1	casein kinase I-alpha
273	36949_at	CSNK1D	U29171	casein kinase 1, delta	casein kinase i delta

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274	38019_at	CSNK1E	L37043	casein kinase 1, epsilon	casein kinase I-epsilon
				CASP2 and RIPK1 domain containing	
275	1211_s_at	CRADD	U84388	adaptor with death domain	death domain containing protein CRADD
276	1867_at	CFLAR	AF005775	CASP8 and FADD-like apoptosis regulator	CASP8 and FADD-like apoptosis regulator caspase-like apoptosis regulatory protein 2
				caspase 4, apoptosis-related cysteine	
277	195_s_at	CASP4	U28014	protease	cysteine protease
				caspase 8, apoptosis-related cysteine	
278	33774_at	CASP8	X98172	protease	MACH-alpha-1
				catenin (cadherin-associated protein),	
279	41156_g_at	CTNNA1	U03100	alpha 1 (102kD)	alpha2(E)-catenin
				catenin (cadherin-associated protein),	
280	41155_at	CTNNA1	U03100	alpha 1 (102kD)	alpha2(E)-catenin
				catenin (cadherin-associated protein),	
281	2085_s_at	CTNNA1	D14705	alpha 1 (102kD)	'human alpha-catenin'
				catenin (cadherin-associated protein),	
282	2069_s_at	CTNNA1	L23805	alpha 1 (102kD)	alpha1(E)-catenin
				catenin (cadherin-associated protein),	
283	35331_at	CTNNAL1	L90260	alpha-like 1	alpha-catenin-like protein
				catenin (cadherin-associated protein),	
284	40777_at	CTNNB1	X87838	beta 1 (88kD)	beta-catenin
				catenin (cadherin-associated protein),	
285	40444_s_at	CTNND1	AB002382	delta 1	
286	38466_at	CTSK	X82153	cathepsin K (pycnodysostosis)	Cathepsin O
287	37391_at	CTSL	X12451	cathepsin L	pro-(cathepsin L)
288	36915_at	CTSO	AI810485	cathepsin O	
289	36119_at	CAV1	AF070648	caveolin 1, caveolae protein, 22kD	
290	339_at	CAV2	AF035752	caveolin 2	caveolin-2
				Cbp/p300-interacting transactivator, with	
291	33113_at	CITED2	U65093	Glu/Asp-rich carboxy-terminal domain, 2	msg-related gene 1
				CCAAT/enhancer binding protein	
292	1052_s_at	CEBPD	M8366/	(C/EBP), della	INF-1L0-Deta protein
293	293 39219_at	CEBPG	U20240	CCAAT/enhancer binding protein (C/EBP), gamma	C/EBP gamma



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294	33861 at	CNOT2	A1123426	CCR4-NOT transcription complex, subunit 2	
				CCR4-NOT transcription complex, subunit	
295	32820_at	CNOT4	U71267	_	potential transcriptional repressor NOT4Hp
296	34819_at	CD164	D14043	CD164 antigen, sialomucin	MGC-24 precursor
	34699_at	CD2AP	AL050105	CD2-associated protein	hypothetical protein
		- <u>-</u>		CD36 antiden (colladen tyne recentor	
			,	thrombospondin receptor)-like 2	
298	33823_at	CD36L2	D12676	(lysosomal integral membrane protein II)	85kDa human lysosomal sialoglycoprotein
				CD44 antigen (homing function and Indian	
299	2036_s_at	CD44	M59040	blood group system)	cell adhesion molecule
				CD81 antigen (target of antiproliferative	•
300	35282_r_at	CD81	M33680	antibody 1)	CD81 antigen
301	39389_at	CD9	M38690	CD9 antigen (p24)	CD9 antigen
				CDC10 cell division cycle 10 homolog (S.	
302	32175_at	CDC10	S72008	cerevisiae)	cell division cycle 10
				CDC16 cell division cycle 16 homolog (S.	
303	40404_s_at	CDC16	U18291	cerevisiae)	CDC16Hs
				CDC23 (cell division cycle 23, yeast,	,
304	304 31877_at	CDC23	AF053977	homolog)	cell division cycle protein 23
305	305 40690 at	CKS2	X54942	CDC28 protein kinase 2	Cks1 protein homologue
306	306 33362_at	CEP3	AF094521	Cdc42 effector protein 3	MSE55-related protein
30	307 32833 at	CLK1	M59287	CDC-like kinase 1	
88	308 41535_at	CDK2AP1	AF006484	CDK2-associated protein 1	putative oral tumor suppressor protein
				CDP-diacylglycerol synthase	
309	41343_at	CDS2	Y16521	(phosphatidate cytidylyltransferase) 2	CDS2 protein
				CDP-diacylglycerolinositol 3-	
		_		phosphatidyltransferase	
310	310 33397_at	CDIPT	AL050383	(phosphatidylinositol synthase)	=
311	311 40591_at	CDC27	S78234	cell division cycle 27	H-NUC
				cell growth regulatory with ring finger	
312	450_g_at	CGR19	U66469	domain	cell growth regulator CGR19
313	313 36514 at	CGR19	U66469	cell growth regulatory with ring finger domain	cell growth regulator CGR19
2	1000 T	2110	200		

Fig 21

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					cellular repressor of E1A-stimulated genes
314	314 35311_at	CREG	AF084523	cellular repressor of E1A-stimulated genes CREG	CREG
315	315 41333 at	CENTB2	D26069	centaurin, beta 2	centaurin, beta 2
316	316 34676 at	CENTG2	AB029022	centaurin, gamma 2	KIAA1099 protein
317	38410 at	CETN2	X72964	centrin, EF-hand protein, 2	caltractin
	t			centrin, EF-hand protein, 3 (CDC31	
318	35232 f at	CETN3	A1056696	homolog, yeast)	
		CENPC1	M95724		centromere autoantigen C
320	320 33805_at	CAP350	AB007949	centrosome-associated protein 350	KIAA0480 protein
				cerebellar degeneration-related protein	
321	36190_at	CDR2	M63256	(62kD)	major Yo paraneoplastic antigen
322		CGI-01	AL049669	CGI-01 protein	hypothetical protein
323	323 40931_at	LOC50999	AL080084	CGI-100 protein	
324	324 38500 at	LOC51014	AB002450	CGI-109 protein	
325	34359_at	LOC51020	AA524058	CGI-130 protein	
326	38667_at	LOC51031	AA189161	CGI-150 protein	
327	41824_at	LOC51096	A1140114	CGI-48 protein	
328	34862_at	LOC51097	AA005018	CGI-49 protein	
329	37199_at	LOC51626	AI760932	CGI-60 protein	
ဗ္ဗ	330 41411_at	LOC51103	AI566877	CGI-65 protein	
331	39814_s_at	LOC51635	A1052724	CGI-86 protein	
				chaperonin containing TCP1, subunit 2	chaperonin-containing TCP-1 beta subunit
332	35759_at	CCT2	AF026166	(beta)	homolog
		-	1	chaperonin containing TCP1, subunit 3	rice condo FOO to the condo
333	40774_at	CCT3	X74801	(gamma)	
			٠	chaperonin containing ICP1, subunit 4	chaperonin containing t-complex polypeptide
334	32594_at	CCT4	AF026291	(delta)	1, delta subunit
L				chaperonin containing TCP1, subunit 6A	
335	38416_at	ССТ6А	L27706	(zeta 1)	chaperonin-like protein
				chaperonin containing TCP1, subunit 7	chaperonin containing t-complex polypeptide
336	38720_at	CCT7	AF026292	(eta)	1, eta subunit
Ľ				chaperonin containing TCP1, subunit 8	chaperonin containing TCP1, subunit 8
337	39767_at	сств	D13627	(theta)	(theta)
338	338 41000_at	CHES1	U68723	checkpoint suppressor 1	checkpoint suppressor 1
339	37855_at	CTBS	M95767	chitobiase, di-N-acetyl-	di-N-acetylchitobiase

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	Α	В	O	O	11
340	38732 at	CLNS1A	X91788	insitive, 1A	Ich protein
341		CLIC4	AL080061	chloride intracellular channel 4	
_	32363 at	CH25H	AF059214	cholesterol 25-hydroxylase	cholesterol 25-hydroxylase
				chondroitin sulfate proteoglycan 2	
343	38112 g at	CSPG2	X15998	(versican)	chondroitin sulfate proteoglycan 2 (versican)
				chondroitin sulfate proteoglycan 2	
344	38111_at	CSPG2	X15998		chondroitin sulfate proteoglycan 2 (versican)
				chondroitin sulfate proteoglycan 6	
345	34763_at	CSPG6	AF020043	(bamacan)	chromosome-associated polypeptide
				chromobox homolog 1 (HP1 beta homolog	
346	37304_at	CBX1	U35451	Drosophila)	heterochromatin protein p25
				chromobox homolog 3 (HP1 gamma	
347	38085_at	CBX3	AI740522	homolog, Drosophila)	
				chromobox homolog 3 (HP1 gamma	
348	38084 at	CBX3	AA648295	homolog, Drosophila)	
				chromodomain helicase DNA binding	
349	36137_at	CHD4	X86691	protein 4	Mi-2 protein
				chromodomain protein, Y chromosome-	
350	32111_at	CDYL	AL050164	like	hypothetical protein
351	39550_at	Clorf17	AB011156	chromosome 1 open reading frame 17	KIAA0584 protein
352	39033 at	C1orf8	278368	chromosome 1 open reading frame 8	
353	32217_at	C12orf22	AF052105	chromosome 12 open reading frame 22	TGF-beta induced apotosis protein 12
354	40979	C14orf3	AJ243310	chromosome 14 open reading frame 3	C14orf3 protein
355	40045_g_at	C18orf1	AF009425	chromosome 18 open reading frame 1	clone 22
356	36860	C19orf7	AB028987	chromosome 19 open reading frame 7	KIAA1064 protein
357	34287_at	C21orf80	AB023175	chromosome 21 open reading frame 80	KIAA0958 protein
358	33406_at	C22orf2	AL050345	chromosome 22 open reading frame 2	hypothetical protein
329	33778	C22orf4	AL096779	chromosome 22 open reading frame 4	hypothetical protein
360	41758_at	C22orf5	AL096879	chromosome 22 open reading frame 5	hypothetical protein
361	38690_at	C3orf4	AL080097	chromosome 3 open reading frame 4	hypothetical protein
362		C4orf1	AF006621	chromosome 4 open reading frame 1	embryonic lung protein
363	36955_at	C5orf8	U10362	chromosome 5 open reading frame 8	GP36b glycoprotein
364	364 41375_at	C6orf28	AJ245416	chromosome 6 open reading frame 28	G7b protein
365	365 41454_at	C6orf34	W27949	chromosome 6 open reading frame 34	
366	366 36139_at	C6orf5	AL050289	chromosome 6 open reading frame 5	hypothetical protein

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	35193_at	CHC1L	AF060219		RCC1-like G exchanging factor RLG
368	34292_at	CXorf12	X92475	chromosome X open reading frame 12	chromosome X open reading frame 12
369	41314_at	SS	AF047042	citrate synthase	citrate synthase
370 4	41159_at	CLTC	D21260	clathrin, heavy polypeptide (Hc)	clathrin heavy chain
371 3	38657 s at	CLTA	M20471	clathrin, light polypeptide (Lca)	clathrin, light polypeptide A, isoform a, clathrin, light polypeptide A, isoform b
_				nylation specific	
372 3	35743_at	CPSF4	U79569	factor 4, 30kD subunit	no arches
				ation factor, 3' pre-RNA,	
373 3	32723_at	CSTF1	L02547		cleavage stimulation factor
				cleavage stimulation factor, 3' pre-RNA,	
374 4	41183_at	CSTF3	U15782	subunit 3, 77kD	cleavage stimulation factor 77kDa subunit
375	38711_at	CLASP2	AB014527	CLIP-associating protein 2	KIAA0627 protein
376	36017_at	LOC57213	AF055016	CLLL6 protein	CLLL6 protein
				clusterin (complement lysis inhibitor, SP-	clusterin (complement lysis inhibitor, SP-
				40,40, sulfated glycoprotein 2,	40,40, sulfated glycoprotein 2, testosterone-
				testosterone-repressed prostate message repressed prostate message 2,	repressed prostate message 2,
377	36780_at	CLU	M25915	2, apolipoprotein J)	apolipoprotein J)
378	378 35180_at	LOC113251	AL050205	c-Mpl binding protein	
379	379 40811_at	COASTER	AB011148	coactivator for steroid receptors	KIAA0576 protein
380	38052_at	F13A1	M14539	coagulation factor XIII, A1 polypeptide	coagulation factor XIII A1 subunit precursor
381	36972_at	RNP24	X92098	coated vesicle membrane protein	transmembrane protein
382	34326_at	COPB	X82103	coatomer protein complex, subunit beta	beta-Coat protein
				coatomer protein complex, subunit beta 2	
383	383 36677_at	COPB2	X70476	(beta prime)	subunit of coatomer complex
384	384 35205_at	COBRA1	AL050280	cofactor of BRCA1	hypothetical protein
				cofactor required for Sp1 transcriptional	
382	36648_at	CRSP9	AF031383	activation, subunit 9 (33kD)	hMed7
386	386 33659_at	CFL1	X95404	cofilin 1 (non-muscle)	cofilin
387	387 40879_at	BICD2	AB014599	coiled-coil protein BICD2	KIAA0699 protein
388	39864_at	CIRBP	D78134	cold inducible RNA binding protein	CIRP
389	39839_at	CSDA	M24069	cold shock domain protein A	cold shock domain protein A
		COL1A2	V00503	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
		COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
392	32305_at	COL1A2	J03464	collagen, type I, alpha 2	apha 2 type i collagen preproprotein



	A	B	O	D	ш
				colladen type III ainha 1 (Ehlers-Danlos	
393	32488_at	COL3A1	X14420	syndrome type IV, autosomal dominant)	prepro-alpha-1 type 3 collagen
394	36659_at	COL4A2	X05610	collagen, type IV, alpha 2	alpha (2) chain
395	38420_at	COL5A2	Y14690	collagen, type V, alpha 2	procollagen alpha 2(V)
396	38722 at	COL6A1	X15880	collagen, type VI, alpha 1	alpha-1 collagen VI (AA 574-1009)
397	38077_at	COL6A3	X52022	collagen, type VI, alpha 3	collagen type VI, alpha 3 chain
398	37459 at	COL8A1	X57527	collagen, type VIII, alpha 1	alpha 1(VIII) collagen
Γ				9	alpha 1 type XI collagen, isoform A
					preproprotein; alpha 1 type XI collagen,
					isoform B preproprotein; alpha 1 type XI
399	37892_at	COL11A1	J04177	collagen, type XI, alpha 1	collagen, isoform C preproprotein
400	35168_f_at	COL16A1	M92642	collagen, type XVI, alpha 1	alpha-1 type XVI collagen
				complement component 1, q	complement component 1, q subcomponent
401	37668_at	C1QBP	M69039	subcomponent binding protein	binding protein precursor
				complement component 1, r	
402	39409_at	C1R	M14058	subcomponent	complement component 1, r subcomponent
				complement component 1, s	
403	403 40496_at	C1S	J04080	subcomponent	complement component 1, s subcomponent
404	404 36638_at	CTGF	X78947	connective tissue growth factor	connective tissue growth factor
				conserved gene amplified in	
405	41202_s_at	0S4	AF000152	osteosarcoma	OS-4 protein
				conserved helix-loop-helix ubiquitous	
406	33770_at	CHUK	AF009225	kinase	IkB kinase alpha subunit
5			0000	COP9 constitutive photomorphogenic	distriction of animals animals and
کے چ	80/1	5000	1151205	CODO bomolog	COPO cignalosomo cubinit 1 CSN1
99	32539_BI	200	021502	goon solong	COL 9 signalosofine subuffit I COLVI
409	409 40138_at	MOV34-34KD	U70735	COP9 subunit 6 (MOV34 homolog, 34 kD) 34 kDa Mov34 homolog	34 kDa Mov34 homolog
410	410 40452 at	CPNE1	U83246	copine I	copine 1
411	39706_at	CPNE3	AB014536	copine III	KIAA0636 protein
412	412 37999 at	CPO	D16611	coproporphyrinogen oxidase (coproporphyria)	coproporphyrinogen oxidase
413	413 37026 at	COPEB	AF001461	core promoter element binding protein	Kruppel-like zinc finger protein Zf9
414	414 41175_at	CBFB	L20298	core-binding factor, beta subunit	transcription factor
415	32803_at	CNIL	AF104398	cornichon-like	cornichon

	A	B	ပ	Q	3
				COX11 homolog, cytochrome c oxidase	
416	34723_at	COX11	U79270	assembly protein (yeast)	COX11 homolog
		٠		CpG island protein; Human nested gene	
		F8A; DXS522E	M34677	protein gene, complete cds.	coagulation factor VIII-associated protein
418	38664_at	CFDP1	AB009285	craniofacial development protein 1	craniofacial development protein 1
				CREB binding protein (Rubinstein-Taybi	
419	33831_at	CREBBP	U47741	syndrome)	CREB-binding protein
420	36948_at	CRI1	AL109701	CREBBP/EP300 inhibitory protein 1	C15or13
421		CRY1	D83702	cryptochrome 1 (photolyase-like)	photolyase
422	37902_at	CRYZ	L13278	crystallin, zeta (quinone reductase)	zeta-crystallin
423	40167_s_at	LOC55884	AF038187	CS box-containing WD protein	
				CSE1 chromosome segregation 1-like	
454	38804_at	CSE1L	AF053641	(yeast)	cellular apoptosis susceptibility protein
425	1768_s_at	CSK	X59932	c-src tyrosine kinase	c-src-kinase
426	41309_g_at	CTBP1	U37408	C-terminal binding protein 1	phosphoprotein CtBP
427	40780_at	CTBP2	AF016507	C-terminal binding protein 2	C-terminal binding protein 2
428	39723_at	CUL1	AF062536	cullin 1	cullin 1
429	429 40141_at	CUL4B	AB014595	cullin 4B	KIAA0695 protein
				cut-like 1, CCAAT displacement protein	
430	430 31823_at	CUTL1	M74099	(Drosophila)	cut-like 1, CCAAT displacement protein
<u>£</u>	431 36872_at	ARPP-19	AL120559	cyclic AMP phosphoprotein, 19 kD	•
				cyclin D binding myb-like transcription	cyclin D binding myb-like transcription factor
432	41808_at	DMTF1	AF052102	factor 1	1
				cyclin D1 (PRAD1: parathyroid	
433	38418_at	CCND1	X59798	adenomatosis 1) '	cyclin
				cyclin D1 (PRAD1: parathyroid	
434	434 2020_at	CCND1	M73554	adenomatosis 1)	bcl-1
435	435 36650_at	CCND2	D13639	cyclin D2	cyclin D2
436	436 40225_at	GAK	D88435	cyclin G associated kinase	HsGAK
437	37723_at	CCNG2	U47414	cyclin G2	cyclin G2
438	1913_at	CCNG2	U47414	cyclin G2	cyclin G2
439	1924_at	CCNH	U11791	cyclin H	cyclin H
440		CCNI	D50310	cyclin I	cyclin I
44	1792_g_at	CDK2	M68520	cyclin-dependent kinase 2	cdc2-related protein kinase

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				cyclin-dependent kinase 7 (MO15	
				homolog, Xenopus laevis, cdk-activating	
442	33317_at	CDK7	L20320	kinase)	protein serine/threonine kinase
				cyclin-dependent kinase 7 (MO15	
	٠			ivating	
443	1969_s_at	CDK7	X77743		CDK activating kinase
444	35140_at	CDK8	R59697	cyclin-dependent kinase 8	
Γ				cyclin-dependent kinase inhibitor 1A (p21,	
445	2031_s_at	CDKN1A	U03106	Cip1)	cyclin-dependent kinase inhibitor 1A
				cyclin-dependent kinase inhibitor 1B (p27,	
446	33847_s_at	CDKN1B	Al304854	Kip1)	
				cyclin-dependent kinase inhibitor 2C (p18,	
447	36053_at	CDKN2C	AF041248	inhibits CDK4)	cyclin-dependent kinase inhibitor
448	448 38700 at	CSRP1	M33146	cysteine and glycine-rich protein 1	cysteine and glycine-rich protein 1
449	449 41401_at	CSRP2	U57646	cysteine and glycine-rich protein 2	cysteine and glycine-rich protein 2
450	450 40936_at	CRIM1	AI651806	cysteine-rich motor neuron 1	
451	38772 at	CYR61	Y11307	cysteine-rich, angiogenic inducer, 61	CYR61 protein
452		CARS	L06845	cysteinyl-tRNA synthetase	cysteinyl-tRNA synthetase
				cytidine monophosphate-N-	
				acetylneuraminic acid hydroxylase (CMP-	
453	39317_at	CMAH	D86324	N-acetylneuraminate monooxygenase)	CMP-N-acetylneuraminic acid hydroxylase
				cytochrome b5 outer mitochondrial	
454	34340_at	CYB5-M	AA173896	membrane precursor	
455	455 35818_at	HCS	D00265	cytochrome c	cytochrome c
456	39921_at	COX5B	AI526089	cytochrome c oxidase subunit Vb	
				cytochrome c oxidase subunit Vla	
457	41206_r_at	COX6A1	A1540925	polypeptide 1	
458	36165 at	coxec	W51774	cytochrome c oxidase subunit VIc	
				cytochrome c oxidase subunit VIIa	
459	39031_at	COX7A1	AA152406	polypeptide 1 (muscle)	
				cytochrome c oxidase subunit VIIa	
460	41760_at	COX7A2	AA978033	polypeptide 2 (liver)	
				cytochrome c oxidase subunit VIIa	
461	461 34330_at	COX7A2L	AB007618	polypeptide 2 like	COX7RP
462	462 34381_at	COX7C	AI708889	cytochrome c oxidase subunit VIIc	



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463	38080_at	COX8	AI525665	cytochrome c oxidase subunit VIII	
464	35819_at	CYC1	X06994	cytochrome c-1	cytochrome c-1
				cytochrome P450, 51 (lanosterol 14-alpha-	
465	33389_at	CYP51	U23942	demethylase)	lanosterol 14-demethylase cytochrome P450
				cytochrome P450, subfamily I (dioxin-	
				inducible), polypeptide 1 (glaucoma 3,	
466	859_at	CYP1B1	U03688	primary infantile)	cytochrome P450
				cytochrome P450, subfamily I (dioxin-	
				inducible), polypeptide 1 (glaucoma 3,	
467	467 40071_at	CYP181	U03688	primary infantile)	cytochrome P450
468	468 37509 at	CRLF3	AF046059	cytokine receptor-like factor 3	cytokine receptor related protein 4
469		KIAA0068	D38549	cytoplasmic FMRP interacting protein 1	
			-	cytoplasmic; Human Ser/Thr protein	
470	1706_at	A-RAF-1	U01337	kinase (A-RAF-1) gene, complete cds.	Ser/Thr protein kinase
471	471 34338 at	CKAP1	D49738	cytoskeleton-associated protein 1	cytoskeleton associated protein
472	32529_at	CKAP4	X69910	cytoskeleton-associated protein 4	P63 protein
473	473 40282 s_at	DF	M84526	D component of complement (adipsin)	adipsin/complement factor D
474	40877_s_at	MN7	AF041080	D15F37 (pseudogene)	
				damage-specific DNA binding protein 2	
475	1243_at	DDB2	U18300	(48kD)	DDBb p48
476	476 36616 at	DAZAP2	D31767	DAZ associated protein 2	DAZ associated protein 2
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
477	37663_at	DDX1	X70649	polypeptide 1	member of DEAD box protein family
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
478	35306_at	DDX15	AB001636	polypeptide 15	ATP-dependent RNA helicase #46
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
479	40490_at	DDX21	U41387	polypeptide 21	Gu protein
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
480	39744_at	DDX3	AF000982	polypeptide 3	dead box, X isoform
				DEAD/H (Asp-Glu-Ala-Asp/His) box	DEAD/H (Asp-Glu-Ala-Asp/His) box
481	34647_at	DDX5	X52104	polypeptide 5 (RNA helicase, 68kD)	polypeptide 5
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
	-			polypeptide 9 (RNA helicase A, nuclear	
482	36153_at	exaa	L13848	DNA helicase II; teukophysin)	RNA helicase A
483	483 41872 at	DFNA5	AF073308	deafness, autosomal dominant 5	nonsyndromic hearing impairment protein

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	0 20	2040	118221	io 3	ionizing radiation resistance conferring
404	1330 at	UALS	0.1832.1		
485	39114 at	DEPP	AB022718	decidual protein induced by progesterone	ОЕРР
486	37638 at	DOCK1	D50857		DOCK 180 protein
487		DAD1	D15057	defender against cell death 1	DAD-1
				deficient in late-infantile neuronal ceroid	
		· · ·		lipofuscinosis; Homo sapiens lysosomal	
				pepstatin insensitive protease (CLN2)	
488	32824_at	CLN2	AF039704	gene, complete cds.	lysosomal pepstatin insensitive protease
				atocyte homolog, lipid	
489	33337_at	DEGS	AF002668		MLD
490	38992_at	DEK	X64229	DEK oncogene (DNA binding)	putative oncogene
491	37951_at	DLC1	AF035119	deleted in liver cancer 1	deleted in liver cancer-1
492	33791 at	DLEU1	Y15227	deleted in lymphocytic leukemia, 1	deleted in lymphocytic leukemia, 1
493	493 38744 at	DSS1	N95406	Deleted in split-hand/split-foot 1 region	
L				delta sleep inducing peptide,	
494	36629_at	DSIPI	A1635895	immunoreactor	
495	35814 at	GA17	AF064603	dendritic cell protein	GA17 protein
496	38385_at	DSTN	S65738	destrin (actin depolymerizing factor)	actin depolymerizing factor
L				development and differentiation enhancing	development and differentiation enhancing development- and differentiation-enhancing
497	39410 at	DDEF2	AB007860	factor 2	factor 2
498	498 39044 s at	DGKD	D73409	diacylglycerol kinase, delta (130kD)	diacylglycerol kinase delta
499	499 38003_s_at	DGKZ	U94905	diacylglycerol kinase, zeta (104kD)	diacylglycerol kinase zeta
200	500 33920 at	DIAPH1	AF051782	diaphanous homolog 1 (Drosophila)	diaphanous 1
L				diazepam binding inhibitor (GABA	
				receptor modulator, acyl-Coenzyme A	
501	37692_at	DBI	AI557240	binding protein)	
				dihydrolipoamide S-acetyftransferase (E2	
				component of pyruvate dehydrogenase	:
502	39041_at	DLAT	Y00978	complex)	PDC-E2 precursor (AA -54 to 561)
23	503 40607_at	DPYSL2	U97105	dihydropyrimidinase-like 2	N2A3
504	36149_at	DPYSL3	D78014	dihydropyrimidinase-like 3	dihydropyrimidinase refated protein-3
505	39503_s_at	DPYSL4	AB006713	dihydropyrimidinase-like 4	dihydropyrimidinase related protein 4
206	38220_at	DPYD	U20938	dihydropyrimidine dehydrogenase	dihydropyrimidine dehydrogenase
507	7 40485_at	HSA249128	IAA176780	DIPB protein	

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				disabled homolog 2, mitogen-responsive	
508	479_at	DAB2	U53446	phosphoprotein (Drosophila)	DOC-2
				discoidin domain receptor family, member	
509	36643 at	DDR1	L20817		tyrosine protein kinase
510	510 40575 at	DLG5	AB011155	discs, large (Drosophila) homolog 5	KIAA0583 protein
				dishevelled associated activator of	
511	33753_at	DAAM1	AB014566	morphogenesis 1	KIAA0666 protein
512	33150_at	SAS10	AI126004	disrupter of silencing 10	
				dJ635G19.1 (LAMR1 (Laminin Receptor 1	
				(67kD) (RPSA, 40S Ribosomal Protein	
				SA, P40)) pseudogene); match: cDNAs:	-
				Em:X15005 Em:J03799 Em:X61156	
				Em:M64923 Em:X06406 Em:AF140348	
				Em:J02870 Em:L16589 Em:Z22749	
				Em:D25224 Em:M14199 Em:M27798;	
513	513 40916_at	dJ635G19.1	AL035494	match: ESTs: Em:AA642	dJ635G19.2.1 (novel protein (isoform 1))
L					
				dJ734P14.1 (KRAB box and C2H2 Zinc	
				finger domain protein pseudogene) match:	
	_	•		cDNAs: Em:M27878 Em:M29580	
				Em:U27186 Em:D31763 Em:AB007872	
				Em:U09366 Em:U09413 Em:X17617	
				Em:AF011573 Em:AF020591 Em:X78925	
				match: proteins: Sw:P52736 Sw:Q06730	
				Sw:P51523 Tr:Q14585 Sw:P15620	
				Sw:Q02386 Sw:P51786 Sw:Q99676	
				Tr:O60792 Sw:Q03923 Sw:O75820	dJ734P14.2.1 (snRNP (small nuclear
514	514 38456_s_at	dJ734P14.1	AL049650	Tr:Q61116 Tr:Q64247	ribonucleoprotein particle) protein B)

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\vdash	4	В	၁	D	ш
515 3	38455_at	dJ734P14.1	AL049650	dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09366 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:Q02386 Sw:P51786 Sw:Q99676 Tr:Q60792 Sw:Q03923 Sw:Q75820 Tr:Q61116 Tr:Q64247	dJ734P14.2.1 (snRNP (small nuclear ribonucleoprotein particle) protein B)
16	516 35809 <u>.g</u> .at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw.P53384 Sw.P52920 Sw.P21590 Sw.O57731 Sw.P40558	dJ862K6.2.2 (splicing factor, arginine/serinerich 6 (SRP55-2)(isoform 2))
517	35808_at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:O57731 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serinerich 6 (SRP55-2)(isoform 2))
				d.J90L6.1 (RPL15 (60S Ribosomal Protein L15) pseudogene); match: proteins: Sw:O74895 Sw:P51417 Sw:P39030 Sw:O17445 Sw:P54780 Sw:O23515 Sw:O65050 Wp:CE12148 Sw:P30736 Sw:P541051 Sw:P54060 Sw:O65082 Sw:P52818 Sw:P79324 Sw:O82712 Sw:O13418 Sw:O82528 Sw:P05748;	
518	518 32433_at	dJ90L6.1	297353	Human DNA sequence from clone RP1- 90L6 on chromosome 22q11.21-11.23 Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence.	

17 Sig

	A	В	C		W)
519	34183_at	DKFZP434C171	AL080169		hypothetical protein
520	40801_at	DKFZP434C212	AA643063	DKFZP434C212 protein	
521	38400_at	DKFZP434D1335 AI920820	A1920820	DKFZP434D1335 protein	
$\overline{}$	33392_at		AL080155		hypothetical protein
523	39411_at	DKFZP434J214	AL080156		hypothetical protein
524	524 40564_at	DKFZP564A043	N42007		
525	37000_at	DKFZP564B167	AL035304		hypothetical protein
526	526 33433 at	DKFZP564F0522	2 AL049943	DKFZP564F0522 protein	hypothetical protein
527	527 41437 at	DKFZP564F1123	3 AL080118	DKFZP564F1123 protein	hypothetical protein
528	528 39442 at	DKFZP564G0222 AL080115	AL080115	DKFZP564G0222 protein	hypothetical protein
529	529 40437 at	DKFZP564G2022 AL049944	AL049944	DKFZP564G2022 protein	hypothetical protein
530	530 36456_at	DKFZP5641052	AL080063	DKFZP5641052 protein	hypothetical protein
531	38033 at	DKFZP564M1416	6 AL049934	DKFZP564M1416 protein	hypothetical protein
532	532 36078 at	DKFZP56400423	3 AL080120	DKFZP56400423 protein	hypothetical protein
533	38256_s_at	DKFZP5640092	W21827	DKFZP5640092 protein	
534	39034_at	DKFZP5640123	AL080122	DKFZP5640123 protein	hypothetical protein
535	535 41662 at	DKFZP566B183	AL050272	DKFZP566B183 protein	hypothetical protein
536	536 32807_at	DKFZP566C134	AF004292	DKFZP566C134 protein	
537	38687_at	DKFZP566D193	AL050051	DKFZP566D193 protein	hypothetical protein
538	538 33776_at	DKFZP566K023	AL050062	DKFZP566K023 protein	hypothetical protein
539	539 41335_at	DC8	AL050084	DKFZP56601646 protein	hypothetical protein
540	540 36961_at	DKFZP586A011	AL050286	DKFZP586A011 protein	hypothetical protein
541	541 38717 at	DKFZP586A0522	2 AL050159	DKFZP586A0522 protein	hypothetical protein
542	542 40831_at	DKFZP586B0923 AL050190	AL050190	DKFZP586B0923 protein	hypothetical protein
543	543 34821 at	DKFZP586D0623	3 AL050197	DKFZP586D0623 protein	hypothetical protein
544	544 39986 at	DKFZP586D0919	9 AL050100	DKFZP586D0919 protein	hypothetical protein
545	545 34269 at		9 AL050102	DKFZp586F1019 protein	hypothetical protein
546	546 35736_at		8 AL050091	DKFZP586F1918 protein	hypothetical protein
547	547 40832_s_at	DKFZP586G011	AL050126	DKFZP586G011 protein	hypothetical protein
548	548 36007 at	DKFZP586L151	AL050137	DKFZP586L151 protein	hypothetical protein
549	549 34833 at		20 AL050157	DKFZP586O0120 protein	hypothetical protein
550	37333_at	DNMT1	X63692	DNA (cytosine-5-)-methyltransferase 1	DNA (cytosine-5-)-methyltransferase
				DNA segment on chromosome X (unique)	
551	40891_f_at	DXS9879E	X92896	9879 expressed sequence	ITBA2 protein
2	550 24015 24	DVVC1EE	1 03426	DNA segment on chromosome X and Y	DNA segment on chromosome X and Y
200	34215_al	IDATO 133E	LU3420	(dilidge) 133 explessed sequelice	ותוומלים וכם כעלים במתמבוות

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	A	В	ပ	O	IJ
553	1252 at	D5S346	M73547	DNA segment, single copy probe LNS- CAI/LNS-CAII (deleted in polyposis	polyposis locus-encoded protein
				DNA segment, single copy, probe pH4	DNA segment, single copy, probe pH4
554	37162_at	D10S170	S72869	(transforming sequence, thyroid-1,	(transforming sequence, thyroid-1,
				DnaJ (Hsp40) homolog, subfamily A,	
555	39118_at	DNAJA1	690807	member 1	DNAJ homologue-2
				DnaJ (Hsp40) homolog, subfamily A,	
556	276_at	DNAJA1	F08069	member 1	DNAJ homologue-2
				DnaJ (Hsp40) homolog, subfamily B,	
222	41233_at	DNAJB6	AB014888	member 6	MRJ
				DnaJ (Hsp40) homolog, subfamily B,	
558	35799_at	DNAJB9	AL080081	member 9	hypothetical protein
				DnaJ (Hsp40) homolog, subfamily C,	
559	36166_at	DNAJC8	AF083190	member 8	SPF31
				docking protein 1, 62kD (downstream of	
560	816_g_at	DOK1	U70987	tyrosine kinase 1)	GAP binding protein p62dok
				docking protein 1, 62kD (downstream of	
561	34433_at	DOK1	AF035299	tyrosine kinase 1)	docking protein 1
9		i	1	dolichyl-phosphate mannosyltransferase	and the state of t
205	348/9_ai	DPIMI	Ar00/6/3	polypepilde 1, catalytic subutilit	delicitor illoriopriospilate lliarinose symmase
563	38957_at	DCAMKL1	AB002367	doublecortin and CaM kinase-like 1	doublecortin and CaM kinase-like 1
564	32168_s_at	DSCR1	U85267	Down syndrome critical region gene 1	Down syndrome critical region protein 1
565	36088_at	DSCR2	AJ006291	Down syndrome critical region gene 2	leucine rich protein
999	35166_at	DSCR3	D87343	Down syndrome critical region gene 3	DCRA
				down-regulator of transcription 1, TBP-	TATA binding protein-associated
267	32621_at	DR1	M97388	binding (negative cofactor 2)	phosphoprotein
268	37981_at	DBN1	D17530	drebrin 1	drebrin E
			-	dual specific protein; Homo sapiens	
				tyrosine phosphatase (cdc14B) mRNA,	
569	40920_at	cdc14B	AF023158	complete cds.	tyrosine phosphatase
				dual specificity phosphatase 11	
570		DUSP11	AF023917	(RNA/RNP complex 1-interacting)	PIR1
571	38272_at	DUSP14	AF038844	dual specificity phosphatase 14	MKP-1 like protein tyrosine phosphatase
572	41225 at	DUSP3	AL049417	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	
;		2 :55			

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	A	В	ပ	G.	
573	41193_at	DUSP6	AB013382	dual specificity phosphatase 6	DUSP6
574	36946_at	DYRK1A	D86550	dual-specificity tyrosine-(Y)- phosphorylation regulated kinase 1A	serine/threonine protein kinase
575	1512_at	DYRK1A	D86550	dual-specificity tyrosine-(Y)- phosphorylation regulated kinase 1A	serine/threonine protein kinase
				dual-specificity tyrosine-(Y)-	dual-specificity tyrosine-(Y)-phosphorylation
2/6	760_at	DYHKZ	Y09216	phosphorylation regulated kinase z dual-specificity tyrosine-(Y)-	regulated kinase z isolorm i
577	39931_at	DYRK3	Y12735	phosphorylation regulated kinase 3	Dyrk3 protein
578	38368_at	DUT	U31930	dUTP pyrophosphatase	deoxyuridine nucleotidohydrolase
579	579 38475_at	DCTN2	U50733	dynactin 2 (p50)	dynamitin
580	34891_at	PiN	AI540958	dynein, cytoplasmic, light polypeptide	
581	34829_at	DKC1	U59151	dyskeratosis congenita 1, dyskerin	Cbf5p homolog
		i i		dystonia 1, torsion (autosomal dominant;	•
585	32234_at	DY11	AF007871	torsin A)	torsinA
				dystroglycan 1 (dystrophin-associated	
583	36989_at	DAG1	L19711	glycoprotein 1)	dystroglycan
787	40488 at	UMU	M18533	dystrophin (muscular dystrophy,	dvetronbin
585	585 40106 at	E18-AP5	AJ007509	E18-55kDa-associated protein 5	E1B-55kDa-associated protein
586	33354 at	SMURF2	AA630312	E3 ubiquitin ligase SMURF2	
587	40375_at	EGR3	X63741	early growth response 3	transcription factor
588	588 36135_at	EBNA1BP2	U86602	EBNA1 binding protein 2	nucleolar protein p40
589	37730_at	p100	U22055	EBNA-2 co-activator (100kD)	100 kDa coactivator
290	33254_at	EVIS	AF008915	ecotropic viral integration site 5	EVI-5 homolog
				ectodermal-neural cortex (with BTB-like	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
591	39542_at	ENC1	AF059611	domain)	nuclear matrix protein NRP/B
				ectonucleotide pyronhoenhatase/nhoenhorliesterase 2	
592	592 41124_r_at	ENPP2	L35594	(autotaxin)	autotaxin
				ectonucleotide pyrophosphodiesterase 2	
593	41123_s_at	ENPP2	L35594	(autotaxin)	autotaxin
594	594 32551_at	EFEMP1	U03877	EGF-containing fibulin-like extracellular matrix protein 1	extracellular protein

	∢	8	C	0	m
595	36488_at	EGFL5	AB011542	EGF-like-domain, multiple 5	MEGF9
296	596 40509 at	FTEA	J04058	electron-transfer-flavoprotein, alpha polypeptide (alutaric aciduria II)	electron transfer flavoprotein, alpha polypeptide
597	597 36881 at	ETFB	X71129	electron-transfer-flavoprotein, beta	electron transfer flavoprotein beta subunit
				elongation factor EF-1-alpha; Human	
000	0000	EEE1 A	104617	elongation factor EF-1-alpha gene,	eukaryotic translation elongation factor 1
599	31853 at	EED	AF080227	embryonic ectoderm development	embryonic ectoderm development protein
				ems1 sequence (mammary tumor and	
	7000	3811	1,000,40	squamous cell carcinoma-associated	amulaxin
3	33001 al	CINIO	14130343	(pool of lost over been of Chichan	
				end of last exon based on GENOCAIN prediction presumably this gene and	
				dJ477H23.2 are part of the same gene	
601	601 41478_at	dJ477H23.1	AL033538	match: ESTs: Em:AA354647	dJ477H23.1 (novel protein)
				endocytic receptor (macrophage mannose	
602	37408_at	ENDO180	AB014609	receptor family)	KIAA0709 protein
				endosome-associated FYVE-domain	
603	37914_at	ENDOFIN	AB002303	protein	endosome-associated FYVE-domain protein
604	39010_at	ENSA	A1658639	endosulfine alpha	
				endothelial differentiation,	
605	40387 at	FDG2	1.180811	lysophosphatidic acid G-protein-coupled recentor, 2	Nsophosphatidic acid receptor homolog
909	40874_at	EDF1	AJ005259	endothelial differentiation-related factor 1	endothelial differentiation-related factor 1
				enhancer of rudimentary homolog	human protein homologous to DROER
607	39079_at	ERH	D85758	(Drosophila)	protein
809	608 2035_s_at	ENO1	M55914	enolase 1, (alpha)	c-myc binding protein
609	609 34335_at	EFNB2	AI765533	ephrin-B2	
				epidermal growth factor receptor pathway	epidermal growth factor receptor pathway
610	37731_at	EPS15	Z29064	substrate 15	substrate 15
				epidermal growth factor receptor pathway	epidermal growth factor receptor kinase
61	1467_at	EPS8	U12535	substrate 8	substrate
612	37762_at	EMP1	Y07909	epithelial membrane protein 1	progression associated protein
613	39631_at	EMP2	U52100	epithelial membrane protein 2	XMP

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	A	В	٥	O	IJ
				EPM1 disease gene; cysteine protease	
			-	inhibitor; Human cystatin B gene,	
614	35816_at	cystatin B	U46692	complete cds.	cystatin B
				erythrocyte membrane protein band 4.1-	
615	32585_at	EPB41L2	AF027299	like 2	protein 4.1-G
616	38375_at	ESD	AF112219	esterase D/formylglutathione hydrolase	esterase D
				estrogen receptor binding site associated,	
617	38283_at	EBAG9	AB007619	antigen, 9	EBAG9
618	37161_at		W28948	ESTs	
619	40885_s_at		N30151	ESTs	
620	33328_at	C1S	W28612	ESTs	
621	33453_at	ATP6S1	AI400326	ESTs	
622	31801_at		AI808712	ESTs	
623	41598		AA890010	ESTs	
				ESTs, Highly similar to RS21_HUMAN	
				40S RIBOSOMAL PROTEIN S21	
624	32744_at	RPS21	AI526078	[H.sapiens]	
				ESTs, Moderately similar to	
				ALUS_HUMAN ALU SUBFAMILY SX	
		-		SEQUENCE CONTAMINATION	
625	39750_at		W61005	WARNING ENTRY [H.sapiens]	
	-			ESTs, Moderately similar to	
				GLK5_HUMAN GLUTAMATE	
				RECEPTOR, IONOTROPIC KAINATE 5	
626	626 34906_g_at		AA977136	PRECURSOR [H.sapiens]	
				ESTs, Moderately similar to T46365	
				hypothetical protein DKFZp434A1518.1	
627	35787_at		A1986201	[H.sapiens]	
				ESTs, Weakly similar to 0903209A	
628	41463_at		AL042729	peptide PD,basic Pro rich [H.sapiens]	
				ESTs, Weakly similar to N-WASP	
629	629 41273_at		AL046940	[H.sapiens]	
630	630 38097_at	PIG8	AF010313	etoposide-induced mRNA	Pig8
634	621 40889 6 25	 EEE184	28170	eukaryotic translation elongation factor 1	
3	140000 1 at	ובבי ואו	IVEDITO	ומוטוומ ו	

Fig 21

	A	В	O	Q	ш
				eukaryotic translation elongation factor 1	
632	632 35175_f_at	EEF1A2	X70940	alpha 2	elongation factor 1 alpha-2
5		0 0 1 1	V60480	eukaryotic translation elongation factor 1	olongation (actor, 1, beta
33	35/48_al	EEF 102	V00403	oeta 2 oukanotic translation elongation factor 1	
				delta (guanine nucleotide exchange	
634	41256_at	EEF10	Z21507		human elongation factor-1-delta
				eukaryotic translation elongation factor 1	
635	1676_s_at	EEF1G	M55409	gamma	pancreatic tumor-related protein
636	36587_at	EEF2	211692	eukaryotic translation elongation factor 2	human elongation factor 2
637	663_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
638	34278_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
930	1154 at	EIE2S1	.102645	eukaryotic translation initiation factor 2, subunit 1 (alpha. 35kD)	eukaryotic translation initiation factor 2, subunit 1 (albha, 35kD)
3	1011			enkarvotic translation initiation factor 28	eukarvotic translation initiation factor 2B.
640	40515_at	EIF2B2	AF035280	subunit 2 (beta, 39kD)	subunit 2 (beta, 39kD)
641		EIF3S2	U36764	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)	TGF-beta receptor interacting protein 1
3	+	60611	I IGARBO	eukaryotic translation initiation factor 3,	translation initiation factor elE3 n40 subunit
240	33321_all	EILOOO	0000	Subalifica (gallinia, 1982)	
643	32576_at	EIF3S5	U94855	subunit 5 (epsilon, 47kD)	translation initiation factor 3 47 kDa subunit
				eukaryotic translation initiation factor 3,	murine mammary tumor integration site 6
644	38681_at	EIF3S6	U62962	subunit 6 (48kD)	(oucogene homolog)
645	35298 at	EIF3S7	U54558	eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD)	translation initiation factor eIF3 p66 subunit
646		FIE3S9	U78525	eukaryotic translation initiation factor 3, subunit 9 (eta. 116kD)	eukaryotic translation initiation factor
				eukarvotic translation initiation factor 4	
647	41785_at	EIF4G2	U73824	gamma, 2	p97
5	20004	FIE 40.2	A E012072	eukaryotic translation initiation factor 4	e E46
8	648 339U/_at	EIF4G3	AL012012	yallılıa, o	



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	٧	Я	S	O	
				eukaryotic translation initiation factor 4A,	
649	1420_s_at	EIF4A2	D30655	isoform 2	eukaryotic initiation factor 4AII
Ç		į.	745050	The refreshment of the rest of	ean-hinding protein
OCO OCO	3//32_dl		10000	Τ	
651	35263 at	EIF4EBP2	N73769	binding protein 2	
652	167_at	EIF5	U49436	ation initiation factor 5	translation initiation factor 5
653	37318 at	ETF1	X81625	eukaryotic translation termination factor 1	C11 protein
				excision repair cross-complementing	excision repair cross-complementing rodent
				rodent repair deficiency, complementation	
				group 3 (xeroderma pigmentosum group	(xeroderma pigmentosum group B
654	1885_at	ERCC3	M31899	B complementing)	complementing)
L				excision repair cross-complementing	
				rodent repair deficiency, complementation	
	,			group 5 (xeroderma pigmentosum,	
		•		complementation group G (Cockayne	
655	2063_at	ERCCS	L20046	syndrome))	excision repair protein
					(atod 11) biogothy works (41)
929	10 V0700	Hen 181	AI 022398	exons 1-4 beyond this clotte; match. profeins P28845 P50172 P51975 Q29608	
25.7	200 04	100 I	270630	exostoses (multiple) 1	
200	מכבטני	1 1 N 1 N 1 N 1 N 1 N 1 N 1 N 1 N 1 N 1	AE000418	exectoses (multiple)-like 2	EXT-like protein 2
650 850	36526_at	EXTL3	AR011091	exostoses (multiple)-like 3	KIAA0519 protein
099	37729 at	XP01	Y08614	exportin 1 (CRM1 homolog, yeast)	exportin 1
				exportin, tRNA (nuclear export receptor for	
661	38753_at	XPOT	AF039022	(tRNAs)	exportin t
				extracellular matrix protein 2, female	
662	39673_i_at	ECM2	AB011792	organ and adipocyte specific	extracellular matrix protein
<u> </u>				extracellular matrix protein 2, female	
663	39674_r_at	ECM2	AB011792	organ and adipocyte specific	extracellular matrix protein
664	35226_at	EYA2	U71207	eyes absent homolog 2 (Drosophila)	Eab1
				family with sequence similarity 8, member	
665	38318_at	FAM8A1	AL050128	A1	
- 5	040	0001	1160107	far upstream element (FUSE) binding	E 1987 Frieding
999	666 318/9_at	Irubrs	009127	proteins	1 OOL DINGING PROCESS O



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Ī				ase (famesyl	farnesyl diphosphate synthase (farnesyl
_			<u></u>		pyrophosphate synthetase,
				rase,	dimethylallyltranstransferase,
1 /99	37325 at	FDPS	D14697	geranyltranstransferase)	geranyltranstransferase)
_				farnesyl-diphosphate farnesyltransferase	
668	34848 at	FDFT1	X69141		farnesyl-diphosphate farnesyltransferase
699	1499 at	FNTA	L10413		farnesyl-protein transferase alpha-subunit
				Fas (TNFRSF6)-associated via death	:
670	38755_at	FADD	X84709	domain	mediator of receptor induced toxicity
				fasciculation and elongation protein zeta 1	
671	37743_at	FEZ1	090090	(zygin I)	FEZ1
				fasciculation and elongation protein zeta 2	
672	38651 at	FEZ2	U60061	(zygin II)	FEZ2
				FAT tumor suppressor homolog 1	
673	40454_at	FAT	X87241	(Drosophila)	homologue of Drosophila Fat protein
				fatty-acid-Coenzyme A ligase, long-chain	
674	40082_at	FACL2	D10040	2	long-chain acyl-CoA synthetase
				fatty-acid-Coenzyme A ligase, long-chain	
675	33880_at	FACL3	D89053	3	Acyl-CoA synthetase 3
				fatty-acid-Coenzyme A ligase, long-chain	
929	33881_at	FACL3	AA977580	3	
677	33360_at	FBXL11	AB023221	F-box and leucine-rich repeat protein 11	KIAA1004 protein
678	37205 at	FBXL7	AB020647	F-box and leucine-rich repeat protein 7	KIAA0840 protein
629	32854_at	FBXW1B	AB014596	F-box and WD-40 domain protein 1B	KIAA0696 protein
680	32169_at	FBX021	AB020682	F-box only protein 21	KIAA0875 protein
681	35337_at	FBXO7	AL050254	F-box only protein 7	hypothetical protein
				FBRNP: heterogeneous ribonucleoprotein	:
				homolog; This sequence comes from Fig.	
				3; D10S102=FBRNP [human, fetal brain,	
682	33817_at	D10S102	S63912	mRNA, 3043 nt].	FBRNP
683		Hill	HG1103-HT1103	Fe protein	dinitrogenase reductase
684		FER1L3	AL096713	fer-1-like 3, myoferlin (C. elegans)	hypothetical protein
				FERM, RhoGEF (ARHGEF) and pleckstrin	
982	685 32148_at	FARP1	AI701049	domain protein 1 (chondrocyte-denved)	

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fetal Alzheimer antigen fibrillin 1 (Marfan syndrome) fibroblast activation protein, alpha fibroblast growth factor 7 (keratinocyte growth factor) fibroblast growth factor 7 (keratinocyte growth factor) fibroblast growth factor receptor 1, isoform 1 precursor; fibroblast growth factor receptor 1, isoform 3 precursor; fibroblast growth factor receptor 1, isoform 4 precursor; fibroblast growth factor receptor 1, isoform 6 precursor; fibroblast growth factor receptor 1, isoform 6 precursor; fibroblast growth factor receptor 1, isoform 7 fibroblast growth factor receptor 1, isoform 8 fibroblast growth factor receptor 1, isoform 7 fi
alpha eratinocyte
related tyrosine kinase 2, Pfeiffer (1, isoform 8 precursor, fibroblast growth
lactor receptor 1, Isolotini 9 precursor
fibronectin 1 fibronectin 1, isoform 2 preproprotein
fibronectin 1
fibronectin leucine rich transmembrane fibronectin leucine rich transmembrane
protein 2
1 (fibulin-1D
UP50
filamin B, beta (actin binding protein 278) beta-filamin
FK506 binding protein 9 (63 kD)
flavin containing monooxygenase 3 flavoprotein
ollistatin precursor; Human follistatin follistatin isoform FST317 precursor;
gene, exon 6. follistatin isoform FST344 precursor

Gig 21

	•		(
	4	٥	>		
				forkhead (Drosophila)-like 7; FREAC3;	
				×-IKe	torkhood/winead balix-like transcription
			1	actor / (FNDL/) gene,	Continued winged new and company
702	702 41027_at		AF078096		Tactor /
703	703 36319_at	FOXF2	U13220	forkhead box F2	forkhead protein FREAC-2
704	40570_at	FOX01A	AF032885	(rnabdomyosarcoma)	Iornieda piotein
705	34740_at	FOXO3A	AF032886	forkhead box O3A	forkhead protein
	32542 at	FHL1	AF063002	four and a half LIM domains 1	LIM protein SLIMMER
707	38422 s at	FHL2	U29332	four and a half LIM domains 2	heart protein
708	41649 at	FHX	AF038177	FOXJ2 forkhead factor	
709	34997 r at	FZD5	U43318	frizzled homolog 5 (Drosophila)	transmembrane receptor
710	34472 at	FZD6	AB012911	frizzled homolog 6 (Drosophila)	Frizzled-6
	33222 at	FZD7	AB017365	frizzled homolog 7 (Drosophila)	frizzled-7
${f -}$	38923 at	FRG1	L76159	FSHD region gene 1	FSHD region gene 1
_	38139 at	FPGT	AF017445	fucose-1-phosphate guanylyltransferase	GDP-L-fucose pyrophosphorylase
	41814 at	FUCA1	M29877	fucosidase, alpha-L- 1, tissue	fucosidase, alpha-L- 1, tissue
				Fukuyama type congenital muscular	,
715	40022 at	FCMD	AB008226	dystrophy (fukutin)	fukutin
716	716 32546_at	迁	U59309	fumarate hydratase	fumarase precursor
7 7 7	26146 24	CIAHBP1	1151586	firse-hinding protein-interacting repressor	siah binding protein 1
1		י ופוועוס	200		
718	40480_s_at	FYN	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES
719	719 2039 s at	FYN	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES FYN oncogene related to SRC, FGR, YES
720	34288 at	RDC1	U67784	G protein-coupled receptor	orphan G protein-coupled receptor
721	37308	GPR107	A1888084	G protein-coupled receptor 107	
722	37298 at	GABARAP	AF044671	GABA(A) receptor-associated protein	MM46
		0	100000	GABA(A) receptor-associated protein like	
723	35/85_at	GABAHAFLI	W 2520 I		
				GABA(A) receptor-associated protein-like	
724	35767_at	GABARAPL2	AI565760	2	
725	37825_at	GALK2	M84443	galactokinase 2	galactokinase
726	726 37742_at	GLB1	M34423	galactosidase, beta 1	galactosidase, beta 1

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				ase,	
727	37263_at	ССН	U55206		human gamma-glutamyi hydrolase
				gap junction protein, alpha 1, 43kD	•
728	32531_at	GJA1	X52947	(connexin 43)	connexin 43
				GCN1 general control of amino-acid	
729	36603_at	GCN1L1	D86973	synthesis 1-like 1 (yeast)	
	35307_at	GDI2	Y13286	GDP dissociation inhibitor 2	GDP dissociation inhibitor beta
				gene predicted from cDNA with a	gene predicted from cDNA with a complete
731	39386_at	KIAA0110	D14811	complete coding sequence	coding sequence
				gene with multiple splice variants near HD	gene with multiple splice variants near HD
732	32180 s at	RES4-22	AB000461	locus on 4p16.3	locus on 4p16.3
					Bruton's tyrosine kinase-associated protein-
733	466 at	GTF2I	U77948	general transcription factor II, i	135
734	35450 s at	GTF2I	AF015553	general transcription factor II, i	TFII-I protein
				general transcription factor IIA, 2 (12kD	
735	37010 at	GTF2A2	A1203737	subunit)	
L				general transcription factor IIA, 2 (12kD	
736	869_at	GTF2A2	U14193	subunit)	transcription factor IIA small 12 kDa subunit
				general transcription factor IIE,	i i
737	37882_at	GTF2E1	X63468	polypeptide 1 (alpha subunit, 56kU)	I FillE-alpha
				general transcription factor IIE,	
738	37295 at	GTF2E2	X63469	polypeptide 2 (beta subunit, 34kD)	TFIIE-beta
				general transcription factor IIH,	
739	38782_at	GTF2H1	M95809	polypeptide 1 (62kD subunit)	basic transcription factor 62kD subunit
_				general transcription factor IIH,	
49	40754_at	GTF2H3	Z30093	polypeptide 3 (34kD subunit)	basic transcription factor 2, 35 KD subunit
741	36188 at	GTF3A	D32257	general transcription factor IIIA	Xenopus transcription factor IIIA homologue
742		GGPS1	AB019036	geranylgeranyl diphosphate synthase 1	geranylgeranyl pyrophosphate synthase
743		GMFB	AB001106	glia maturation factor, beta	glia maturation factor
744	39793_at	GBAS	AF029786	glioblastoma amplified sequence	GBAS
				glucan (1,4-alpha-), branching enzyme 1	
				(glycogen branching enzyme, Andersen	
				disease, glycogen storage disease type	
745	32643_at	GBE1	L07956	1V)	1,4-alpha-glucan branching enzyme
746	746 34332 at	GNPI	D31766	glucosamine-6-phosphate isomerase	glucosamine-6-phosphate isomerase
				(

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	(2		glucosaminyl (N-acetyl) transferase 1,	
747	38218_at	GCNT1	M97347		beta-1,6-N-acetylglucosaminyltransferase
748	at		K03515		neuroleukin
749	38986 at		Z49835	glucose regulated protein, 58kD	protein disulfide isomerase
750	at		X03674	glucose-6-phosphate dehydrogenase	glucose-6-phosphate dehydrogenase
751	at		M15182	glucuronidase, beta	glucuronidase, beta
752	at	GLUD1	M20867	glutamate dehydrogenase 1	glutamate dehydrogenase 1
	35485_at		X80818	glutamate receptor, metabotropic 4	metabotropic glutamate receptor type 4
Γ				glutamate-ammonia ligase (glutamine	
754	40522_at	פרחר	X59834	synthase)	glutamateammonia ligase
				glutamate-cysteine ligase, catalytic	-
755	31850_at	GCLC	M90656	subunit	gamma-glutamylcysteine synthetase
				glutamate-cysteine ligase, modifier	gamma-glutamylcysteine synthetase light
756	33163_r_at	GCLM	L35546	subunit	subunit
				glutamic-oxaloacetic transaminase 1,	
757	35343_at	GOT1	M37400	soluble (aspartate aminotransferase 1)	aspartate aminotransferase 1
				glutamic-oxaloacetic transaminase 2,	
				mitochondrial (aspartate aminotransferase	
758	40764 at	GOT2	M22632	2)	aspartate aminotransferase 2 precursor
759	34719 at	GLS	AB020645	glutaminase	KIAA0838 protein
				glutamine-fructose-6-phosphate	glutamine:fructose-6-phosphate
760	32626 at	GFPT1	M90516	transaminase 1	amidotransferase
				glutamine-fructose-6-phosphate	Glutamine:fructose-6-phosphate
761	39640 at	GFPT2	AB016789	transaminase 2	amidotransferase
762	762 35300 at	EPRS	X54326	glutamyl-prolyl-tRNA synthetase	glutaminyl-tRNA synthetase
763	763 34311 at	GLRX	X76648	glutaredoxin (thioltransferase)	glutaredoxin
764	37033 s at	GPX1	X13710	glutathione peroxidase 1	
765	765 40508 at	GSTA4	AF025887	glutathione S-transferase A4	glutathione S-transferase A4-4
992	38386 r at	GSS	U34683	glutathione synthetase	glutathione synthetase
				glutathione-S-transferase like; glutathione	
767	824_at	GSTTLp28	U90313	transferase omega	glutathione-S-transferase homolog
				glyceraldehyde-3-phosphate	
768	AFFX-HUMGAP(GAPD	(GAPD	M33197	dehydrogenase	giyceraldehyde-3-phosphate dehydrogenase
769	769 35905 s. at	GAPD	U34995	glyceraldehyde-3-phosphate dehydrogenase	
		2 :: (2)			

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		-		glyceraldehyde-3-phosphate	
22	770 AFFX-HUMGAP(GAPD	GAPD	M33197	dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase
771	39392 at	GNPAT	A.Inn2190	niveronenhosnhate 0-acyltransferase	dihydroxyacetone phosphate acytransferase
	10000			altaino alonomo anatom anatom E	alkaino obostano ottobre processio L
İ				giyome cleavage system protein n	giyciile cleavage system protein a
772		GCSH	D00723	(aminomethyl carrier)	(aminomethyl carrier)
773	39665_at	GLRB	U33267	glycine receptor, beta	glycine receptor beta subunit
774	40645_at	GSK3B	L33801	glycogen synthase kinase 3 beta	protein kinase
775	40876_at	GYG	U31525	glycogenin	glycogenin
776	35334_at	GYG2	U94362	glycogenin 2	glycogenin-2 alpha
777	38379_at	GPNMB	X76534	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb
8//	37251_s_at	GPM6B	AF016004	glycoprotein M6B	
622	33126_at	AD-017	L13435	glycosyltransferase AD-017	
780	780 36582_g_at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase
187	36581_at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase
782	36201_at	GL01	D13315	glyoxalase I	lactoyl glutathione lyase
				glyoxylate reductase/hydroxypyruvate	
783	40133_s_at	GRHPR	W28944	reductase	
					guanine nucleotide binding protein (G
					protein), alpha stimulating activity
					polypeptide 1, isoform alpha-s-2;
					neuroendocrine secretory protein 55;
					guanine nucleotide binding protein (G
					protein), alpha stimulating activity
				-	polypeptide 1, isoform XL-alpha-s; guanine
					nucleotide binding protein (G protein), alpha
			•		stimulating activity polypeptide 1, isoform
784	784 37449_i_at	GNAS	X04409	GNAS complex locus	alpha-s-1.
785	785 37448_s_at	GNAS	X26009	GNAS complex locus	alpha subunit of GsGTP binding protein

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Γ					guanine nucleotide binding protein (G
					protein), alpha stimulating activity
					polypeptide 1, isoform alpha-s-2;
					neuroendocrine secretory protein 55;
					guanine nucleotide binding protein (G
					protein), alpha stimulating activity
					polypeptide 1, isoform XL-alpha-s; quanine
					nucleotide binding protein (G protein) alpha
					etimulating activity polypentide 1 isoform
700	27.450	OVINO	X04400	SNAS complex locus	alpha-s-1
3	0) 100 - at	2	COLLON		ADP-ribosylation factor binding protein 3.
			-	golgi associated, gamma adaptin ear	isoform short; ADP-ribosylation factor
787	37959 at	GGA3	D63876	containing, ARF binding protein 3	binding protein 3, isoform long
	788 32713 at	GOLGA1	U51587	golgi autoantigen, golgin subfamily a, 1	Golgi complex autoantigen golgin-97
789	32150 at	GOLGA4	X82834	golgi autoantigen, golgin subfamily a, 4	256 kD golgin
790	790 36827_at	GOLPH1	AF020762	golgi phosphoprotein 1	unknown protein
791	38620_at	GOSR2	AA905543	golgi SNAP receptor complex member 2	
792	34737 at	GOI TC1	AE058718	goldi transport complex 1 (90 kD subunit)	putative 13 S Golgi transport complex 90kD subunit brain-specific isoform
793	793 41767 r at	KIAA0855	AB020662	golgin-67	KIAA0855 protein
794	36950 at	HSGP25L2G	X90872	gp25L2 protein	
				GPAA1P anchor attachment protein 1	glycosylphosphatidylinositol anchor
795	36035_at	GPAA1	AB002135	homolog (yeast)	attachment 1 (GPAA1)
796	32595_at	GRSF1	U07231	G-rich RNA sequence binding factor 1	G-rich sequence factor-1
				growth arrest and DNA-damage-inducible, growth arrest and DNA-damage-inducible	growth arrest and DNA-damage-inducible
797	39822_s_at	GADD45B	AF078077	beta	protein GADD45beta
				growth arrest and DNA-damage-inducible,	
798	39821_s_at	GADD45B	N95168	beta	
799	799 661_at	GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
800	800 41839_at	GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
801	ļ	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
802	1598_g_at	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
803	37615_at	GRB10	D86962	growth factor receptor-bound protein 10	growth factor receptor-bound protein 10
				growth hormone inducible transmembrane	
804	804 41752 at	GHITM	W28190	protein	

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	¥	8	C	D	TI.
802	160030_at	GHR	X06562	growth hormone receptor	growth hormone receptor
	40113_at	GS3955	D87119	GS3955 protein	GS3955
				GTP binding protein overexpressed in	
807	37279_at	GEM	U10550	skeletal muscle	Gem
				guanine nucleotide binding protein (G	
				protein), alpha inhibiting activity	the mother fraction
808	33809_at	GNAIT	AL049933	polypeptide i	nypomencal protein
				ein (G	guanine nucleotide binding protein (G
				a inhibiting activity	protein), alpha inhibiting activity polypeptide
808	37307_at	GNAI2	X04828		2
				guanine nucleotide binding protein (G	
810	34608_at	GNB2L1	M24194	protein), beta polypeptide 2-like 1	MHC B complex protein 12.3
				guanine nucleotide binding protein (G	
811	35272_at	GNG5	AI541042	protein), gamma 5	
812	812 37735_at	GNG10	U31383	guanine nucleotide binding protein 10	G protein gamma-10 subunit
				guanylate binding protein 1, interferon-	
813	at		M55542	inducible, 67kD	guanylate binding protein isoform l
814			L76200	guanylate kinase 1	guanylate kinase
815	815 32249_at	HFL1	M65292	H factor (complement)-like 1	factor H homologue
816	at		X07523	H factor 1 (complement)	complement factor H
				H.sapiens ACTH-R gene for	candidate adrenocorticotropic hormone
817	420_at	ACTH-R	X65633	adrenocorticotropic hormone receptor.	receptor
818	31673_s_at	sion r	egu X65784	H.sapiens CAR gene.	cell matrix adhesion regulator
819	37003 at	CD63; MLA1; ME4	ME4X62654	H.sapiens gene for Me491/CD63 antigen.	ME491 /CD63 antigen
				H conjone none for mitorhondrial ATP	ATP synthase, H+ transporting, mitochandrial F0 complex subunit c (subunit
820	38076_at	P1 gene for c sub	2069X)qns	synthase c subunit (P1 form).	9), isoform 1
821	35125 at	hro S6	60EZ9X	H.sapiens gene for ribosomal protein S6.	ribosomal protein S6
822	822 34646_at	npS7	225749	H.sapiens gene for ribosomal protein S7.	ribosomal protein S7
823	823 31510 s at	hH3.3B	248950	H.sapiens hH3.3B gene for histone H3.3.	histone H3.3

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				H.sapiens lactate dehydrogenase B gene	
				exon 1 and 2 (EC 1.1.1.27) (and joined	
824	824 33820_g_at	ldhB	X13794	CDS).	lactate dehydrogenase B
				H.sapiens lactate dehydrogenase B gene	
				exon 1 and 2 (EC 1.1.1.27) (and joined	•
825	33819_at	ldhB	X13794	CDS).	lactate dehydrogenase B
826	34787_at	ORF1	X93209	H.sapiens mRNA for NRD1 convertase.	NRD1 convertase
				H.sapiens mRNA for PIBF1 protein,	
827	36012_at	PIBF1	Y09631	complete.	PIBF1 protein
				H.sapiens mRNA for tre oncogene (clone	
828	828 31526_f_at	tre	X63547	213).	oncogene
829	40471_at	PxF	Y09048	H.sapiens PxF gene.	PxF protein
				H.sapiens PXMP1 gene, exon 1 (and	70kD peroxisomal integral membrane
830	37038_at	PXMP1	X83467	joined CDS).	protein
				H.sapiens rpS8 gene for ribosomal protein	
831	31583_at	rpS8	X67247		ribosomal protein S8
				H.sapiens SPHAR gene for cyclin-related	
832	1685_at	SPHAR	X82554	protein.	S-phase response (cyclin-related)
833	38127_at	syndecan-1	248199	H.sapiens syndecan-1 gene (exons 2-5).	syndecan 1
834	37310_at	uPA	X02419	H.sapiens uPA gene.	urokinase-plasminogen activator
835	34308_at	HZAFL	U90551	H2A histone family, member L	histone 2A-like protein
988	39337_at	HZAFZ	M37583	H2A histone family, member Z	H2A histone family, member Z
837	33458_r_at	H2BFL	AI688098	H2B histone family, member L	
838	838 40818_at	LOC51580	D14041	H-2K binding factor-2	H-2K binding factor-2
839	839 254_at	H3F3A	M11353	H3 histone, family 3A	H3 histone, family 3A
840	39969_at	H4FG	AA255502	H4 histone family, member G	*
841	32591_at	HCDI	AI494623	HCDI protein	
842	35215_at	HDCMA18P	AL049996	HDCMA18P protein	hypothetical protein
				heat shock 10kD protein 1 (chaperonin	
843	39353_at	HSPE1	Al912041	10)	
844	844 37720_at	HSPD1	M22382	heat shock 60kD protein 1 (chaperonin)	mitochondrial matrix protein
				heat shock 70kD protein 5 (glucose-	heat shock 70kD protein 5 (glucose-
845	36614_at	HSPA5	X87949	regulated protein, 78kD)	regulated protein, 78kD)
846	846 41510 c at	Норав	15189	heat shock 70kD protein 9B (mortalin-2)	MTHSP75
		2007 1011	20:0:1		



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847	32316_s_at	HSPCA	X15183	heat shock 90kD protein 1, alpha	heat shock 90kD protein 1, alpha
848	33984_at	HSPCB	M16660	heat shock 90kD protein 1, beta	heat shock 90kD protein 1, beta
849	31906_at	HSBP1	AF068754	heat shock factor binding protein 1	meat snock factor binding protein I nobri
850	1468 at	TRAP1	U12595	heat shock protein 75	associated protein
821	38054_at		AF029890	hepatitis B virus x interacting protein	hepatitis B virus X interacting protein
				hepatoma-derived growth factor (high-	
852	852 38779_r_at	HDGF	D16431	mobility group protein 1-like)	hepatoma-derived GF
853	853 35644_at	НЕРН	AB014598	hephaestin	KIAA0698 protein
				heterogeneous nuclear ribonucleoprotein	
854	38094_at	HNRPAB	M65028	A/B	hnRNP type A/B protein
i.		0400141	200001	heterogeneous nuclear ribonucleoprotein	A distraction in the property of the property
822	3/334_at	HINHFAO	023803	AU.	יופופוסלפוופסים ווססוותכופסלווסנפוון עס
				heterogeneous nuclear ribonucleoprotein	
856	34987_s_at	HNRPA1	X79536	A1	hnRNPcore protein A1
					heterogeneous nuclear ribonucleoprotein
_				heterogeneous nuclear ribonucleoprotein	A2/B1, isoform A2; heterogeneous nuclear
857	36654_s_at	HNRPA2B1	M29065	A2/B1	ribonucleoprotein A2/B1, isoform B1
					heterogeneous nuclear ribonucleoprotein C,
				heterogeneous nuclear ribonucleoprotein	isoform b; heterogeneous nuclear
828	33666_at	HNRPC	M16342	C (C1/C2)	ribonucleoprotein C, isoform a
L				heterogeneous nuclear ribonucleoprotein	
		!		D (AU-rich element RNA binding protein 1,	
829	38016_at	HNRPD	M94630	37kU)	UNA-binding protein
				heterogeneous nuclear ribonucleoprotein	
860	33845_at	HNRPH1	W28483	H1 (H)	
		. 2		heterogeneous nuclear ribonucleoprotein	
861	41132_r_at	HNRPH2	U01923	H2 (H')	heterogeneous nuclear ribonucleoprotein H2
	:		-	hadranania nuclear ribanialanzatain	heterogeneous nuclear ribonucleoprotein
862	41283_at	HNRPH3	AF052131	H3 (2H9)	
863	863 40836 s at	HNRPH3	W26677	heterogeneous nuclear ribonucleoprotein H3 (2H9)	
	11 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -				

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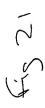
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	A	Я	၁	O	
864	39415_at	HNRPK	X72727	heterogeneous nuclear ribonucleoprotein K	transformation upregulated nuclear protein
				heterogeneous nuclear ribonucleoprotein	
865	35201_at	HNRPL	X16135		heterogeneous nuclear ribonucleoprotein L
	1	A CONTRACT	1 03533	heterogeneous nuclear ribonucleoprotein	M. protein
000	3//1/_al	ואורטאורו	L03332	hotorogonie niclost ribonicloorotein	
867	39792_at	HNRPR	AF000364	neterogeneous nacrear montacreoprotein R	heterogeneous nuclear ribonucleoprotein R
		•		heterogeneous nuclear ribonucleoprotein	
898	38654_at	HNRPU	X65488	U (scaffold attachment factor A)	hnRNP U protein
698	32818_at	HXB	X78565	hexabrachion (tenascin C, cytotactin)	human tenascin-C
870	39827_at	RTP801	AA522530	HIF-1 responsive RTP801	
				high density lipoprotein binding protein	
871	31504_at	HDLBP	M64098	(vigilin)	high density lipoprotein binding protein
				high-mobility group (nonhistone	
872	32220_at	HMG1	D63874	chromosomai) protein 1	רואומ-ו
				high-mobility group (nonhistone	high-mobility group (nonhistone
873	306_s_at	HMG14	J02621	chromosomal) protein 14	chromosomal) protein 14
				high-mobility group (nonhistone	
874	35738_at	HMG17L3	Al347088	chromosomal) protein 17-like 3	
				high-mobility group (nonhistone	high-mobility group (nonhistone
875	38065_at	HMG2	X62534	chromosomal) protein 2	chromosomal) protein 2
876		HMG2L1	AL079310	high-mobility group protein 2-like 1	hypothetical protein
877	_	HPCAL1	AF070616	hippocalcin-like 1	BDP-1 protein
878	1009 at	HINT1	U51004	histidine triad nucleotide binding protein 1	protein kinase C inhibitor
879	34231_at	HBOA	AF074606	histone acetyltransferase	histone acetyltransferase
880	41855	HAT1	AF030424	histone acetyltransferase 1	histone acetyltransferase 1
881	38771_at	HDAC1	D50405	histone deacetylase 1	RPD3 protein
882	-	HDAC2	U31814	histone deacetylase 2	transcriptional regulator homolog RPD3
883	38271_at	HDAC4	AB006626	histone deacetylase 4	KIAA0288 protein
884	1 39046_at	H2AV	AL049324	histone H2A.F/Z variant	
882	39092_at	H2AV	AW007731	histone H2A.F/Z variant	
886		HTATIP2	AF039103	HIV-1 Tat interactive protein 2, 30 kD	Tat-interacting protein TIP30
887	7 40220_at	HIS1	AB021179	HMBA-inducible	HEXIM1 protein
				(



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888	39809_at	HBP1	AF019214	HMG-box containing protein 1	HMG box containing protein 1
				HMG-domain containing protein which is the 57 kd subunit within SWI/SNF-related	
				BAF complexes; contains a proline-rich N-	
				terminus, a kinesin-like coiled-coil region,	
				and a highly acidic c-terminus; Homo	
				sapiens BAF57 (BAF57) gene, complete	
889	33828_at	BAF57	AF035262		BAF57
				HMT1 hnRNP methyltransferase-like 1 (S.	
890	39348_at	HRMT1L1	X99209	cerevisiae)	arginine methyltransferase
				HMT1 hnRNP methyltransferase-like 2 (S.	
891	32825_at	HRMT1L2	Y10805	cerevisiae)	arginine methyltransferase
				HNRNP Core Protein A1 LIKE	
				pseudogene; match: proteins P04256	
				Q28521 P49312 P09651 P51991 P51992	
892	31463_s_at	dJ256G22.1	AL022097	P51968 P17130 P22626	
				holocytochrome c synthase (cytochrome c	
893	38943_at	HCCS	U36787	heme-lyase)	holocytochrome c-type synthetase
894	894 39610_at	HOXB2	X16665	homeo box B2	homeo box B2
895	895 40674_s_at	нохсе	S82986	homeo box C6	homeo box C6
8		0	1000001		
988	38233_at	HOMEH-3	AF093265	Homer, neuronal Immediate early gene, 3	nomer-s
				Homo sapiens (clone f17252) ubiquinol cytochrome c reductase Rieske iron-	
897	34401_at	UQCRFS1	L32977	sulphur protein (UQCHFS1) gene, exon 2. Hieske Fe-S protein	Rieske Fe-S protein
				Homo sapiens (clone FFE-7) type II inosine monophosphate dehydrogenase (IMPDH2) gene, exons 1-13, complete	inosine monophosphate dehydrogenase type
898	36624_at	IMPDH2	L33842	cds.	
				Homo sapiens aldehyde oxidase (AOX1)	
833	37599_at	AOX1	AF017060	gene, exon 35 and complete cds.	aldehyde oxidase
900	900 39740 q at	NACA	AF054187	Homo sapiens alpha NAC mRNA, complete cds.	alpha NAC

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	A	B	O	g	Ξ
901	39739_at	NACA	AF054187	Homo sapiens alpha NAC mRNA, complete cds.	alpha NAC
902	902 41154 r at	CTNNA1	AF102803	Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds.	alphaE-catenin
903	903 41153_f_at	CTNNA1	AF102803	TNNA1)	alphaE-catenin
904	39324 at		AL050078	Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746	
905			D45288	Homo sapiens cDNA FLJ13267 fis, clone OVARC1000964	
906	35754 at		L40391	Homo sapiens cDNA FLJ13553 fis, clone PLACE1007454	
				Homo sapiens cDNA FLJ14821 fis, clone OVARC1000556, highly similar to RIBOSOMAL PROTEIN S6 KINASE II	
907	907 33325_at		W26667 W28575	ALPHA 2 (EC 2.7.1) Homo sapiens cDNA FLJ25016 fis, clone CBL01574	
606	41253_s_at		A1983043	Homo sapiens cDNA FLJ30436 fis, clone BRACE2009037	
910	39162_at		AA156987	Homo sapiens cDNA' FLJ30544 fis, clone BRAWH2001412	-
911	41807_at		AL040137	Homo sapiens cDNA FLJ31959 fis, clone NT2RP7007422	
912	38643_at		W87466	Homo sapiens cDNA FLJ33151 fis, clone UTERU2000263	
913	34246_at		AA418437	Homo sapiens cDNA: FLJ21175 fis, clone CAS11071	
914	914 40813_at		AI768188	Homo sapiens cDNA: FLJ21243 fis, clone COL01164	



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-				Homo sapiens cDNA: FLJ21449 fis, clone COI 04483 hinhly similar to AE010235	
				Homo sapiens mRNA from chromosome	
915	915 40923_at	,	AA290994	5q31-33 region	
2	- 00000		MOZEDO	Homo sapiens cDNA: FLJ21904 fis, clone	
916	916 38993 L at		VV 2 / 3 / 2 / 2 / 2 / 2 / 2 / 2 / 2 / 2 /	20000131	
				Homo sapiens cDNA: FLJ21927 fis, clone	
			•	HEP04178, highly similar to HSU90909	
917	38093_at		60606N	Human clone 23722 mRNA sequence	
918	918 34840 at		A1700633	Homo sapiens cDNA: FLJ22642 fis, clone HSI06970	
				Homo sapiens cDNA: FLJ23324 fis, clone	
				HEP12482, highly similar to	
				cle myosin	osin heavy chain isoform
919	32838_at	smooth muscle m S67247	S67247	heavy chain-B (MYH10) mRNA SMemb	
				Homo sapiens cervical cancer suppressor-	
920	920 33737_f_at		AI871359.	1 mRNA, complete cds	
				Homo sapiens clone 23570 mRNA	
921	921 41663_at		AF038202	sequence	
				Homo sapiens clone 23700 mRNA	
922	36815_at		AF038185	sednence	
				Homo sapiens clone 23718 mRNA	
923	923 41841_at		AF052138	sednence	
				Homo sapiens clone 23903 mRNA	
924	37794_at		AF035281	sednence	
				Homo sapiens clone 23938 mRNA	
925	925 38764_at		AF007142	sednence	
				Homo sapiens clone 24416 mRNA	•
926	926 35342_at		AF052159	sequence	
				Homo sapiens clone 24630 mRNA	
927	31867_at		AF052174	sednence	
				Homo sapiens clone 24674 mRNA	
928	36758_at		AF070578	sednence	
				Homo sapiens clone 24790 mRNA	
929	929 41864_at		AF052181	sednence	

930 38070_at)	
930 38070				Homo sapiens clone FBD3 Cri-du-chat	
	at	7	AL080234	critical region mRNA	
				Homo sapiens cofactor A protein mRNA,	
	_at	TBCA //	AF038952	complete cds.	cofactor A protein
				Homo sapiens cytochrome c oxidase	
				subunit IV precursor (COX4) gene,	
				nuclear gene encoding mitochondrial	
932 39027_at	a	COX4	AF017115	protein, complete cds.	cytochrome c oxidase subunit IV precursor
				Homo sapiens D15F37 pseudogene, S4	
933 40878_f_at	_f_at	D15F37 /	AF041081	allele, mRNA sequence.	
				Homo sapiens deoxycytidylate deaminase	
934 631_g_at	_at	рстр	L39874	gene, complete cds.	deoxycytidylate deaminase
				ycytidylate deaminase	
935 630_at	*	DCTD	L39874		deoxycytidylate deaminase
				Homo sapiens DNA for	
				galactocerebrosidase, exon 17 and	
936 33936_at	,_at	GALC	D86181		galactocerebrosidase
				Homo sapiens F1Fo-ATPase synthase f	
937 40134_at	at	ATP5J2; ATP5JL;	JL; AF047436	subunit mRNA, complete cds.	F1Fo-ATPase synthase f subunit
				Homo sapiens gene for LD78 alpha	
938 36103_at	3 at	SCYA3; LD78ALP D90144	D90144	precursor, complete cds.	LD78 alpha precursor
				Homo sapiens GOS28/P28 protein	
939 40725_at	5_at	GOSR1; P28; GS2	3S2AF047438	mRNA, complete cds.	GOS28/P28 protein
				Homo sapiens GTP binding protein	
940 38708_at	3_at	RAN; TC4; ARA24AF054183	AF054183	mRNA, complete cds.	GTP binding protein
				Homo sapiens H beta 58 homolog mRNA,	
941 35790_at)_at	VPS26; HB58; HB	HB AF054179	complete cds.	H beta 58 homolog
				Homo sapiens histone macroH2A1.2	
942 36576_at	3_at	H2AFY; H2A.y; H2	H2AF054174	mRNA, complete cds.	histone macroH2A1.2
				Homo sapiens insulin induced protein 1	
943 35303_at	3_at	INSIG1	U96876	(INSIG1) gene, complete cds.	insulin induced protein 1
				Homo sapiens interferon-gamma receptor	
				alpha chain gene, exon 7 and complete	,
944 1038_s_at	s at	interferon-gamma U19247	U19247	cds.	interferon-gamma receptor alpha chain

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	4	8	ပ	O	Ш
945	945 895_at	FIE	L19686	Homo sapiens macrophage migration inhibitory factor (MIF) gene, complete cds. macrophage migration inhibitory factor	macrophage migration inhibitory factor
				Homo sapiens mitochondrial proteolipid	
		,		osivir nomolog minity, nacieal gene encodina mitochondrial protein, complete	
946	946 38967_at	C14orf2; MP68; P	P AF054175	cds.	mitochondrial proteolipid 68MP homolog
				Homo sapiens mRNA for Hmob33 protein,	
947	947 31881_at		Y14155	3' untranslated region	
948	at	1132	AJ012755	Homo sapiens mRNA for TL132	TL132 protein
				Homo sapiens mRNA full length insert	
949	949 38786_at		AL079279	cDNA clone, EUROIMAGE 248114	
				Homo sapiens mRNA; cDNA	
	•			DKFZp434A012 (from clone	
950	950 33418_at		AL096752	DKFZp434A012)	
				Homo sapiens mRNA; cDNA	
				DKFZp434B102 (from clone	
951	38630_at		AL080192	DKFZp434B102)	
				Homo sapiens mRNA; cDNA	
				DKFZp434M162 (from clone	
952	41529_g_at		W72239	DKFZp434M162)	
				Homo sapiens mRNA; cDNA	
				DKFZp434M245 (from clone	
953	36451_at		AI743299	DKFZp434M245)	
				Homo sapiens mRNA; cDNA	
				DKFZp564A026 (from,clone	•
954	36821_at	DKFZp564A026	AL050367	DKFZp564A026)	hypothetical protein
				Homo sapiens mRNA; cDNA	
				DKFZp564A072 (from clone	
955	37366_at		AL049969	DKFZp564A072)	
				Homo sapiens mRNA; cDNA	
				DKFZp564B222 (from clone	
926	39506_at		AA933984	DKFZp564B222)	
				Homo sapiens mRNA; cDNA	
				DKFZp564D016 (from clone	
957	957 39748_at		AL050021	UKFZp564U016)	

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38357_at	ľ			Ĩ		
35301_at AL049321 DD 33716_at N95443 DD 35301_at AL049941 DD 35301_at AL049987 DD 35303_at AL049962 DD 35290_at AL049962 DD 35290_at AL049367 DD 3679_at AL049367		٧	B		Ŋ	J
35301_at AL049321 D 35301_at N95443 D 35301_at AL049941 D 36502_s_at AL049965 D 34303_at AL049962 D 35290_at AL049962 D					Homo sapiens mRNA; cDNA	
38357_at AL049321 PH					DKFZp564D156 (from clone	
35301_at	58	38357_at		AL049321	DKFZp564D156)	
35301_at					Homo sapiens mRNA; cDNA	
35301_at AL049941 C AL049265 C AL049987 C AL049987 C AL049987 C AL049987 C AL049987 C AL049987 C AL049988 C Al04988 C Al0498		8			DKFZp564E122 (from clone	
35301_at AL049941	59	33716_at		N95443	DKFZp564E122)	
35301_at AL049941	Γ				Homo sapiens mRNA; cDNA	
35301_at AL049941			*		DKFZp564E2222 (from clone	
39170_at AL049265	980	35301_at		AL049941	DKFZp564E2222)	
35842_at AL049265 C AL049987 C AL049987 C AL049987 C AL049987 C AL049949 C C AL049989 C C AL049962 C C C AL049962 C C C AL049962 C C C C AL049962 C C C C C C C C C C C C C C C C C C C	Γ				Homo sapiens mRNA; cDNA	
39170_at AL049965 AL049965 Al049962 Al					DKFZp564F053 (from clone	
40552_s_at AL049987		35842 at		AL049265	DKFZp564F053)	
40552_s_at 39170_at AL049987 39170_at AL049957 6 36509_at AL049962 6 35290_at AL049962 6 10 10 10 10 10 10 10 10 10 10 10 10 10	_	1			Homo sapiens mRNA; cDNA	
40552_s_at AL049987 39170_at AL049957 6 34303_at AL049962 6 35290_at AL049962 6 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18					DKFZp564F112 (from clone	
34303_at AL049957 [5] 34303_at AL049962 [6] 40353_at AL049962 [6] 35290_at AL050081 [6] 38079_at AL049367	962	40552 s at		AL049987	DKFZp564F112)	
34303_at AL049957 [5] 34303_at AL049949 [6] 36509_at AL049962 [6] 35290_at AL050081 [6] 38079_at AL05081					Homo sapiens mRNA; cDNA	
34303_at AL049957 [136509_at AL049962 [140353_at AL049962 [140353_at AL049962 [14050081 [1405008]			•		DKFZp564J0323 (from clone	
34303_at AL049949 [] 36509_at AL049962 [] 35290_at AL050081 [] 38079_at AL049367	963	39170 at		AL049957	DKFZp564J0323)	
34303_at AL049949 [1] 36509_at AL049962 [1] 35290_at AL050081 [1] 38079_at AL049367		!			Homo sapiens mRNA; cDNA	
36509_at AL049962 AL049962 AL049962 AL049962 AL049962 AL049962 AL050081 AL050081 AL049367 AL					DKFZp564L0822 (from clone	
35290_at AL049998 [1] 35290_at AL050081 38079_at AL049367	964	34303 at		AL049949	DKFZp564L0822)	
35290_at AL049998 [6] 40353_at AL049962 [6] 35290_at AL050081 AL049367		ľ			Homo sapiens mRNA; cDNA	
35290_at AL049998 [1] 35290_at AL050081 38079_at AL049367				·	DKFZp564L222 (from clone	
40353_at AL049962 1 35290_at AL050081 38079_at AL049367	965	36509 at		AL049998	DKFZp564L222)	
40353_at AL049962 AL050081 AL050081 AL050081 AL049367 AL04957 A					Homo sapiens mRNA; cDNA	
40353_at AL049962 135290_at AL050081 38079_at AL049367					DKFZp564P0823 (from clone	
35290_at AL050081	996	40353 at		AL049962	DKFZp564P0823)	
35290_at AL050081 38079_at AL049367					Homo sapiens mRNA; cDNA	
38079_at AL049367					DKFZp566J2146 (from clone	
38079_at AL049367	296	35290 at		AL050081	DKFZp566J2146)	
38079_at AL049367					Homo sapiens mRNA; cDNA	
38079_at AL049367					DKFZp586B0918 (from clone	
- 1000 PM	968	38079 at		AL049367	DKFZp586B0918)	
- CONTRACTOR OF THE CONTRACTOR					Homo sapiens mRNA; cDNA	
000001				à.	DKFZp586B1922 (from clone	
32195_at	696	32195_at	-	AL049450	DKFZp586B1922)	

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35379_at AL049397 37575_at AL050192 34283_at AL080110 34752_at AL080111 35103_s_at AL080213 35187_at AL080216 35363_at DDX17 AL080113 41690_at AL049471 40349_at AL04942					Homo sapiens mRNA; cDNA	
39579_at ALO50192 ALO50125 ALO50125 ALO50125 ALO50125 ALO50125 ALO5022_at ALO80111 ALO80213 ALO80213 ALO80213 ALO80213 ALO80216 ALO80213 ALO80216 AL		1		700001	DKFZp586C1019 (from clone	
37575_at AL050192 C C C C C C C C C	श्री	39379_at		AL049397		
37575_at AL050192 34283_at AL050125 1000_at AL080110 34752_at AL080111 1000_at AL080111 1000_at AL080111 1000_at AL080213 1000_at AL080213 1000_at AL080216 1000_at AL080113 1000_at AL080113 1000_at AL080114 1000_at AL080114 1000_at AL080114 1000_at AL080114 1000_at AL080114 1000_at AL080114					Homo sapiens mRNA; cUNA	
39600_at AL080110 [39600_at AL080111 [34752_at AL080111 [35103_s_at AL080213 [35187_at AL080216 [41013_at DDX17 AL080113 [41690_at AL049471 AL04942		37575 at		AL050192	DKFZp586C1723)	
AL050125 C AL050125 C AL080110 C C AL080111 C C C C C C C C C C C C C C C C C C					Homo sapiens mRNA; cDNA	
AL050125 C AL060110 C AL080111 C AL080111 C AL080213 C AL080213 C AL080216 C AL080216 C AL080217 AL080113 C AL080114 C AL					DKFZp586F071 (from clone	
AL080110 [C AL080111 [C AL080111] [C AL080111] [C AL080213] [C AL080216] [C AL080113] [C AL080113] [C AL080113] [C AL080114] [C AL08011	972	34283_at		AL050125	DKFZp586F071)	
AL080110 [C AL080111 [C AL080111] [C AL080111] [C AL080213 [C AL080213 [C AL080213 [C AL080113 [C AL080113 [C AL080113 [C AL080113 [C AL080471 [C AL089471 [C AL049471 [C AL049442 [C AL080114 [C AL049442 [C AL080114 [C AL049442 [C AL049444] [C AL0494442 [C AL049444] [C AL0494442 [C AL049444] [C AL0494442 [C AL049444] [C AL0494442 [C AL049444] [C AL049444] [C AL049444] [C AL049444] [C AL0494442 [C AL049444] [C AL049444] [C AL049444] [C AL0494444 [C AL049444] [C AL049444] [C AL049444] [C AL049444] [C AL0494444] [C AL049					Homo sapiens mRNA; cDNA	
AL080110 [C AL080111 [C AL080111] [C AL080111] [C AL080213] [C AL080216] [C AL080113] [C AL080113] [C AL080114] [C AL08011					DKFZp586G1922 (from clone	
35103_s_at AL080111 [] 36092_at AL080213 [] 35187_at AL080216 [] 41013_at AL080114 AL0803 at AL080114 AL0803 at AL080114	973	39600_at		AL080110	DKFZp586G1922)	
35103_s_at AL080111 [39103_s_at H98552 [36092_at AL080213 [35363_at DDX17 AL080113 [41013_at AL080114 AL08942]					Homo sapiens mRNA; cDNA	
35103_s_at AL080111 [36092_at AL080213 [35187_at AL080216 [35363_at DDX17 AL080113 [41013_at AL080114 AL080144 AL0842]					DKFZp586G2222 (from clone	
35103_s_at H98552 [36092_at AL080213 [35187_at AL080216 41013_at AL080113 41690_at AL049471 40349_at AL049442	974	34752_at		AL080111	DKFZp586G2222)	
36092_at AL080213 135187_at AL080216 141013_at DDX17 AL080114 141090_at AL04942					Homo sapiens mRNA; cDNA	
35103_s_at H98552 1					DKFZp58610523 (from clone	
35187_at AL080213 35363_at DDX17 AL080113 41690_at AL049471 40349_at AL049442	975	39103_s_at		H98552	DKFZp586l0523)	
35187_at AL080213 35363_at DDX17 AL080113 41690_at AL049471 40349_at AL049442					Homo sapiens mRNA; cDNA	
35187_at AL080213 35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471 40349_at AL049442					DKFZp58611823 (from clone	
35187_at AL080216 35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471 40349_at AL049442	976			AL080213	DKFZp58611823)	
35187_at AL080216 35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471 40349_at AL049442					Homo sapiens mRNA; cDNA	
35187_at AL080216 35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471 40349_at AL049442					DKFZp586K1123 (from clone	
35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471 40349_at AL049442	977	35187_at		AL080216	DKFZp586K1123)	
35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471 40349_at AL049442					Homo sapiens mRNA; cDNA	
35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471 40349_at AL049442					DKFZp586K2322 (from clone	
41013_at AL080114 41690_at AL049471 40349_at AL049442	978	35363_at	DDX17	AL080113	DKFZp586K2322) '	
41013_at AL080114 41690_at AL049471 40349_at AL049442					Homo sapiens mRNA; cDNA	
41013_at AL080114 41690_at AL049471 40349_at AL049442		•			DKFZp586M2022 (from clone	
AL049471 AL049442	979	41013_at		AL080114	DKFZp586M2022)	
AL049471 AL049442					Homo sapiens mRNA; cDNA	
AL049471 AL049442					DKFZp586N012 (from clone	
AL049442	980	41690_at		AL049471	DKFZp586N012)	
AL049442					Homo sapiens mRNA; cDNA	
AL049442					DKFZp586N1720 (from clone	
	981	40349_at		AL049442	DKFZp586N1720)	

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				Collid Sapiens mindy, Collyd	
(7)	982 32672 at		AL049387	DAFZp366N1918 (IIOIII CIONE DKFZp586N1918)	
11				Homo sapiens NADH-cytochrome b5	
ന	36668_at	DIA1	M28713	reductase (b5R) gene, exon 9.	NADH-cytochrome b5 reductase
l				Homo sapiens nucleophosmin	
				phosphoprotein (NPM) gene, 3' flanking	
က	38542_at		U89322	sequence.	
I_				Homo sapiens p18 protein mRNA,	
_4	40587_s_at	EEF1E1; P18	AF054186	complete cds.	p18 protein
				Homo sapiens PAC clone RP1-170019	even-skipped homeo box 1 (homolog of
986	41448_at	HOXA4	AC004080	from 7p15-p21, complete sequence.	Drosophila)
L				Homo sapiens prion protein (PrP) gene,	
987	36159_s_at	PrP	U29185	complete cds.	prion protein
_				Homo sapiens putative dienoyl-CoA	
_				isomerase (ECH1) gene, exons 7-10, and	
988	32756_at	ECH1	AF030249	complete cds.	putative dienoyl-CoA isomerase
				Homo sapiens RP58 gene, complete	
989	35824_at	RP58	AJ223321	CDS.	RP58 protein
_				Homo sapiens Sec61 gamma mRNA,	
990	39169_at	SEC61G	AF054184	complete cds.	Sec61 gamma
		,		Homo caniene signal transducer and	
				CHAPO.	
		į	1	activator of transcription 6 (SIAI6) gene,	signal transducer and activator of
99	41222_at	STAT6	AF067575	exons 15 through 23 and complete cds.	transcription 6
				Homo sapiens sperm acrosomal protein	
992	38817_at	SPAG7; ACRP; F:	2; F\$AF047437	mRNA, complete cds.	sperm acrosomal protein
-				Homo sapiens splicing factor,	
				arginine/serine-rich 12 (SFRS12) mRNA,	
993	36033_at		AL049309	complete cds	
				Homo sapiens thymosin beta-10 gene,	
994	31481_s_at	TMSB10	M92383	3'end.	thymosin beta-10
				Homo sabiens TIMP gene for tissue	
	995 1693 s at	TIMP	D11139	inhibitor of metalloproteinases, partial cds. Itssue inhibitor of metalloproteinases	tissue inhibitor of metalloproteinases

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				Homo sapiens transaldolase-related	
				protein gene, exons 3-8 and complete	
966	37311_at	TALDO1; TAL-H; AF010400		cds.	transaldolase-related protein
				Homo sapiens translation initiation factor	
266	32229_at	EIF4EL3; 4EHP; 4AF038957	AF038957	4e mRNA, complete cds.	translation initiation factor 4e
866	1323 at	UBB	X04803	Homo sapiens ubiquitin gene.	ubiquitin
666	999 32153_s_at	UBB	U49869	Homo sapiens ubiquitin gene.	ubiquitin
1000	1000 38372 at		U66042	Homo sapiens unknown mRNA	
			1.00001	Homo sapiens vacuolar H(+)-ATPase	inidia ese ATO actions
9	1001 38814_at	A L P6V1G1; A I P6	F6 AF038954	subunit meny, complete cus.	אמכעטומן דו(ד) און מאם אחסתווונ
1002	1002 41597 s. at	SEC221 1: SEC22 AE047442	AF047442	sec22b mRNA, complete cds.	vesicle trafficking protein sec22b
1003	อั	X5L	Y18504	Homo sapiens X5L gene.	XAP-5-like protein
				Homo sapiens, clone IMAGE:3028427,	
1004	1004 38662_at		AL047596	mRNA, partial cds	
				Homo sapiens, clone IMAGE:3140802,	
1005	1005 38312_at		AL050002	mRNA	
				Homo sapiens, clone IMAGE:3855224,	
1006	1006 33388_at		AL080223	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4132509,	
1007	1007 38676_at		AA059408	mRNA	
				Homo sapiens, clone IMAGE:4150198,	
1008	1008 40238_at		AI674208	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4182947,	
1005	1009 32119_at		AL049423	mRNA	
				Homo sapiens, clone IMAGE:4183312,	
101	1010 38650_at	IGFBP5	L27560	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4183312,	
101	1011 1396_at	IGFBP5	L27560	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4391536,	*.
1012	1012 40432_at		AA522891	mRNA	
				Homo sapiens, Similar to RNA helicase-	
_				related protein, clone MGC:9246	
101	1013 36130_f_at	MT1E	R92331	IMAGE:3892441, mRNA, complete cds	

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				Homo sapiens, Similar to serine (or	
				cysteine) proteinase inhibitor, clade E	
				(nexin, plasminogen activator inhibitor	
				type 1), member 2, clone MGC:23129	
1014	1014 41246 at		AI743134	IMAGE:4578406, mRNA, complete cds	
				Homo sapiens, similar to unknown, clone	
			-	MGC:39325 IMAGE:5440447, mRNA,	
1015	1015 41533 at		U79298	complete cds	
				-inducible, endoplasmic	homocysteine-inducible, endoplasmic
				9	reticulum stress-inducible, ubiquitin-like
1016	1016 39733 at	HERPUD1	AF055001	domain member 1	domain member 1
				homolog of yeast mutL gene; Human	
				homolog of yeast mutL (hPMS1) gene,	
1017	1017 525 g_at	hPMS1	U13695	complete cds.	postmeiotic segregation 1
				homologous to mouse Rsu-1; putative;	
				Human RSU-1/RSP-1 mRNA, complete	
1018	1018 32545 r_at	RSU-1	L12535	cds.	ras suppressor protein 1
			- 34	homologous to mouse Rsu-1; putative;	
		-		Human RSU-1/RSP-1 mRNA, complete	
1019	1019 32544_s_at	RSU-1	L12535	cds.	ras suppressor protein 1
1020	1020 39800 s at	HAX1	U68566	HS1 binding protein	HAX-1
				Human 2,4-dienoyl-CoA reductase gene,	
1021	1021 38104 at	DECR1; NADPH	U78302	exon 10 and complete cds.	2,4-dienoyl-CoA reductase
				Human alcohol dehydrogenase chi	
				polypeptide (ADH5) gene exons 8-9,	
1022	1022 37708_r_at	ADH5	M81118	complete cds.	alcohol dehydrogenase
				Human alcohol dehydrogenase chi	
			9	polypeptide (ADH5) gene exons 8-9,	
1023	1023 37707_i_at	ADHS	M81118	complete cds.	alcohol dehydrogenase
				Human alpha-1 collagen type IV gene,	
1024	1024 39333_at	COL4A1	M26576	exon 52.	alpha-1 type IV collagen
1025	1025 38417_at	AMPD2	M91029	Human AMP deaminase (AMPUZ) mRIVA.	Human AMP deaminase (AMPU2) mHNA. AMP deaminase isolorm L splicing variant
1026	1026 37747 at	ANX5	005770	Human annexin V (ANX5) gene, exon 13.	annexin V

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2	1000	L WING	600611	Human calmodulin (CALM1) gene, exons 2.3.4.5 and 6. and complete cds.	calmodulin
ž Ž				Human cathepsin D (catD) gene, exons 7,	
1028	1028 239_at	CTSD	M63138	8, and 9.	cathepsin D
Γ				Human cellular oncogene c-fos (complete v-fos FBJ murine osteosarcoma viral	v-fos FBJ murine osteosarcoma viral
1029	1029 1916_s_at	c-fos	V01512	sequence).	oncogene homolog
				ular oncogene c-fos (complete	v-fos FBJ murine osteosarcoma viral
1030	1030 1915_s_at	c-los	V01512	sequence).	oncogene nomolog
				Human c-jun proto oncogene (JUN),	v-jun avian sarcoma virus 17 oncogene
1031	32583_at	NON	J04111	complete cds, clone hCJ-1.	homolog
3		4	104444	Human c-jun proto oncogene (JUN),	v-jun avian sarcoma virus 17 oncogene bomolog
23	1032 1695_81			Complete cos, clorid rico-1:	Society
1033	1033 41604_at		0/929/	Human clone 23589 mRIVA sequence	
				Human clone A9A2BRB5 (CAC)n/(GTG)n	
1034	1034 32185 at		U00946	repeat-containing mRNA	•
				Human cyclophilin gene for cyclophilin	
1035	1035 33667_at	PPIA	X52851	(EC 5.2.1.8).	peptidylprolyl isomerase
				Human cytochrome b5 (CYB5) gene, exon	
1036	1036 38459_g_at	CYB5	L39945	6 and complete cds.	cytochrome b5
				Human cytochrome b5 (CYB5) gene, exon	
1037	1037 38458_at	CYB5	L39945	6 and complete cds.	cytochrome b5
				Human dihydrolipoamide dehydrogenase	
1038	1038 36163_at	DLD; E3; LAD; DL	AD; DLL13761	gene, exon 14.	dihydrolipoamide dehydrogenase
		ı		Human DNA for 14-3-3 protein eta chain,	-
1039	1039 1424 s at	YWHAH; YWHA1	YWHA1 D78577	exon2 and complete cds'.	14-3-3 protein eta chain
				Human DNA sequence from clone 73H22	
			•	on chromosome 6q23, complete	
1040	1040 31797_at	dJ73H22.1	AL035699	sednence.	dJ73H22.1 (TBP-like protein)
				Human ENO2 gene for neuron specific	
1041	1041 40193_at	ENO2	X51956	(gamma) enolase.	human gamma enolase
1042	1042 38326_at	G0S2	M69199	Human G0S2 protein gene, complete cds. G0S2 protein	GOS2 protein
104	1043 40567 at	TUBA3: EL.125113 X01703	X01703	Human gene for alpha-tubulin (b alpha 1). alpha-tubulin	alpha-tubulin
Ś	1000t	10000, 10001	201100	/	

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1044	1044 39775_at	SERPING1; C1IN	N X54486		C1 inhibitor
				gene for creatine kinase B (EC	
1045	1045 40862 i_at	CKB; CKBB	X15334		creatine kinase B
				gene for hepatitis C-associated	
				microtubular aggregate protein p44, exon	hepatitis C-associated microtubular
1046	1046 37641_at	IF144; p44; MTAP D28915		_	aggregate protein p44
				Human gene for heterogeneous nuclear	
				ribonucleoprotein (hnRNP) core protein	
1047	1047 40211_at	HNRPA1; HNRNP X12671	X12671	A1.	hnrnp a1 protein
				growth	melanoma growth stimulatory activity
1048	1048 408_at	MGSA	X54489	一	preprotein
				Human gene for ornithine decarboxylase	
1049	1049 36203_at	00001	X16277	ODC (EC 4.1.1.17).	ornithine decarboxylase (ODC)
				Human gene for very low density	
1050	1050 36873_at	VLDLR	D16532		very low density lipoprotein receptor
1051	1051 34759_at		U68494	Human hbc647 mRNA sequence	
L				Human hepatic dihydrodiol	
1052	1052 32805_at	AKR1C1; DD1; DE	DI U05861	dehydrogenase gene, exon 9.	hepatic dihydrodiol dehydrogenase
				Human HMG-17 gene for non-histone	
1053	1053 41231 f at	HMG17; MGC562 X13546	X13546		put. HMG-17 protein
				Human HOX 5.1 gene for HOX 5.1	
1054	1054 38294 at	HOXD4; HOX4; H	i; HX17360	protein.	hox 5.1 protein
				Human hsc70 gene for 71 kd heat shock	
1055	1055 40637_at	HSP73 HSC70 HS	HS Y00371	cognate protein.	71 Kd heat shock cognate protein
1056	1056 232 at	LAMB2	M55210	Human laminin B2 chain gene, exon 28.	laminin B2 chain
				Human lipoprotein-associated coagulation	
				inhibitor (LACI) gene, exon 9 and	
1057	1057 40767 at	TFPI	M59499	complete cds.	lipoprotein-associated coagulation inhibitor
1058	1058 38637_at	LOX	L16895	Human lysyl oxidase (LOX) gene, exon /. lysyl oxidase	lysyl oxidase
				Human medium-chain acyl-CoA	
1050	1059 37532_at	MCAD	M91432	dehydrogenase (MCAD) gene, exon 12.	medium-chain acyl-CoA denydrogenase
106	1060 870 f at	MT3: GIF: GIFB	M93311	Human metallothionein-III gene, complete cds.	metallothionein-III
2	1010	1			

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				Human metaxin (MTX) gene, complete	
1061	1061 40890_at	MTX	U46920	cds.	metaxin
				Human mRNA for erythrocyte adducin	
1062	1062 32145_at	ADD1	X58141	alpha subunit.	erythrocyte alpha adducin
				Human mRNA for general transcription	
1063	1063 37381_g_at	TF2B	X59268	factor IIB.	IIB protein
1064	1064 33683_at	TI-227H	D50525	Human mRNA for TI-227H.	
					myocyte-specific enhancer factor 2A, C9
				ene, last coding exon, and	form; myocyte-specific enhancer factor ZA,
1065	1065 41747_s_at	MEF2A	U49020	complete cds.	C4 torm
				Human NAD(P)H:quinone oxireductase	
1066	1066 38066_at	NQ01	M81600	gene, exon 6.	NAD(P)H:quinone oxireductase
				Human natural killer cell enhancing factor	
1067	1067 39729_at	NKEFB	L19185	(NKEFB) mRNA, complete cds.	enhancer protein
				:	
				Human nonmuscle/smooth muscle alkall	non-muscie myosin light chain; smooth
1068	1068 33994_g_at	MLC	M22919	myosin light chain gene, complete cds.	muscle myosin light chain
				Human nucleic acid binding protein gene,	
1069	1069 32841_at	ZNF9; DM2; CNB U19765	U19765	complete cds.	nucleic acid binding protein
1070	1070 32590 at	NCL	M60858	Human nucleolin gene, complete cds.	nucleolin
				Human oncoprotein 18 (Op18) gene,	
1071	1782 s at	Op18	M31303	complete cds.	oncoprotein 18
				Human prostaglandin D2 synthase gene,	
1072	1072 216_at	PTGDS	M98539	exon 7.	prostaglandin D2 synthase (21kD, brain)
				Himan protein phoenhatase 24 catalvic	protein phosphatase-2A catalytic subunit-
1073	1073 237 s at	PPP2CA	M60483	subunit-alpha gene, complete cds.	alpha
				Human protein phosphatase inhibitor 2	
				(PPP1R2) gene, exon 6 and complete	
1074	1074 812 at	PPP1R2	U68111	cds.	protein phosphatase inhibitor 2
				Human protein phosphatase inhibitor 2	
				(PPP1R2) gene, exon 6 and complete	
107	1075 33180_at	PPP1R2	U68111	cds.	protein phosphatase inhibitor 2
10,	10 2020 050	·	14/01894	Human putative ribosomal protein S1	
	132320_at		VV Z 1004	ZAILIIII.	

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1077 491_at PTPRG 1078 492_g_at PTPRG 1079 36611_at ACP1 1080 174_s_at SH3P18 1081 241_g_at SRM	U46116 U46116 U25849	Human receptor tyrosine phosphatase gamma (PTPRG) gene, exon 30 and complete cds.	
		4	
	U46116 U25849 U61167	for two sine phoenhatese	
	U46116 U25849 U61167	Himan recentor tyrocine phoenhatece	receptor tyrosine phosphatase gamma
	U46116 U25849 U61167	וחווומוו ובכפלוכו ולוספוווב לווספלוומומפ	
	U25849 U61167	gamma (PTPRG) gene, exon 30 and	
	U25849 U61167	complete cds.	receptor tyrosine phosphatase gamma
	U25849 U61167	Human red cell-type low molecular weight	
	U25849 U61167	acid phosphatase (ACP1) gene, exon 6	red cell-type low molecular weight acid
		and 7, complete cds.	phosphatase
	U61167	Human SH3 domain-containing protein	
		SH3P18 mRNA, complete cds	SH3 domain-containing protein SH3P18
		Human spermidine synthase gene,	
	M64231	complete cds.	spermidine synthase
		Human sterol carrier protein-X/sterol	
		carrier protein-2 (SCP-X/SCP-2) gene,	-
	P-2 U11313	exon 16, and complete cds.	sterol carrier protein-X/sterol carrier protein-2
1083 32587_at ZFP36L2; BRF	BRF2; {U07802	Human Tis11d gene, complete cds.	Tis11d
1084 31680 at TOP1P2	M55630	Human topoisomerase I pseudogene 2.	
		Human transformation-related protein	
1085 36446_s_at HMG1L2	L24521	mRNA, 3' end	transformation-related protein
		Human transmembrane protein (CD59)	
1086 39351_at CD59	M84349	gene, exon 4.	CD59 protein
1087 38727 at THE1	M23161	Human transposon-like element mRNA	
		Human vascular cell adhesion molecule-1	
1088 41433 at VCAM1	M73255	(VCAM1) gene, complete CDS.	vascular cell adhesion molecule-1
	U58522	huntingtin interacting protein 2	huntingtin interacting protein
1090 35973 at HYPH	AB023163	Huntingtin interacting protein H	KIAA0946 protein
1091 40196_at HYA22	D88153	HYA22 protein	HYA22
·	-	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A	enoyl-CoA hydratase/3-hydroxyacyl-CoA
1092 36952_at HADHA	D16480	thiolase/enoyi-Coenzyme A nydratase (trifunctional protein), alpha subunit	denydrogenase alpha-subunit oi triiunctional protein

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1093	1093 39741_at	НАОНВ	D16481	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein
1094	1094 36626_at	HSD17B4	X87176	hydroxysteroid (17-beta) dehydrogenase 4 17beta-hydroxysteroid dehydrogenase	17beta-hydroxysteroid dehydrogenase
				Hypothetical protein of unknown function;	
		٠		Hypothetical 52 KDa protein; Hypothetical	
				protein exhibits similarity to motils tound in (1179010) delta 6 desaturase, a	
				hypothetical cytochrome b5 containing	
				fusion protein, and hypotetical proteins	
				encoded by (Z81122) T13F2.1	
				[Caenorhabditis elegans] and (Z70271)	
				W08D2.4 [Caenorhabditis elegans]; DNA	
				structure-specific endonuclease FEN1;	
				FLAP ENDONUCLEASE-1;	
				MATURATION FACTOR 1 (MF1); DNase	
				IV; RAD2_HUMAN; Hypothetical human	
				Best's macular dystrophy relatedprotein;	
				Simulated translation extends ORF of	
				previously reported partial coding	
				sequence for Best's macular dystrophy	
			•.	related protein (AF038536); Homo	
				sapiens chromosome 11, BAC CIT-HSP-	
				311e8 (BC269730) containing the hFEN1	BC269730_1; BC269730_2; FEN1_HUMAN;
1095	1095 41583_at	FEN1	AC004770	gene, complete sequence.	BC269730_4

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Е	BC269730_1; BC269730_2; FEN1_HUMAN;	BC269730_4	hypothetical protein CG018	hypothetical protein AF038182
Q	Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypotetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy relatedprotein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1	gene, complete sequence.	hypothetical gene CG018	hypothetical gene supported by AF038182; BC009203
၁		AC004770	U50527	AF038182
8		FEN1	CG018	LOC90355
A	·	1096 34224_at	1097 1527_s_at	1098 33466_at
		1096	60	109

Fig 21

ш		Noc 104_1, Noc 104_5, Noc 104_5	hypothetical protein, similar to (AC007017) putative RNA helicase A [Arabidopsis thaliana]		
D	Hypothetical human protein (partial CDS); CDS constructed from combination of BLASTX, EST matches and Xgrail predictions. N-terminus of protein likely encoded in flanking cosmid R29942. Predicted protein exhibits weak similarity to hypothetical protein PIDIe1226191 (AL021106) from Drosophila melanogaster; Hypothetical human protein most similar to Rat ionotropic glutamate receptor (L34938); CDS constructed primarily from XGRAIL predictions and BLASTX similarity to (L34938) ionotropic glutamate receptor [Rattus norvegicus] and gil2160125 (U29873) NMDAR-L [Rattus norvegicus]. Also exhibits similarity to PIDIe258718 (Z78413) T01C3.10 (Caenorhabditis elegans). C-terminus of hypothetical protein is ill-defined at this point; definition will require identification and characterization of appropriate cDNAs: Hypothetical 59.8 kDa human protein; CDS constructed from EST matches and Xgrail predictions. C-terminus of predicted protein not fully confirmed by EST or cDNA coverage.	hypothetical protein	hypothetical protein	hypothetical protein hypothetical protein 23851	hypothetical protein 24636
၁		AC004528 AA015605	AL079292	AF007130 AF035313	Al651368
В		MGC2436 FI 120811	LOC54505	LOC54104 LOC56007	LOC55977
A		1099 35983_at	1101 39140 at	37819 39517	1104 41561_s_at



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1105 41128_at	LOC92703	AF070537	hypothetical protein BC013073	
1106 38972 at	LOC115207	AF052169	hypothetical protein BC013764	
1107 34864 at	CGI-57	AF070638	hypothetical protein CGI-57	hypothetical protein CGI-57
1108 39960_at	CL640	AF091086	hypothetical protein CL640	hypothetical protein CL640
1109 38837_at	DJ971N18.2	W26226	hypothetical protein DJ971N18.2	
1110 35142_at	DKFZP564D172	AF070617	hypothetical protein DKFZp564D172	
1111 34830_at	DKFZP564K0822	K0822 W25986	hypothetical protein DKFZp564K0822	
1112 31852 at	DKFZP5640043	O043 AL050390	hypothetical protein DKFZp5640043	
1113 33895_at	DKFZP586F1318 AL050373	AL050373	hypothetical protein DKFZP586F1318	hypothetical protein
1114 39692 at	DKFZP586F2423 AL080209	AL080209	hypothetical protein DKFZp586F2423	
1115 35682_at	FLB6421	AI133727	hypothetical protein FLB6421	
1116 36647_at	FLJ10326	AA526812	hypothetical protein FLJ10326	
1117 34804_at	FLJ10618	AL049246	hypothetical protein FLJ10618	
1118 36840 at	FLJ10737	AF052158	hypothetical protein FLJ10737	
1119 35283_at	FLJ10738	H05692	hypothetical protein FLJ10738	
1120 37610_at	FLJ10803	AI765280	hypothetical protein FLJ10803	
1121 33173 g at	FLJ10849	T75292	hypothetical protein FLJ10849	
1122 39923 at	FLJ10971	A1935420	hypothetical protein FLJ10971	
			hypothetical protein FLJ11021 similar to	
1123 38105_at	FLJ11021	W26521	splicing factor, arginine/serine-rich 4	
1124 33394 at	FLJ11126	AA034074	hypothetical protein FLJ11126	
1125 35709_at	FLJ11149	AF038172	hypothetical protein FLJ11149	
1126 38141_at	FLJ11193	AF038176	hypothetical protein FLJ11193	
	FLJ11806	AI561196	hypothetical protein FLJ11806	
1128 41177_at	FLJ12443	AW024285	hypothetical protein FLJ12443	
1129 41434 at	FLJ12552	AF070557	hypothetical protein FLJ12552	hypothetical protein FLJ12552
1130 36580_at	FLJ13910	AL050139	hypothetical protein FLJ13910	hypothetical protein FLJ13910
1131 32222 at	FLJ14639	AA152202	hypothetical protein FLJ14639	
1132 38710 at	FLJ20113	AL096714	hypothetical protein FLJ20113	
1133 38652_at	FLJ20154	AF070644	hypothetical protein FLJ20154	
1134 40868_at	FLJ20274	AA442799	hypothetical protein FLJ20274	
1135 34739_at	FLJ20275	W26023	hypothetical protein FLJ20275	
1136 34857_at	FLJ20986	224724	hypothetical protein FLJ20986	
1137 32251_at	FLJ21174	AA149307	hypothetical protein FLJ21174	
1138 40615_at	FLJ21439	AA780049	hypothetical protein FLJ21439	
139 33915_at	FLJ23027	W22655	hypothetical protein FLJ23027	

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11403	1140 35198_at	LOC57146		4796	hypothetical protein from clone 24796
11413	1141 38483 at	HSA011916	AJ011916	5	hypothetical protein
11424	1142 41236_at	HSU79252	U79252		hypothetical protein HSU79252
1143 38443	18443_at	MGC14433	U79291	hypothetical protein MGC14433	
1144 39811	19811_at	MGC2749	AA402538	hypothetical protein MGC2749	
				hypothetical protein MGC2840 similar to a	
1145	1145 32051_at	MGC2840	AJ224875	putative glucosyltransferase	glucosyltransferase
1146 35219	15219 at	MGC3047	AL050202	hypothetical protein MGC3047	
1147	1147 41696 at	MGC3077	AI620381	hypothetical protein MGC3077	
T				hypothetical protein MGC4276 similar to	hypothetical protein MGC4276 similar to
1148	1148 41147_at	MGC4276	AF038186	CG8198	CG8198
1149	1149 37242 at	MGC5149	U79260	hypothetical protein MGC5149	
1150	1150 36975 at	MGC8721	W26659	hypothetical protein MGC8721	
1151	1151 35677_at	MGC9084	AL035369	hypothetical protein MGC9084	hypothetical protein
1152	1152 32504 at	MY014	AW024812	hypothetical protein My014	
1153	1153 38106_at	YR-29	AJ012409	hypothetical protein YR-29	hypothetical protein
1154	1154 37640 at	HPRT1	M31642	hypoxanthine phosphoribosyttransferase 1 (Lesch-Nyhan syndrome)	hypoxanthine phosphoribosyltransferase 1
1155	1155 1039 s at	HIF1A	U22431	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	hypoxia-inducible factor 1 alpha
			•	IGF binding protein-4; Human insulin-like	
		200	290001	growin factor binding protein 4 (1911 of 4)	insulin-like growth factor hinding protein-4
1157	1155 39781 at	Igror4	A,1005579	IK cytokine, down-regulator of HLA II	Prer protein
1158	1158218 at	≅	S74221	IK cytokine, down-regulator of HLA II	IK factor
1159	1159 37690 at	ILVBL	U61263	ilvB (bacterial acetolactate synthase)-like	acetolactate synthase homolog
1160	1160 36097_at	ETR101	M62831	immediate early protein	immediate early protein
1161	1161 1237 at	(EB3	S81914	immediate early response 3	immediate early response 3, isoform short; immediate early response 3, isoform long
1162	1162 34301 at	logo.	VOR915	immunoclobulin (CD79A) binding protein 1 alpha 4 protein	alpha 4 protein
701	34391_at	l labil	010001		

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	A	В	ပ	O	ı
				perfamily containing	
1163	1163 38636_at	ISLR	AB003184		ISLR
				IMP (inosine monophosphate)	IMP (inosine monophosphate)
1164	1164 40695_at	IMPDH1	J05272		dehydrogenase 1
1165	1165 36875_at	IBTK	AL050018		hypothetical protein
				nant	inhibitor of DNA binding 1, dominant
1166	1166 36617_at	<u></u>	X77956		negative helix-loop-helix protein
			-	inhibitor of DNA binding 2, dominant	
1167	1167 41215_s_at	ID2	D13891	negative helix-loop-helix protein	Id-2H
				inhibitor of kappa light polypeptide gene	
				enhancer in B-cells, kinase complex-	
1168	1168 34344_at	IKBKAP	AF044195	associated protein	IkappaB kinase complex associated protein
				inner membrane protein, mitochondrial	
1169	1169 37659 at	IMMI	L42572	(mitofilin)	transmembrane protein
					human type 1 inositol 1,4,5-trisphosphate
1170	1170 755_at	ITPR1	D26070	inositol 1,4,5-triphosphate receptor, type 1	receptor
					human type 1 inositol 1,4,5-trisphosphate
1171	1171 32778 at	ITPR1	D26070	inositol 1,4,5-triphosphate receptor, type 1	receptor
1172	1172 36154_at	IHPK1	D87452	inositol hexaphosphate kinase 1	KIAA0263 protein
					lithium-sensitive myo-inositol
1173	1173 32697_at	IMPA1	AF042729	inositol(myo)-1(or 4)-monophosphatase 1	monophosphatase A1
1174	1174 36496_at	IMPA2	AF014398	inositol(myo)-1(or 4)-monophosphatase 2	myo-inositol monophosphatase 2
1175	1175 35833_at	LOC51141	AL080184	insulin induced protein 2	
1176	1176 41049_at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
1177	1177 851_s_at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
				insulin-like growth factor 1 (somatomedin	
1178	1178 38737_at	IGF1	X57025	(C)	insulin-like growth factor I
				insulin-like growth factor 1 (somatomedin	
1179	1179 1501_at	IGF1	X57025	(c)	insulin-like growth factor I
1180	1180 160027_s_at	IGF2R	Y00285	insulin-like growth factor 2 receptor	insulin-like growth factor 2 receptor
				insulin-like growth factor binding protein 2	insulin-like growth factor binding protein 2 insulin-like growth factor binding protein 2
1181	1181 40422_at	IGFBP2	X16302	(36kD)	(36KD)
	. [
1182	1182 1737_s_at	IGFBP4	M62403	insulin-like grown factor binding protein 4	insulin-like growth factor binding protein 4 insulin-like growth factor binding protein 4

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1183	2062 at	IGFBP7	L19182	insulin-like growth factor binding protein 7	
1184	1184 37991_at	ITM1	L38961	integral membrane protein 1	integral membrane protein 1
				integral membrane protein; swiss-prot	
1185	1185 37326 at	A4	U93305	differentiation in intestinal epithelium	LIM domain only 6
1186	1186 41163 at	P24B	AL109672	integral type I protein	p24B protein
					integrin beta 1 isoform 1A precursor; integrin
		,			isoform 1C-1 precursor; integrin beta 1
1187	1187 32808 at	ITGB1: CD29: FN X07979	87979	integrin beta 1 subunit precursor; Human mBNA for integrin beta 1 subunit.	isoform 1D precursor, integrin beta 1 isoform 1C-2 precursor
				integrin cytoplasmic domain-associated	integrin cytoplasmic domain associated
1188	1188 1195_s_at	ICAP-1A	AF012024	protein 1	protein
1189	189 120 at	ITGA1	X68742	integrin, alpha 1	
1190	1190 37484_at	ITGA1	X68742	integrin, alpha 1	
1191	1191 36892_at	ITGA7	AF032108	integrin, alpha 7	integrin alpha-7
				integrin, alpha V (vitronectin receptor,	integrin, alpha V (vitronectin receptor, alpha
1192	1192 39071_at	ITGAV	M14648	alpha polypeptide, antigen CD51)	polypeptide, antigen CD51)
1193	1193 39754_at	ITGB5	X53002	integrin, beta 5	
1194	1194 2058_s_at	ITGB5	M35011	integrin, beta 5	integrin, beta 5
				integrin, beta-like 1 (with EGF-like repeat	
1195	1195 40681_at	ITGBL1	AB008375	domains)	osteoblast specific cysteine-rich protein
1196	196 35365_at	آج ا	U40282	integrin-linked kinasė	integrin-linked kinase
				interacts with adenovirus E3-14.7KDa, a	
				TNF-alpha cytolysis antagonist; leucine	
				John form: interacts with adenovirus E3-	
				14.7KDa, a TNF-alpha cytolysis	
				antagonist; leucine zipper protein;	
				alternatively translated; short form; Homo	
1107	1107 41743 i et	OPTN: NRP: FIP	P2 AF061034	sapiens FIP2 alternatively translated mRNA complete cds	FIP2
	11/40-1-01				



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				interacts with adenovirus E3-14.7KDa, a	
				TNF-alpha cytolysis antagonist; leucine	
				zipper protein; alternatively translated;	
				long form; interacts with adenovirus E3-	
				14.7KDa, a TNF-alpha cytolysis	
				antagonist; leucine zipper protein;	
_				alternatively translated; short form; Homo	
				sapiens FIP2 alternatively translated	
1198	1198 41742 s at	OPTN; NRP; FIP2	P2 AF061034		FIP2
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 1
1199	1199 676 q at	IFITM1	J04164	1 (9-27)	(9-27)
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 1
1200	1200 675 at	IFITM1	J04164	1 (9-27)	(9-27)
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 3
1201	1201 41745_at	IFITM3	X57352	3 (1-8U)	(1-8U)
1202 1456	1456 s at	IF116	M63838		interferon-gamma induced protein
1203	925 at	IFI30	J03909	interferon, gamma-inducible protein 30	interferon, gamma-inducible protein 30
1204	1204 39728 at	IFI30	J03909	interferon, gamma-inducible protein 30	interferon, gamma-inducible protein 30
				interferon-induced protein with	interferon-induced protein with
1205	1205 32814 at	IFIT1	M24594	tetratricopeptide repeats 1	tetratricopeptide repeats 1
				interferon-related developmental regulator	
1206	1206 37679 at	IFR01	Y10313		PC4 protein
1207	1368_at	IL1R1	M27492	interleukin 1 receptor, type I	interleukin 1 receptor, type I
1208	1208 33228 q at	IL10RB	A1984234	interleukin 10 receptor, beta	
1209	1209 33227_at	IL10RB	Al984234	interleukin 10 receptor, beta	
1210	1210 38969_at	11.27	A1828168	interleukin 27	
1211	1211 38299_at	11.6	X04430	interleukin 6 (interferon, beta 2)	interleukin 6 (interferon, beta 2)
1212	1212 35372 r at		M17017	interleukin 8	interleukin 8
				interleukin enhancer binding factor 2,	
1213	1213 36189_at	ILF2	U10323	45kD	NF45 protein
1214	1214 36030_at	DKFZP58612223	AL080214	intermediate filament-like MGC:2625	hypothetical protein
1215	1215 35776_at	ITSN1	AF064243	intersectin 1 (SH3 domain protein)	intersectin short form
1216	1216 41431_at	ICK	AB023153	intestinal cell kinase	KIAA0936 protein
				IQ motif containing GTPase activating	:
1217	1217 1825_at	IQGAP1	L33075	protein 1	ras GTPase-activating-like protein

Fig 21

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				te dehydrogenase 1 (NADP+),	
1218	1218 39023_at	IDH1	AF020038	soluble	NADP-dependent isocitrate dehydrogenase
1219	1219 40112 at	Прнзв	AA522698	isocitrate dehydrogenase 3 (NAD+) beta	
	;;				NAD+-specific isocitrate dehydrogenase
1220	1220 40111 g at	IDH3B	U49283	ta	beta precursor
1221		KIAA1162	AL021396	isoform 1 match: proteins: Tr:Q9UJA1	hypothetical protein
1222	1222 32695 at	dJ196E23.1	297632	isoform 2 match: protein Q99991	bombesin-like receptor 3
1223	1223 40827_at	IARS	U04953	isoleucine-tRNA synthetase	isoleucyl-tRNA synthetase
1224	1224 36985 at	IDI1	X17025	isopentenyl-diphosphate delta isomerase	isopentenyl-diphosphate delta isomerase
				isoprenylcysteine carboxyl	
1225	1225 41775_at	ICMT	AF064084	methyltransferase	prenylcysteine carboxyl methyltransferase
1226	1226 34877_at	JAK1	AL039831	Janus kinase 1 (a protein tyrosine kinase)	
1227		JM4	AJ005896	JM4 protein	JM4 protein
1228	1228 40957_at	JJAZ1	D63881	joined to JAZF1	joined to JAZF1
1229	41250_at	JTV1	U24169	JTV1 gene	JTV-1
1230	1230 41483_s_at	ONOL	X56681	jun D proto-oncogene	junD protein
1231	1612_s_at	ONOC	X56681	jun D proto-oncogene	junD protein
1232	1232 40464_g_at	KPNB2	U70322	karyopherin (importin) beta 2	transportin
1233	1233 39028_at	KPNB3	Y08890	karyopherin (importin) beta 3	Ran_GTP binding protein 5
1234	1234 35725_at	KPNA3	D89618	karyopherin alpha 3 (importin alpha 4)	karyopherin alhph 3
1235	235 32487_s_at	KPNA4	AB002533	karyopherin alpha 4 (importin alpha 3)	Qip1
				katanin p60 (ATPase-containing) subunit	-
1236	1236 32708_g_at	KATNA1	AI191768	A 1	
				KDEL (Lys-Asp-Glu-Leu) endoplasmic	
1237	37386_i_at	KDELR1	X55885	reticulum protein retention receptor 1	KDEL receptor
				KDEL (Lys-Asp-Glu-Leu) endoplasmic	
1238	39080_at	KDELR2	M88458	reticulum protein retention receptor 2	KDEL receptor 2
				KDEL (Lys-Asp-Glu-Leu) endoplasmic	
1235	1239 33402_at	KDELR3	AL035081	reticulum protein retention receptor 3	hypothetical protein
1240	1240 37150_at	AB026190	AB026190	Kelch motif containing protein	Kelch motif containing protein
124	1241 32329_at	KRTHB6	X99142	keratin, hair, basic, 6 (monilethrix)	type II intermediate filament of hair keratin
124%	1242 39346 at	KHDRBS1	M88108	KH domain containing, RNA binding, signal transduction associated 1	p62

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1243	1243 32679_at	KIAA0009	D13634	KIAA0009 gene product	KIAA0009 gene product
1244	1244 34760_at	KIAA0022	D14664	KIAA0022 gene product	KIAA0022 gene product
1245	1245 41129_at	KIAA0033	D26067	KIAA0033 protein	
1246	1246 38797_at	KIAA0062	D31887	KIAA0062 protein	-
1247	1247 36978_at	KIAA0077	D38521	KIAA0077 protein	
1248	1248 37718_at	KIAA0096	D43636	KIAA0096 protein	
1249	1249 37293_at	KIAA0097	D43948	KIAA0097 gene product	KIAA0097 protein
				KIAA0098 is a human counterpart of	
				mouse chaperonin containing TCP-1	
				gene. Start codon is not identified.	
				ha01413 cDNA clone for KIAA0098 has a	
				2-bp insertion between 736-737 of the	
-				sequence of KIAA0098.; Homo sapiens	
1250	250 40417_at	KIAA0098	D43950	mRNA for KIAA0098 protein, partial cds.	KIAA0098 protein
1251	1251 39783_at	KIAA0100	D43947	KIAA0100 gene product	KIAA0100 protein
1252	1252 37359_at	KIAA0102	D14658	KIAA0102 gene product	KIAA0102 gene product
1253	1253 38031_at	KIAA0111	D21853	KIAA0111 gene product	KIAA0111 gene product
1254	1254 40279_at	KIAA0121	D50911	KIAA0121 gene product	KIAA0121 protein
1255	1255 36845_at	KIAA0136	D50926	KIAA0136 protein	
1256	1256 32099_at	KIAA0138	D50928	KIAA0138 gene product	KIAA0138 gene product
1257	1257 38472_at	KIAA0143	D63477	KIAA0143 protein	
1258	1258 41728_at	KIAA0152	D63486	KIAA0152 gene product	KIAA0152 gene product
1259	1259 37642_at	KIAA0157	D63877	KIAA0157 protein	KIAA0157 protein
1260	1260 32661_s_at	KIAA0170	D79992	KIAA0170 gene product	KIAA0170 gene product
1261	37225_at	KIAA0172	D79994	KIAA0172 protein	
1262	1262 36942_at	KIAA0174	D79996	KIAA0174 gene product	KIAA0174 gene product
1263	31863_at	KIAA0179	D80001	KIAA0179 protein	-
1264	37734_at	KIAA0184	D80006	KIAA0184 protein	
1265	1265 41669 at	KIAA0191	D83776	KIAA0191 protein	
1266	1266 36192_at	KIAA0193	D83777	KIAA0193 gene product	KIAA0193 gene product
1267	1267 38056 at	KIAA0195	D83779	KIAA0195 gene product	KIAA0195 gene product
1268	1268 38419_at	KIAA0196	D83780	KIAA0196 gene product	KIAA0196 gene product
1269	1269 38067_at	KIAA0202	D86957	KIAA0202 protein	
1270	1270 32586_at	KIAA0217	D86971	KIAA0217 protein	
1271	1271 38728_at	KIAA0225	D86978	KIAA0225 protein	

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1272 40971_at	KIAA0229	D86982	KIAAU229 protein	
1273 37748_at	KIAA0232	D86985	KIAA0232 gene product	KIAA0232 protein
1274 38892_at	KIAA0240	D87077	KIAA0240 protein	
1275 40765_at	KIAA0251	D87438	KIAA0251 protein	
1276 41634_at	KIAA0256	D87445	KIAA0256 gene product	KIAA0256 protein
1277 36971_at	KIA'A0257	D87446	KIAA0257 protein	
1278 32237_at	KIAA0265	D87454	KIAA0265 protein	
1279 39405_at	KIAA0266	D87455	KIAA0266 gene product	KIAA0266 gene product
1280 35039 at	KIAA0276	D87466	KIAA0276 protein	
1281 38592 s_at	KIAA0284	Al828210	KIAA0284 protein	
1282 41381_at	KIAA0308	AB002306	KIAA0308 protein	
1283 37943 at	KIAA0321	AB002319	KIAA0321 protein	
1284 32592 at	KIAA0323	AB002321	KIAA0323 protein	
1285 39797 at	KIAA0349	AB002347	KIAA0349 protein	
1286 34661_at	KIAA0350	AB002348	KIAA0350 protein	KIAA0350 protein
32208_at	KIAA0355	AB002353	KIAA0355 gene product	KIAA0355 gene product
1288 32223_at	KIAA0365	AB002363	KIAA0365 gene product	
1289 33442_at	KIAA0367	AB002365	KIAA0367 protein	
35830_at	KIAA0370	AB002368	KIAA0370 protein	
1291 40517_at	KIAA0372	AB002370	KIAA0372 gene product	KIAA0372 gene product
34837_at	KIAA0376	AB002374	KIAA0376 protein	
1293 41457_at	KIAA0423	AB007883	KIAA0423 protein	-
67_at	KIAA0433	AB007893	KIAA0433 protein	KIAA0433 protein
	KIAA0438	AB007898	KIAA0438 gene product	KIAA0438 gene product
1296 40805_at	KIAA0440	AB007900	KIAA0440 protein	KIAA0440 protein
1297 32091_at	KIAA0446	AB007915	KIAA0446 gene product	KIAA0446 protein
298 41243_at	KIAA0447	AB007916	KIAA0447 gene product	KIAA0447 protein
1299 32206_at	KIAA0451	AB007920	KiAA0451 gene product	KIAA0451 protein
1300 36069_at	SRGAP2	AB007925	KIAA0456 protein	KIAA0456 protein
37230_at	KIAA0469	AB007938	KIAA0469 gene product	KIAA0469 protein
33893_r_at	KIAA0470	AB007939	KIAA0470 gene product	KIAA0470 protein
34445 at	KIAA0471	AB007940	KIAA0471 gene product	KIAA0471 protein
35318_at	KIAA0475	AB007944	KIAA0475 gene product	KIAA0475 protein
35786_at	KIAA0476	AB007945	KIAA0476 gene product	KIAA0476 protein
35762_at	KIAA0483	AB007952	KIAA0483 protein	KIAA0483 protein
41830 at	KIAA0494	AB007963	KIAA0494 gene product	KIAA0494 protein

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1308 35534_at	KIAA0514	AB011086	KIAA0514 gene product	KIAA0514 protein
1309 38724_at	KIAA0515	AB011087	KIAA0515 protein	KIAA0515 protein
1310 34192 at	KIAA0532	AB011104	KIAA0532 protein	KIAA0532 protein
1311 33787_at	KIAA0537	AB011109	KIAA0537 gene product	KIAA0537 protein
1312 35184_at	KIAA0546	AB011118	KIAA0546 protein	KIAA0546 protein
1313 31849_at	KIAA0564	AB011136	KIAA0564 protein	KIAA0564 protein
1314 39434_at	KIAA0592	AB011164	KIAA0592 protein	KIAA0592 protein
1315 41379 at	KIAA0594	AB011166	KIAA0594 protein	KIAA0594 protein
1316 32866_at	KIAA0605	AB011177	KIAA0605 gene product	KIAA0605 protein
1317 39852 at	KIAA0610	AB011182	KIAA0610 protein	KIAA0610 protein
1318 40160 at	KIAA0618	AL080109	KIAA0618 gene product	hypothetical protein
U'	KIAA0625	AB014525	KIAA0625 protein	KIAA0625 protein
11	KIAA0626	AB014526	KIAA0626 gene product	KIAA0626 protein
1321 39376_at	KIAA0630	AB014530	KIAA0630 protein	KIAA0630 protein
1322 34353_at	KIAA0648	AB014548	KIAA0648 protein	KIAA0648 protein
1323 38082 at	KIAA0650	AB014550	KIAA0650 protein	KIAA0650 protein
1324 39117 at	KIAA0662	AB014562	KIAA0662 gene product	KIAA0662 protein
1325 41170_at	KIAA0663	AB014563	KIAA0663 gene product	KIAA0663 protein
1326 31826_at	KIAA0674	AB014574	KIAA0674 protein	KIAA0674 protein
1327 39403 at	KIAA0678	AB014578	KIAA0678 protein	KIAA0678 protein
1328 39519_at	KIAA0692	AB014592	KIAA0692 protein	KIAA0692 protein
1329 39380_at	KIAA0697	AB014597	KIAA0697 protein	KIAA0697 protein
1330 39705_at	KIAA0700	AB014600	KIAA0700 protein	KIAA0700 protein
1331 41620_at	KIAA0716	AB018259	KIAA0716 gene product	KIAA0716 protein
1332 33835_at	KIAA0721	AB018264	KIAA0721 protein	KIAA0721 protein
1333 35177_at	KIAA0725	AB018268	KIAA0725 protein	KIAA0725 protein
1334 41218 at	KIAA0729	AB018272	KIAA0729 protein	KIAA0729 protein
1335 38694_at	KIAA0738	AB018281	KIAA0738 gene product	KIAA0738 protein
1336 39771_at	KIAA0740	AB018283	KIAA0740 gene product	KIAA0740 protein
1337 41585_at	KIAA0746	AB018289	KIAA0746 protein	KIAA0746 protein
1338 38424_at	KIAA0747	AB018290	KIAA0747 protein	KIAA0747 protein
1339 40848 g at	KIAA0750	AB018293	KIAA0750 gene product	KIAA0750 protein
1340 32224_at	KIAA0769	AB018312	KIAA0769 gene product	KIAA0769 protein
1341 36474_at	KIAA0776	AB018319	KIAA0776 protein	KIAA0776 protein
1342 33251_at	KIAA0779	AB018322	KIAA0779 protein	KIAA0779 protein
1343 35999_r_at	KIAA0781	AB018324	KiAA0781 protein	KIAA0781 protein
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KIAA0788	8 AB018331	KIAA0788 protein	KIAA0788 protein
KIAA0795		KIAA0795 protein	KIAA0795 protein
KIAA0802		KIAA0802 protein	KIAA0802 protein
KIAA0810		KIAA0810 protein	KIAA0810 protein
KIAA0826	6 AB020633	KIAA0826 protein	KIAA0826 protein
KIAA0830	-	KIAA0830 protein	KIAA0830 protein
KIAA0831	1 AB020638	KIAA0831 protein	KIAA0831 protein
KIAA0841	1 AB020648	KIAA0841 protein	KIAA0841 protein
KIAA0843	3 AB020650	KIAA0843 protein	KIAA0843 protein
KIAA0854	4 AB020661	KIAA0854 protein	KIAA0854 protein
KIAA0864	4 AB020671	KIAA0864 protein	KIAA0864 protein
KIAA0877		KIAA0877 protein	KIAA0877 protein
KIAA0878	_	KIAA0878 protein	KIAA0878 protein
KIAA0882		KIAA0882 protein	KIAA0882 protein
KIAA0893	13 AB020700	KIAA0893 protein	KIAA0893 protein
KIAA0903	13 AB020710	KIAA0903 protein	KIAA0903 protein
KIAA0909	9 AB020716	KIAA0909 protein	KIAA0909 protein
KIAA0911	1 AB020718	KIAA0911 protein	KIAA0911 protein
KIAA0916	16 AF075587	KIAA0916 protein	protein associated with Myc
KIAA0931	31 AB023148	KIAA0931 protein	KIAA0931 protein
KIAA0934	34 AB023151	KIAA0934 protein	KIAA0934 protein
KIAA0937	37 AB023154	KIAA0937 protein	KIAA0937 protein
KIAA0938	38 AB023155	KIAA0938 protein	KIAA0938 protein
Rab11-FIP2	-IP2 AB023158	KIAA0941 protein	KIAA0941 protein
KIAA0942	42 AB023159	KIAA0942 protein	KIAA0942 protein
KIAA0947	47 AB023164	KIAA0947 protein	KIAA0947 protein
KIAA0970	70 AB023187	KIAA0970 protein	KIAA0970 protein
KIAA0978		KIAA0978 protein	KIAA0978 protein
KIAA0981		KIAA0981 protein	KIAA0981 protein
KIAA0982		KIAA0982 protein	KIAA0982 protein
KIAA0993		KIAA0993 protein	KIAA0993 protein
KIAA0997	97 AI970189	KIAA0997 protein	
KIAA0999	99 AB023216	KIAA0999 protein	KIAA0999 protein
KIAA1001	01 AW052084	KIAA1001 protein	
KIAA1012	12 AB023229	KIAA1012 protein	KIAA1012 protein
KIAA1014	14 AB023231	KIAA1014 protein	KIAA1014 protein

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380 39615	9615_at	KIAA1026	AB028949	KIAA1026 protein	KIAA1026 protein
3813	381 34089 at	KIAA1030	AB028953	KIAA1030 protein	KIAA1030 protein
382 41651	4	KIAA1033	AB028956	KIAA1033 protein	KIAA1033 protein
3834	ا ۔۔	KIAA1034	AB028957	KIAA1034 protein	KIAA1034 protein
3843		KIAA1041	AB028964	KIAA1041 protein	KIAA1041 protein
3853	385 38778 at	KIAA1046	AB028969	KIAA1046 protein	KIAA1046 protein
3864	386 41268 q at	KIAA1049	AB028972	KIAA1049 protein	KIAA1049 protein
3874	387 40855 at	KIAA1053	AB028976	KIAA1053 protein	KIAA1053 protein
388	1388 39400 at	KIAA1055	AB028978	KIAA1055 protein	KIAA1055 protein
389	1389 33877 s at	KIAA1067	AB028990	KIAA1067 protein	KIAA1067 protein
3903	1390 34688 at	KIAA1078	AB029001	KIAA1078 protein	KIAA1078 protein
391	1391 33924 at	KIAA1091	AB029014	KIAA1091 protein	KIAA1091 protein
392	1392 32508 at	KIAA1096	AL096857	KIAA1096 protein	hypothetical protein
393	1393 41179 at	KIAA1100	AB029023	KIAA1100 protein	KIAA1100 protein
1394	1394 34839 at	KIAA1104	AB029027	KIAA1104 protein	KIAA1104 protein
1395	1395 33457 at	RAP140	AB029028	KIAA1105 protein	KIAA1105 protein
1396	1396 36814 at	KIAA1109	AB029032	KIAA1109 protein	KIAA1109 protein
1397	34274 at	KIAA1116	AB029039	KIAA1116 protein	KIAA1116 protein
1398	398 37617 at	KIAA1128	U90912	KIAA1128 protein	
1399	1399 33358 at	KIAA1157	W29087	KIAA1157 protein	
1400	1400 40308_at	KIAA1240	A1830496	KIAA1240 protein	
1401	1401 33811_at	KIAA1254	AI761567	KIAA1254 protein	
1402	1402 38674_at	KIAA1354	AA115140	KIAA1354 protein	
1403	1403 32730_at	KIAA1750	AL080059	KIAA1750 protein	
1404	1404 32171 at	KIAA1856	AL080102	KIAA1856 protein	hypothetical protein
1405	1405 39897_at	KIAA1966	N36997	KIAA1966 protein	
1406	1406 32846 s at	KTN1	D13629	kinectin 1 (kinesin receptor)	kinectin 1
1407	1407 39057_at	KNS2	L04733	kinesin 2 (60-70kD)	kinesin light chain
1408	1408 32079 at	KIF13B	AB014539	kinesin family member 13B	KIAA0639 protein
1409	1409 33345_at	KIF3C	AF035621	kinesin family member 3C	kinesin-related protein
1410	1410 34294 at	KIFC3	AL041493	kinesin family member C3	
1411	1411 41474 at	KIF2	Y08319	kinesin heavy chain member 2	kinesin-2
1412	1412 40779_at	KIFAP3	U59919	kinesin-associated protein 3	SMAP
1413	1413 34216_at	KLF7	AA478904	Kruppel-like factor 7 (ubiquitous)	-
	10 00700	Candau	V067E3	L-3-hydroxyacyl-Coenzyme A	3-hydroxyacyl-CoA dehydrogenase
414	141438/68 at	INAUTION	76/06/1	deliyalogerase, short chair	

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1415 41485	1485 at	I DHA	X02152	lactate dehydrodenase A	lactate dehydrogenase A
1416 288 s	88 s at	LBR	L25931	lamin B receptor	lamin B receptor
	1			laminin receptor 1 (67kD, ribosomal	
14172	1417 256_s_at	LAMR1	M14199	protein SA)	laminin receptor 1
14183	1418 37671_at	LAMA4	S78569	laminin, alpha 4	laminin alpha 4 chain
1419 581_at	81_at	LAMB1	M61916	laminin, beta 1	laminin B1
-				LanC lantibiotic synthetase component C-	
1420 39441	19441_at	LANCL1	Y11395	like 1 (bacterial)	lanthionine synthetase C-like protein 1
				latent transforming growth factor beta	latent transforming growth factor beta
1421 1	1421 1495_at	LTBP1	M34057	binding protein 1	binding protein 1 precursor
_				latent transforming growth factor beta	11
1422 3	1422 37906_at	LTBP2	Z37976	binding protein 2	LTBP-2 precursor
-				lectin, galactoside-binding, soluble, 1	
1423	1423 33412_at	LGALS1	AI535946	(galectin 1)	
				lectin, galactoside-binding, soluble, 3	
1424	1424 35367_at	LGALS3	AB006780	(galectin 3)	galectin-3
				lectin, galactoside-binding, soluble, 3	
1425	1425 37754_at	LGALS3BP	L13210	binding protein	Mac-2 binding protein
				lectin, galactoside-binding, soluble, 8	
1426	1426 1846 at	LGALS8	L78132	(galectin 8)	prostate carcinoma tumor antigen
1427	1427 34267_r_at	LEPR	U50748	leptin receptor	leptin receptor
1428	1428 33830_at	HSOBRGRP	AW026535	leptin receptor gene-related protein	
1429	1429 33829_at	HSOBRGRP	Y12670	leptin receptor gene-related protein	leptin receptor gene-related protein
7,00	10000	1 EDBOTT 1	AEOGREOF	lentin recentor overlanning transcript-like 1 brain mv047 protein	brain my047 protein
3	3			leucine rich repeat (in FLII) interacting	
1431	41320_s_at	LRRFIP1	0969A	protein 1	transcription repressor
,	00000	500	A DO 10 F 9 7	lauring zinner down-regulated in cancer 1 DOC1 protein	I DOG1 protein
1132	1432 33307 at	1 BPPRC	M92439	leucine-rich PPR-motif containing	leucine-rich PPR-motif containing protein
1434	37470	LAIR1	AF013249	leukocyte-associated Iq-like receptor 1	leukocyte-associated Ig-like receptor-1
1435	38081	LTA4H	J03459	leukotriene A4 hydrolase	leukotriene A4 hydrolase
1436	1436 36062 at	LPXN	AF062075	leupaxin	leupaxin
				libtest16.A02.r bvnorm Homo sapiens	
1437	1437 35278_at	RPS29	AI541542	cDNA 5', mRNA sequence.	
1438	1438 39687_at	E46L	AI524873	like mouse brain protein E46	

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1439	439 39686 g at		AL050282	like mouse brain protein E46	hypothetical protein
440	1440 39685 at		AL050282	like mouse brain protein E46	hypothetical protein
				likely homolog of rat kinase D-interacting	
1441	1441 39163 at	KIDINS220	W27233	substance of 220 kDa	
				likely ortholog of mouse suppressors of	
1442	1442 32669_at	SOCS5	AB014571	cytokine signalling 5	KIAA0671 protein
1443	1443 40555_at	TC10	AL043108	likely ortholog of mouse TC10-alpha	
				likely ortholog of mouse TPR-containing,	
1444	1444 40844_at	TSBP	D63875	SH2-binding phosphoprotein	KIAA0155 gene product
				likely ortholog of mouse variant	
1445	1445 41248_at	CSTF2T	AB014589	polyadenylation protein CSTF-64	KIAA0689 protein
			,	likely ortholog of rat golgi stacking protein	
1446	1446 35805_at	GRASP55	AA447263	homolog GRASP55	
				LIM and senescent cell antigen-like	
1447	1447 39232 at	LIMS1	U09284	domains 1	PINCH protein
1448	1448 36181 at	LASP1	X82456	LIM and SH3 protein 1	LIM and SH3 domain protein
1449		LIMK2	D45906	LIM domain kinase 2	LIMK-2
1450	1450 1452 at	LM04	U24576	LIM domain only 4	breast turnor autoantigen
1451	1451 31936 s. at	LKAP	AB007890	limkain b1	KIAA0430 protein
				lipase A, lysosomal acid, cholesterol	
1452	1452 38745_at	LIPA	X76488	esterase (Wolman disease)	lysosomal acid lipase
1453	1453 38098 at	LPIN1	D80010	lipin 1	
1454	1454 37542_at	LHFPL2	D86961	lipoma HMGIC fusion partner-like 2	
1455	1455 41209_at	LPL	M15856	lipoprotein lipase	lipoprotein lipase precursor
1456	1456 1798 at	LIV-1	U41060	LIV-1 protein, estrogen regulated	estrogen regulated LIV-1 protein
				liver form; Homo sapiens glycogen	
				phosphorylase (PYGL) gene, exon 20 and	
1457	1457 37215 at	PYGL	AF046798	complete cds.	glycogen phosphorylase

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				long tailed isoform; individual exons 6-14	
-	_			are alternative exons any of which can be	
	_			spliced out of the mRNA.; putative; long	
	_			tailed isoform; putative; long tailed	
-				isoform; hemopoietic variant; putative;	
				long tailed isoform; epithelial form;	
				putative; Human cell surface glycoprotein	
				CD44 (CD44) gene, 3' end of long tailed	
1458 40493 at	193_at	CD44	L05424		cell surface glycoprotein CD44
				low density lipoprotein-related protein-	-
				associated protein 1 (alpha-2-	
				macroglobulin receptor-associated protein alpha-2-macroglobulin receptor-associated	alpha-2-macroglobulin receptor-associated
1459 36194_al	194_at	LRPAP1	M63959	1)	protein
				low molecular mass ubiquinone-binding	
1460 34400_at	100_at	OP-C	AI540957	protein (9.5kD)	
1461 37C	37025_at	PIG7	AL120815	LPS-induced TNF-alpha factor	
1462 39017		LSM1	AJ238094	Lsm1 protein	Lsm1 protein
1463 38038_al	338_at	LUM	U21128	lumican	lumican
1464 38115 at	115_at	FUS1	AF055479	lung cancer candidate	lung cancer candidate FUS1
1465 39428 at	428 at	LNK	AF055581	otein	adaptor protein Lnk
1466 39396 at	396_at	LYPLA1	AF081281	lysophospholipase I	lysophospholipase
1467 33788_at	788_at	LYSAL1	AB002390	lysosomal apyrase-like 1	lysosomal apyrase-like 1
1468 39758_1	758_f_at	LAMP1	J04182	lysosomal-associated membrane protein 1 lysosomal membrane glycoprotein-1	lysosomai memorane glycoprotein- i
1469 38403_at	403_at	LAMP2	X77196	lysosomal-associated membrane protein 2	lysosomal-associated membrane protein 2 lysosome-associated membrane protein-2
1470 38402 at	402 at	LAMP2	U36336	lysosomal-associated membrane protein 2	lysosomal-associated membrane protein 2 lysosome-associated membrane protein-2b
				lysosomal-associated protein	lysosomal-associated protein
1471 39019 at	019_at	LAPTM4A	D14696	transmembrane 4 alpha	transmembrane 4 alpha
1472 33127	127_at	LOXL2	U89942	lysyl oxidase-like 2	lysyl oxidase-related protein
1473 34336	336_at	KARS	D32053	lysyl-tRNA synthetase	Lysyl tRNA Synthetase
1474 32832_at	832_at	MAEA	AF084928	macrophage erythroblast attacher	erythroblast macrophage protein EMP
1475 36174	174 at	MACMABOKS	X70326	macrophage myristoylated alanine-rich C kinase substrate	macrophage myristoylated alanine-rich C kinase substrate
2010	14 81	CALCULOUM	101000		

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				MAD, mothers against decapentaplegic	
1476	1476 1453_at	MADH2	U68018	homolog 2 (Drosophila)	mad protein homolog
				MAD, mothers against decapentaplegic	
1477	1477 38944_at	MADH3	U68019	homolog 3 (Drosophila)	mad protein homolog
				MAD, mothers against decapentaplegic	
1478	1478 1433_g_at	MADH3	U68019	homolog 3 (Drosophila)	mad protein homolog
				MAD, mothers against decapentaplegic	
1479	1479 36953 at	MADH4	U44378	homolog 4 (Drosophila)	Dpc4
	1			MAD, mothers against decapentaplegic	
1480	1480 1013 at	MADHS	U59913	homolog 5 (Drosophila)	Smad5
				MAD, mothers against decapentaplegic	
1481	1481 1955_s_at	MADH6	AF035528	homolog 6 (Drosophila)	Smad6
				MAD, mothers against decapentaplegic	
1482	1482 1857_at	MADH7	AF010193	homolog 7 (Drosophila)	MAD-related gene SMAD7
				major histocompatibility complex, class I,	
1483	1483 41237_at	HLA-A	D32129	А	HLA-A26
				major histocompatibility complex, class II,	
1484	1484 41609_at	HLA-DMB	U15085	DM beta	HLA-DMB
				major histocompatibility complex, class II,	
1485	1485 38096_f_at	HLA-DPB1	M83664	DP beta 1	HLA-DPB1
				major histocompatibility complex, class II,	
1486	1486 38095_i_at	HLA-DPB1	M83664	DP beta 1	HLA-DPB1
				major histocompatibility complex, class II,	
1487	1487 37039_at	HLA-DRA	J00194	DR alpha	DR alpha precursor
				major histocompatibility complex, class II,	
1488	1488 33261_at	HLA-DRB1	M16941	DR beta 1	
				major histocompatibility complex, class I-	
1489	1489 34425_at	HLALS	AF031469	like sequence	MHC class I-related protein 1 isoform D
				major receptor for HIV-1; member of	
				immunoglobulin supergene family; T cell	
1490	1490 34003_at	CD4	U47924	surface glycoprotein T4	protein 'A', isoform 1
1491	1491 36608 at	MDH1	D55654	malate dehydrogenase 1, NAD (soluble)	cytosolic malate dehydrogenase
				malic enzyme 1, NADP(+)-dependent,	
1492	1492 837_s_at	ME1	U43944	cytosolic	cytosolic NADP(+)-dependent malic enzyme

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				malic enzyme 2, NAD(+)-dependent,	mitochondrial NAD(P)+ -dependent malic
1493	1493 36599 at	ME2	M55905	mitochondrial	епгуте
1494	1494 36673 at	MPI	X76057	mannose phosphate isomerase	phosphomannose isomerase
	l			MAP kinase-interacting serine/threonine	
1495	1495 35299_at	MKNK1	AB000409	kinase 1	MNK1
				MAP/microtubule affinity-regulating kinase	
1496	1496 40826_at	MARK3	M80359		protein p78
				MAPK-activated protein kinase; PRK;	
				Homo sapiens mitogen activated protein	
				kinase activated protein kinase gene,	mitogen activated protein kinase activated
1497	1497 41506_at	MAPKAPK5; PRA AF032437	AF032437	complete cds.	protein kinase
				match proteins: Sw. P04040 Sw. P04762	
_				SwrP04270 Tr:062839 SwrP00432	
_		-		O D 11: C 12: C 13:	
				SW:P1/336 11:P90682 11:02/46/	
				Sw:061235 Tr:018193 Tr:077229	
				Tr:Q49133 Sw:P26901 Sw:P55306	
	,			Sw:P30263 Tr:P95631, Sw:P44390	
				Tr:Q27710 Sw:Q96528 Sw:O13289	-
				Sw:P07820 Sw:P30265 Sw:P77872	
				Tr:Q59602 Tr:P77924 Sw:Q59170	
				Sw:P15202 Tr:Q59296 Tr:O33613	
				Sw:Q92405 Sw:Q59635 Sw:P81138	
1498	1498 37009 at	CAT	AL035079	match ESTs: W94164 N28621	dJ53C18.1 (Catalase)
				match to ESTs AA316181	
				(NID:g3165221), AA032221	
				(NID:g1502183), and Al167942	
				(NID:g3701112); H_RG041D11.1; Homo	
				sapiens BAC clone CTB-41D11 from	six transmembrane epithelial antigen of the
1495	1499 40297 at	WUGSC:H_RG04 AC005053	4 AC005053	7q21, complete sequence.	prostate

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				match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283	
			_=	D38535 D38595 match: proteins Q06033	
_			-	P97280 O54882 O35802 Q61704 Q14624	
_		-		P79263 Q63416 Q42141 P19823 Q02668	P79263 Q63416 Q42141 P19823 Q02668 hepatocellular carcinoma associated protein;
500	500 34860 g at	BCG1	298046	Q61703 P97279 Q29052	breast cancer associated gene 1
				match: cDNAs: Em:AL050345 match:	
				ESTs: Em:AA304885 Em:AA447346	
				Em:AA314213 Em:AA209368	
				Em:AA209372 Em:T84723 Em:H23039	
				Em:AA542125 Em:W41686	
501	501 35336 at	HS508115A	AL021707	Em:AA384854 Em:AA492678	chromosome 22 open reading frame 2
502	502 32658 at	dJ1033B10.1	AL031228	match: protein 015214	BING4
503	503 31545 at	dJ1033B10.1	AL031228	match: protein 015214	BING4
1504	504 36986 at	dJ886K2.1	AL031295	match: protein SPTREMBL; Q14241	UDP-galactose-4-epimerase
				match: proteins CE02000 O59733	
				CE01999; supported by FGENES and	
1505	1505 38072 at	dJ465N24.1	AL031432	GENSCAN	hypothetical protein dJ465N24.2.1
				match: proteins O15037 CE16881	
				supported by GENSCAN possibly this	-
				partial gene and dJ281H8.1 are part of	dJ281H8.2 (PUTATIVE novel protein similar
1506	1506 32478 f at	dJ281H8.1	AL031133	one gene	to KIAA0323 and worm C30F12.1)

	**************************************	9. Z. X.	
	dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-77 (isoform 2))	dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-77 (isoform 2))	cytochrome c oxidase subunit VIa polypeptide 1
U	match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51/12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.	match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.	match: proteins P13182 P12074 P10818 P43024 Q02221 P07471 P10817 P43023 cytochrome c oxidase subunit Vla P13182 O13085 O13082
O	AL031781	AL031781	AL021546
В	dJ51J12.1	dJ51J12.1	COX6A
A	1507 39759_at	508 39760_at	1509 32573_at
	1507	1508	1509



	A	В	O	Q	B
1510	1510 33443 at	HSF2	Z99129	match: proteins P38533 Q03933 P38530 P41154 Q00613 P38529 P38531 Q63717 P38532 Q99472	heat shock transcription factor 2
				match: proteins Q14189 P15924 Q03001	
				P97395 P97396 P97394; Human UNA	
				sequence from clone 512B11 on	
				chromosome 6p24-25. Contains the	,
				Desmoplakin I (DPI) gene, ESTs, STSs	
1511	1511 36133 at	dJ512B11.1	AL031058	and GSSs, complete sequence.	dJ512B11.1 (Desmoplakin I (DPI))
				match: proteins Q14209 Q16254 O35261	
				O00716 Q61501 Q90977 Q01094	
1512	1512 37043 at	E2F-2	AL021154	027368	E2F transcription factor 2
				match: proteins Q15774; match: protein	
				Q01968 P32019; Homo sapiens DNA	
		-		sequence from PAC 454M7 on	
	-			chromosome Xq25-26.3. Contains the	
				OCRL1 gene for Lowe Oculocerebrorenal dJ454M7.1.2 (Lowe Oculocerebrorenal	dJ454M7.1.2 (Lowe Oculocerebrorenal
				Syndrome protein OCRL-1. Contains	Syndrome protein OCRL-1) (isoform 2);
				ESTs, STSs and GSSs, complete	dJ454M7.1.1 (Lowe Oculocerebrorenal
1513	1513 41227 at	OCRL1	AL022162	sednence.	Syndrome protein OCRL-1) (isoform 1)
					dJ341E18.1 (Serine/Threonine Protein
				match: proteins Q62726 P20793 Q04859	Kinase (presumptive isolog of Rat protein
151	1514 38990 at	dJ341E18.1	AL031178	Q39423 P43294 O49669	Q62726))

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	IFNOMOL	AL021938	match: proteins Q92833 Q62315; protein Q92833 has a different stop codon 19 aa further downstream because it jumps frame twice, circumventing the stopcodon in this entry. This could be due to a sequence error in the cDNA sequence; Homo sapiens DNA sequence from PAC 232K4 on chromosome 6p22.3. Contains the JUMONJI gene for a hypothetical 141.7 kD protein. Contains ESTs, STSs, a CA repeat polymorphism and genomic marker D6S260', complete sequence.	dJ232K4.1 (hypothetical 141.7 kD protein JUMONJI)
1516 37350_at	dJ889N15.1	AL031177	665 Q91664 1667 O60939 0426 P06907 573 P10522 uence 180040 I FGENES	dJ889N15.1 (novel protein similar to X. laevis Cortical Thymocyte Marker CTX)
1517 39738_at	APOL2	282215	match: proteins: 5w:014791	apolipoprotein L
151831824 at	Σ Π	AL049699	match: proteins: Sw:P06801 Sw:P28227 Sw:Q29558 Sw:P13697 Sw:P40927 Sw:Q16798 Tr:Q16797 Sw:P48163	dJ747H23.1 (malic enzyme 1, soluble (NADP-dependent malic enzyme, małate oxidoreductase, EC 1.1.1.40))
32766 at	OTK27 SSFA1	Z83840		non-histone chromosome protein 2 (S. cerevisiae)-like 1
a at	XBP1	293930	match: proteins: Sw.P17861 Tr.O35426; Human DNA sequence from clone CTA- 292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete sequence.	bK292E10.1 (X-box binding protein 1 (TREB5))
1520 39756_g_at	Abri	753220	sednelice.	////

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match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA- 292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, GSSs	match: proteins: Sw:P17861 Tr:C Human DNA sequence from clon 292E10 on chromosome 22q11-1 Contains the XBP1 gene for X-bc protein 1 (TRE85), ESTs, STSs,	match: proteins: Sw:P17861 Tr:C Human DNA sequence from clon 292E10 on chromosome 22q11-1 Contains the XBP1 gene for X-bo protein 1 (TREB5), ESTs, STSs,	match: proteins: Sw:P17861 Tr:C Human DNA sequence from clon 292E10 on chromosome 22q11-1 Contains the XBP1 gene for X-bo protein 1 (TREB5), ESTs, STSs,	βι	Y Y biodical series
521 39755_at XBP1 Z93930 sequence.	Z93930		sequence.		(TREB5))
match: proteins: Sw:P26038 Tr:O35763 Sw:P26041 Sw:P26042 Sw:P26044	match: proteins: Sw:P26038 Ti Sw:P26041 Sw:P26042 Sw:P2	match: proteins: Sw:P26038 Ti Sw:P26041 Sw:P26042 Sw:P2	match: proteins: Sw:P26038 Ti Sw:P26041 Sw:P26042 Sw:P2	r:035763 6044	
Sw.P35241 Sw.P26043 Sw.P15311 Sw.P31976 Sw.P26040 Tr.O26520	Sw:P35241 Sw:P26043 Sw:P1 Sw:P31976 Sw:P26040 Tr:O26	SW:P35241 SW:P26043 SW:P1 SW:P31976 SW:P26040 Tr:Q26	Sw:P35241 Sw:P26043 Sw:P1 Sw:P31976 Sw:P26040 Tr:O26	5311	
Tr:Q24788 Tr:Q24796 Tr:Q94815; Human	Tr:Q24788 Tr:Q24796 Tr:Q94	Tr:Q24788 Tr:Q24796 Tr:Q94	Tr:Q24788 Tr:Q24796 Tr:Q94	815; Human	
DNA sequence from clone 376D21 on	DNA sequence from clone 37	DNA sequence from clone 370	DNA sequence from clone 370	5D21 on	
chromosome Xq11.1-12 Contains the	chromosome Xq11.1-12 Con	chromosome Xq11.1-12 Con	chromosome Xq11.1-12 Con	tains the	,
MSN gene for Woesin (Wembrane	MSN gene for Moesin (Mem	MSN gene for Moesin (Mem	MSN gene for Moesin (Mem	orane-	
organizing Extension Spike protein), ESTs. STSs. GSSs. genomic marker	organizing Extension Spike	organizing Extension Spike ESTs, STSs, GSSs, denon	organizing Extension Spike ESTs, STSs, GSSs, genon	protein), nic marker	
DXS8029 and a putative CpG island,	DXS8029 and a putative C	DXS8029 and a putative C	DXS8029 and a putative C	pG island,	dJ376D21.1 (Moesin (Membrane-organizing
1522 40771_at MSN Z98946 complete sequence.	298946		complete sequence.		Extension Spike protein))
match: proteins: Sw:P39023 Sw:O16797	match: proteins: Sw.P390	match: proteins: Sw:P390	match: proteins: Sw:P390	23 Sw:O16797	
Sw:P21531 Sw:P39872 Sw:P27659	Sw:P21531 Sw:P39872 S	Sw:P21531 Sw:P39872 S	Sw:P21531 Sw:P39872 S	w:P27659	
Sw. Q92901 Sw: P49149 Sw: P22738	Sw:Q92901 Sw:P49149 S	Sw:Q92901 Sw:P49149 S	Sw:Q92901 Sw:P49149 S	w:P22738	
31722_at RPL3 AL022326 Sw:P35684 Sw:P17094 Wp:CE05598	AL022326		Sw:P35684 Sw:P17094 V	Vp:CE05598	ribosomal protein L3
	match: proteins: Sw;P505	match: proteins: Sw;P505	match: proteins: Sw;P505	50 Sw:O09181	
Tr: O62622 Sw: P40984 Sw: P50623	Tr: 062622 Sw: P40984 Sw	Tr:062622 Sw:P40984 Sw	Tr: O62622 Sw: P40984 Sw	.P50623	
Tr.Q42551 Tr.O24240 Tr.Q42973	Tr:Q42551 Tr:O24240 Tr:C	Tr:Q42551 Tr:O24240 Tr:C	Tr:Q42551 Tr:O24240 Tr:C	242973	
SW. P524/8 SW. QUZ159 SW.F15/32	SW:P52478 SW:QUZ159 SW	SW:P5Z478 SW:Q0Z159 SV:P5Z478 SW:Q0Z159 SW	SW:P524/8 SW:Q02159 SV	V:P 15/32	
Sw.P49427 Tr.O17424 SwrP5867	Sw.P4047 Tr.O17404 Sw	Sw. P49427 Tr.O17424 Sw	Sw: 000102 11:010042	27.843 rP25867	C358B7.1 (ubiquitin-conjugating enzyme E2I
1524 33136 at UBE21 AL031714 Sw.P52490	AL031714		Sw:P52490		(homologous to yeast UBC9))
0000000.m3 0770100.m3 10010000 140000	Cor Consideration of the Corporation of the Corpora	C. C. C. C. C. C. C. C. C. C. C. C. C. C	ZOLOWING CONTOURS	70 Cur. 0e0400	
525 36607 at [hK250D10.3 799716 Sw:P36956 Sw:Q60416 Tr:O15352	799716		Sw: P36956 Sw:Q60416 T	72 SW. 3352 r:015352	septin 3
			match: proteins: Sw:Q280	38 Sw:Q16674	small nuclear ribonucleoprotein polypeptide
1526 38399_at SNRPB2 AL034428 Tr:P97591 Sw:Q61865	AL034428	-	Tr:P97591 Sw:Q61865		В"

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T				match: proteins: Tr:O54791 Sw:Q90595	
				Sw:Q61827 Sw:Q90596 Tr:O54790	
				Tr:O15525 Sw:Q90889 Tr:O73679	•
527	1527 36711 at	HS506A DKFZP5	5 AL021977	Sw:Q00056 Sw:Q10060 Sw:Q15427	chromosome 22 open reading frame 5
528	1528 39561 at	1	AL008583	_	chromobox homolog 6
					dJ738P15.2 (CD39-like 2 (a nucleoside
1529	1529 39876 at	dJ738P15.1	AL035252	Tr:Q9QYC9	phosphatase))
		,		match: proteins: Tr:094136 Sw:099798	
				Sw:P49609 Sw:P20004 Sw:P16276	dJ347H13.1 (aconitase 2, mitochondrial
				Tr:O75809 Tr:O74699 Wp:CE00516	(Aconitate Hydratase, EC 4.2.1.3, Citrate
1530	1530 37189 at	ACO2	AL023553	Sw:P19414 Tr:O75944 Sw:O13966	Hydrolyase))
				match: proteins: Tr:P70386 Sw:Q02527	
1531	1531 41235 at	TAXREB67 TXRE	IE AL022312	Sw:Q10470 Sw:Q09327	activating transcription factor 4
		1			dJ117516.1 (Ras inhibitor JC265 (Ras
				match: proteins: Tr:Q00425 Sw:Q13671	association (RalGDS/AF-6) domain
1532	1532 36550 at	dJ1175l6.1	AL049538	Tr:O15010 Tr:P97680	containing protein))
				match: proteins: Tr:Q14621 Tr:Q64012	
				Sw:P07910 Sw:P19600 Tr:O60812	RNA-binding protein (autoantigenic) long
1533	1533 39368 at	P542	AL031668	Sw:Q14011 Sw:P26686	isoform
				match: proteins: Tr:Q9Y3M0 Tr:Q9WU14	
1534	1534 33821 at	dJ483K16.1	AL034374	Sw:P39540 Tr:Q9Y396	dJ483K16.1.1 (novel protein (isoform 1))
1535	39029 at	G10	U11861	maternal G10 transcript	maternal G10 transcript
1536	1536 35145 at	MNT	X96401	MAX binding protein	ROX protein
					MAX interacting protein 1, isoform a; MAX
1537	1537 39072 at	MXI1	L07648	MAX interacting protein 1	interacting protein 1, isoform b
					MAX interacting protein 1, isoform a; MAX
1538	1538 654_at	MXI1	L07648	MAX interacting protein 1	interacting protein 1, isoform b
				MCM2 minichromosome maintenance	
1539	35312_at	MCM2	D21063	deficient 2, mitotin (S. cerevisiae)	
				MCM3 minichromosome maintenance	
		,		deficient 3 (S. cerevisiae) associated	
1540	1540 40469_at	MCM3AP	AB011144	protein	KIAA0572 protein

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1541 40117_at 1542 41388_at				Atomorphism opening mointonon	
1541 401				MCIVIO minicuromosome maintenance	
1541 401 1542 413				deficient 6 (MIS5 homolog, S. pombe) (S.	
1542 413	17_at	MCM6	D84557	cerevisiae)	HsMcm6
1542 413				viral integration	
	88_at	MEIS2	AF017418		homeobox protein MEIS2
				Meis1, myeloid ecotropic viral integration	
1543 37486_f_at	86_f_at	MEIS3	U68385	site 1 homolog 3 (mouse)	Meis1-related protein 2
				mel transforming oncogene (derived from	
1544 35340_at	40_at	MEL	AI819948	cell line NK14)- RAB8 homolog	
_				melanoma antigen, family A, 2, copy a;	,
-				similar to GenBank Accession Number	
1545 36500_at	00_at	MAGEA2A	AF027974	L18920	melanoma antigen family A2a
1546 41139_at	39_at	MAGED1	W26633	melanoma antigen, family D, 1	
1547 39327_at	127_at	D2S448	D86983	Melanoma associated gene	
_				membrane cofactor protein (CD46,	membrane cofactor protein (CD46,
			0	live	trophoblast-lymphocyte cross-reactive
1548 38441_s_at	141_s_at	MCP	X59408	antigen)	antigen)
 				membrane component, chromosome 11,	
1549 39471_at	171_at	M11S1	Z48042	surface marker 1	GPI-anchored protein p137
				membrane component, chromosome 17,	
				suface marker 2 (ovarian carcinoma	membrane component, chromosome 17,
1550 33444_at	144_at	M17S2	D30756	antigen CA125)	surface marker 2
				membrane metallo-endopeptidase	
				(neutral endopeptidase, enkephalinase,	
1551 1389_at	39_at	MME	J03779	CALLA, CD10)	membrane metallo-endopeptidase
				mesenchyme homeo box 2 (growth arrest-	
1552 40399_r_at	399_r_at	MEOX2	AI743406	specific homeo box)	
				Met at bp 326 also used as initiation	
				codon in vitro; Met at bp 248 also used as	
				initiation codon in vitro; Homo sapiens	
				porin (por) mRNA, complete cds and	
1553 370	1553 37697_s_at	por	L08666	truncated cds.	porin
1554 40244	244_s_at	MPPE1	AI743654	metallo phosphoesterase	

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Ш	metallothionein		metal-regulatory transcription factor	metastasis associated protein	metaxin 2	nolomod esetedtavs ANOt broiden toon	year meniony in the symmetres meniors		methyl-CpG binding protein	methyl-CpG binding protein MBD2	methyl-CpG binding protein MBD4	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate	cyclohydrolase, precursor	methylenetetrahydrofolate dehydrogenase		methenyltetrahydrofolate cyclohydrolase,	formyltetrahydrofolate synthetase	methylmalonyl-CoA mutase				MHC class I molecule	associated microfibrillar protein	A-type microphthalmia associated	transcription factor	microsomal glutathione S-transferase 2	KIAA0465 protein		
d	ike gene; H.sapiens lothionein and ent.		anscription factor 1		metaxin 2	VI VI	memorine-third symmetase	methionyl aminopeptidase 1	methyl-CpG binding domain protein 1	methyl-CpG binding domain protein 2	methyl-CpG binding domain protein 4	methylene tetrahydrofolate dehydrogenase (NAD+ dependent),	methenyltetrahydrofolate cyclohydrolase	methylenetetrahydrofolate dehydrogenase	(NADP+ dependent),	methenyltetrahydrofolate cyclohydrolase,	formyltetrahydrofolate synthetase	methylmalonyl Coenzyme A mutase	MHC class I chain-related gene B; cDNA	sequence deposited under GenBank	Accession Number X91625; Human Minu	class i molecule (ivilob) gene, complete	cas.	microphthalmia-associated transcription	factor	microsomal glutathione S-transferase 2	microtubule-actin crosslinking factor 1	microtishing accordated protein 1A	ווווכוסומסמים מפפסים ליים היים ויים
C	×55503	AI547258	X78710	U35113	AF053551		X94754	D42084	Y10746	AF072242	AF072250		X16396				J04031	M65131				077	104200	207100	AB006909	U77604	AB007934	Mocest	120071
۵		MT2A	MTF1	MTA1	MTX2		MAHS	METAP1	MBD1	MBD2	MBD4		MTHFD2				MTHFD1	MUT					MICE	INILAL	MITE	MGST2	MACF1	MANDAM	
<	7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1556 39081 at	1557 38945 at	1643 g at	1559 35642_at		1560 39342_at	1561 37619_at	1562 41828_at	33905_at	1564 34386_at		1565 40074_at				3 674 g at	1567 40105 at				1	1568 35937_at	1009 30332 at	1570 38228 r. at	1571 820 at	1572 38704 at	45 70 05047 04	313381/ BE
	+ 4 4 4	1556	1557	1558	1559		1560	1561	1562	1563	1564		1565				1566	156			_	ļ	156	001	157	157	157	-	2

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Γ	∢	Ä	ပ	O	ш
				microtubule-associated protein, RP/EB	
1575	1575 33456_at	MAPRE1	U24166		EB1
				microtubule-associated proteins 1A/1B	
1576	1576 39370_at	MAP1A/1BLC3	W28807		
1577	1577 34296_at	MID1	AF041210		midline 1 fetal kidney isoform 3
1578	1578 34403_at	MFGE8	U58516		BA46
Γ				mitochondrial ATP synthase regulatory	
1579	1579 40027_at	ATPW	W52999		
1580	1580 37174_at	MRPL19	D14660	mitochondrial ribosomal protein L19	mitochondrial ribosomal protein L19
1581	1581 37726 at	MRPL3	X06323	mitochondrial ribosomal protein L3	mitochondrial ribosomal protein L3
1582	39717 g at	MRPL33	AI597616	mitochondrial ribosomal protein L33	
1583	1583 32221_at	MRPS18B	AL050361	mitochondrial ribosomal protein S18B	mitochondrial ribosomal protein S18B
1584	1584 38899_s_at	MFN1	U95822	mitofusin 1	putative transmembrane GTPase
1585	1585 34369 at	MFN2	D86987	mitofusin 2	KIAA0214 protein
1586	1586 36577 at	MIG2	224725	mitogen inducible 2	mitogen inducible gene mig-2
1587	37733 at	MAPK14	L35263	mitogen-activated protein kinase 14	CSaids binding protein
1588	1588 36926 at	MAPK6	X80692	mitogen-activated protein kinase 6	p97mapk
1589	1589 38431 at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1590	1590 1238 at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1591	1591 1130_at	MAP2K1	L11284	mitogen-activated protein kinase kinase 1	mitogen-activated protein kinase kinase 1
				mitogen-activated protein kinase kinase	
1592	1592 1327_s_at	MAP3K5	U67156	kinase 5	mitogen-activated kinase kinase kinase 5
				mitogen-activated protein kinase kinase	
1593	1593 36905_at	MAP3K7	AB009356	kinase 7	TGF-beta activated kinase 1a
				mitogen-activated protein kinase kinase	
1594	1594 38980_at	MAP3K7IP2	AB018276	kinase 7 interacting protein 2	KIAA0733 protein
				mitogen-activated protein kinase kinase	
1595	1595 35694_at	MAP4K4	AB014587	kinase kinase 4	KIAA0687 protein
				mitogen-activated protein kinase-activated	
1596	1596 36179_at	MAPKAPK2	U12779	protein kinase 2	MAP kinase activated protein kinase 2
				mitogen-activated protein kinase-activated	
1597	1637_at	MAPKAPK3	U09578	protein kinase 3	MAPKAP kinase
1598	1598 41220_at	MSF	AB023208	MLL septin-like fusion	KIAA0991 protein
1599	1599 38437_at	MLN51	X80199	MLN51 protein	MLN51 protein

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A B C Cerevisiae MMS19-Like (MET18 homolog, S. MMS19 (MET18 S. Liter) MAS19-Like (MET18 homolog, S. MMS19-Like (MET18 Liter) MAS1-T-at MAS-1	MMS19l MAP-1 at MAOA	O	0	y
MMS19L AF007151 cerevisiae) MMS19L AF007151 cerevisiae) MAD-1 AI670788 monoamine oxidase A MAD-1 AI670788 monoamine oxidase A MAD-2	at			
MMS19L AF007151 cerevisiae) MAP-1 Al670788 modulator of apoptosis 1 MAOA AA420624 monoamine oxidase A r MAOA MA620624 monoamine oxidase A r MAOB MA6177 monoamine oxidase B r MAOB M69177 monoamine oxidase B r MMD X85750 associated B r MMD X85750 associated B r MPGX D14812 MORF-related gene X MPDR-related Gene X MRGX D14812 MORF-related gene X MPDR-related Gene X MRSX D14812 MORF-related gene X MPDR-related Gene X MBNL AR007888 muscleblind-like (Drosophila) muscleblind-like (Drosophila) MSC AF087036 muscleblind-like (Drosophila) muscleblind-like (Drosophila) MSC AF087036 muscleblind-like (Drosophila) muscleblind-like (Drosophila) MSH6 U28946 muscleblind-like (Drosophila) muscleblind-like (Drosophila) MCL1 L08246 <t< td=""><td>ä</td><td>_</td><td> MMS19-like (MET18 homolog, S.</td><td></td></t<>	ä	_	MMS19-like (MET18 homolog, S.	
MAP-1 AIGT0788 modulator of apoptosis 1 MAOA AA420624 monoamine oxidase A MAOA M68840 monoamine oxidase A MAOA AA420624 monoamine oxidase A MAOB MAG9177 monoamine oxidase B MAOB M69177 monoamine oxidase B MADB X85750 associated MADB MORF-related gene X MBNL MORF-delated gene X MBNL MAD0788 MSC AF087036 MUSC AF087036 MSC AF087036 MSHE U28846 MCL1 L08246 MCL1 L08246 MCL1 L08246 MCL1 L08246 MYO1B MYO1B MYO1B MA1	at	AF007151	cerevisiae)	MMS19 (ME118 S. cerevisiae)-iike
MAOA AA420624 monoamine oxidase A Indexed MAOA M68840 monoamine oxidase A Indexed MAOB M68840 monoamine oxidase B Indexed MAOB M68177 monocyte to macrophage differentiation-in monocyte to macrophage differentiation-in monocyte to macrophage differentiation-in monocyte to macrophage differentiation-in monocyte to macrophage differentiation-in monocyte to macrophage differentiation-in monocyte to macrophage differentiation-in monocyte to macrophage differentiation-in monocyte to macrophage differentiation-in monocyte to macrophage differentiation-in monocyte in	at	AI670788	modulator of apoptosis 1	
MACOA M68840 monoamine oxidase A In Indoamine oxidase A MAOB AA420624 monoamine oxidase B In MAOB MAOB M69177 monoamine oxidase B In MODB MAD X85750 associated In MODB MAD D14812 MORF-related gene X In MODB MRGX D14812 MORF-related gene X In MODB MRDX D14812 MORF-related gene X In MODB MRDX AF087036 musculin cativated B-cell factor.1) MRSC AF087036 musculin cativated B-cell factor.1) MSC AF087036 musculin cativated B-cell factor.1) MSHE U28946 musculin cativated B-cell factor.1) MSHE U28946 musculin cativated B-cell factor.1) MCL1 L08246 myelin protein zero-like 1 MCL1 L08246 myelin cell leukemia sequence 1 (BCL2-leated) MCL1 L08246 myelind cell leukemia sequence 1 (BCL2-leated) MYO1B AJ001381 myeloid cell leukemia sequence 1 (BCL2-leated) MYO1B AJ001381 <td></td> <td>AA420624</td> <td>monoamine oxidase A</td> <td></td>		AA420624	monoamine oxidase A	
MAOA AA420624 monoamine oxidase A MAOB M69177 monoamine oxidase B MADB X85750 associated B MMD X85750 associated Gene X MRGX D14812 MORF-related gene X MPOR-related gene X M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) MBNL AB007888 muscleblind-like (Drosophila) MSC AF087036 muscleblind-like (Drosophila) MSC AF087036 mult homolog 3 (E. coli) MSC AF087030 mult3 homolog 2, colon cancer, nonpolyposis type 1 (E. coli) MSHE U28946 mult3 homolog 6 (E. coli) MSHE U28946 myelin protein zero-like 1 MCL1 L08246 myelin protein zero-like 1 MCL1 L08246 myeloid cell leukemia sequence 1 (BCL2-related) MYO1B AJ001381 myeloid c		M68840	monoamine oxidase A	monoamine oxidase A
MAOB M69177 monoamine oxidase B MMD X85750 associated MRGX D14812 MORF-related gene X MRGX D14812 MORF-related gene X MPHOSPH10 X98494 mucleolar irlonucleoprotein 10 (U3 small mucleolar irlonucleoprotein) MBNL AB007888 mucleolar irlonucleoprotein) MSC AF087036 muscellind-like (Drosophila) MSC AF087036 muschin (activated B-cell factor-1) MSC AF087036 muth homolog 2, colon cancer, MSH6 U03911 nonpolyposis type 1 (E. coli) MSH6 U28946 muth homolog 6 (E. coli) MSH6 U28946 muth homolog 6 (E. coli) MSH6 U28946 muth homolog 6 (E. coli) MCL1 L08246 related) MCL1 L08246 related) MCL1 L08246 related) MYLTE AF108145 MYLE protein MYO1B AB018270 myosin IB MYO1D AB018270 myosin IB MYO1D		AA420624		
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MSC AF087036 musculin (activated B-cell factor-1) MLH3 L40399 mutL homolog 3 (E. coli) MSH2 U03911 nonpolyposis type 1 (E. coli) MSH6 U28946 mutS homolog 6 (E. coli) MPZL1 AF087020 myelin protein zero-like 1 MCL1 L08246 myelin protein zero-like 1 MCL1 L08246 related) MCL1 L08246 myeloid cell leukemia sequence 1 (BCL2-related) MYCL1 L08246 myeloid/lymphoid or mixed-lineage teukemia (trithorax homolog, Drosophila); MYO1B AJ001381 myosin IB MYO1B AJ001381 myosin IB MYO1D AB018270 myosin IB MYO1D AB018342 myosin Ight chain 1 slow a myosin Ight chain 1 slow a myosin Ight polypeptide, regulatory, non-x54304 MYO10 AB018342 myosin Ight polypeptide, regulatory, non-x54304 </td <td></td> <td></td> <td>muscleblind-like (Drosophila)</td> <td>muscleblind (Drosophila)-like</td>			muscleblind-like (Drosophila)	muscleblind (Drosophila)-like
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MSH2 U03911 mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) MSH6 U28946 mutS homolog 6 (E. coli) MSH6 U28946 myelin protein zero-like 1 MCL1 L08246 myelin protein zero-like 1 MCL1 L08246 related) MXCL1 L08246 related) MXCL2 related) myeloid/lymphoid or mixed-lineage L13773 translocated to, 2 , MYO1B AJ001381 MYLE protein MYO1B AJ001381 myosin IB MYO1D AB018270 myosin IB MYO1E U14391 myosin IB MYO1C U14391 myosin IB MYO1D AB018342 myosin Ight chain 1 slow a MYO10 AB018342 myosin Ight polypeptide, regulatory, non- MYO10 AB018342 myosin, light optypetide, regu		L 40399	mutt. homolog 3 (E. coli)	mutL homolog 3
MSH2 U03911 nonpolyposis type 1 (E. coli) MSH6 U28946 mulS homolog 6 (E. coli) MPZL1 AF087020 myelin protein zero-like 1 MCL1 L08246 related) MYCL1 L08246 related) MYCL1 L08246 related) MYCL1 L08246 related) MYCL2 L13773 translocated to, 2 MYO1B AF108145 MYLE protein MYO1B AB018270 myosin IB MYO1E U14391 myosin IB MC1SA A1127424 myosin IB MYO10 AB018342 myosin regulatory light chain MYO10 AB018342 myosin, light polypeptide, regulatory, non- MICR A8018342 myosin, light polypeptide, regulatory, non-	·		mutS homolog 2, colon cancer,	
MSH6 U28946 mutS homolog 6 (E. coli) MPZL1 AF087020 myelin protein zero-like 1 MCL1 L08246 related) myeloid cell leukemia sequence 1 (BCL2-related) myeloid/lymphoid or mixed-lineage MLT2 L13773 translocated to, 2 related) MYO1B AF108145 MYLE protein MYO1B AB018270 myosin IB MYO1D AB018270 myosin IE MLC1SA A127424 myosin IE MYO10 AB018342 myosin regulatory light chain MYO10 AB018342 myosin regulatory light polypeptide, regulatory, non-sarcomeric (20KD)		U03911	nonpolyposis type 1 (E. coli)	mutS homolog 2
MPZL1 AF087020 myelin protein zero-like 1 MCL1 L08246 related) myeloid cell leukemia sequence 1 (BCL2-related) related) myeloid/lymphoid or mixed-lineage teukemia (trithorax homolog, Drosophila): MYLT2 L13773 translocated to, 2 , cosophila): MYO1B AF108145 MYLE protein MYO1B AB018270 myosin IB MKO1D AB018270 myosin IE MLC1SA A127424 myosin IE MYO10 AB018342 myosin regulatory light chain MYO10 AB018342 myosin regulatory light polypeptide, regulatory, non-myosin, light polypeptide, regulatory, non-sarcomeric (20KD)		U28946	mutS homolog 6 (E. coli)	G/T mismatch binding protein
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37 at MLLT2 L13773 translocated to, 2 translocated to, 2 AF108145 MYLE protein 37 at MYLE AF108145 MYLE protein AF10801381 MYLE protein 39 at MYO1B AB018270 myosin IB 29 at MYO1E U14391 myosin IE 51 at MLC1SA A1127424 myosin Ight chain 1 slow a 87 at MLC-B U26162 myosin Regulatory light chain 62 at MYO10 AB018342 myosin X MYO10 AB018342 myosin Ight polypeptide, regulatory, non-sarcomeric (20kD)	,	L08246	related)	related)
MLLT2			myeloid/lymphoid or mixed-lineage	myeloid/lymphoid or mixed-lineage leukemia
MLLT2 L13773 translocated to, 2 MYLE AF108145 MYLE protein MYO1B AJ001381 myosin IB MYO1D AB018270 myosin ID MYO1E U14391 myosin IE MLC1SA A1127424 myosin Ight chain 1 slow a MLC-B U26162 myosin regulatory light chain MYO10 AB018342 myosin X MYO10 AB018342 myosin Iight polypeptide, regulatory, non-sarcomeric (20kD)	-		leukemia (trithorax homolog, Drosophila);	(trithorax homolog, Drosophila); translocated
MYLE AF108145 MYLE protein MYO1B AJ001381 myosin IB MYO1D AB018270 myosin ID MYO1E U14391 myosin IE MLC1SA A1127424 myosin Ight chain 1 slow a MLC-B U26162 myosin regulatory light chain MYO10 AB018342 myosin X MYO10 AB018342 myosin X MYO10 AS4304 sarcomeric (20kD)	aţ	L13773	translocated to, 2	to, 2
MYO1B AJ001381 myosin IB MYO1D AB018270 myosin ID MYO1E U14391 myosin IE MLC1SA A1127424 myosin Ight chain 1 slow a MLC-B U26162 myosin regulatory light chain MYO10 AB018342 myosin X MYO10 AB018342 myosin, light polypeptide, regulatory, non-sarcomeric (20kD)	at	AF108145	MYLE protein	DEXI
MYO1D AB018270 myosin ID MYO1E U14391 myosin IE MLC1SA A1127424 myosin light chain 1 slow a MLC-B U26162 myosin regulatory light chain 2 myosin X MYO10 AB018342 myosin X MYO10 X54304 sarcomeric (20kD)		AJ001381	myosin IB	myh-1c
MYO1EU14391myosin IEMLC1SAA1127424myosin light chain 1 slow aMLC-BU26162myosin regulatory light chainMYO10AB018342myosin XMYO10X54304sarcomeric (20kD)		AB018270	Myosin ID	KIAA0727 protein
MLC1SA A1127424 myosin light chain 1 slow a MLC-B U26162 myosin regulatory light chain MYO10 AB018342 myosin X myosin X MYO10 X54304 sarcomeric (20kD)	, te	U14391	myosin IE	myosin-IC
MLC-B U26162 myosin regulatory light chain MYO10 AB018342 myosin X myosin X myosin X myosin X x54304 sarcomeric (20kD)		A1127424	myosin light chain 1 slow a	
MYO10 AB018342 myosin X myosin X myosin, light polypeptide, regulatory, non-x54304 sarcomeric (20kD)		U26162	myosin regulatory light chain	myosin regulatory light chain
myosin, light polypeptide, regulatory, non-sarcomeric (20kD)		AB018342	myosin X	KIAA0799 protein
		YE4304	myosin, light polypeptide, regulatory, non-	
A ATTACO A DOCCOSEO MONOTUBLIA PER PROPERTY SECURITIES OF THE PERSON OF	a	V54504	myotuhularin related protein 3	myotubularin related protein 3

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1627	39707_at	MTMR4	AB014547		KIAAU647 protein
1628	38035 at	MTMR6	AF072928		myotubularin related protein 6
1629	39607 at		AL080178		hypothetical protein
1630			AF052099	myotubularin related protein 8	
				ein kinase C	
1631	32434_at	MARCKS	D10522	substrate	80K-L protein
1632 39267	39267 at	AGM1	AF102265	N-acetylglucosamine-phosphate mutase	N-acetylglucosamine-phosphate mutase
	11			N-acylsphingosine amidohydrolase (acid	
1633	1633 36938_at	ASAH	U70063	ceramidase)	acid ceramidase
1634 AE1	/61 of	HASA	070063	N-acylsphingosine amidohydrolase (acid ceramidase)	acid ceramidase
3	5			NADH dehydrogenase (ubiquinone) 1	
1635	1635 36169_at	NDUFA1	N47307	alpha subcomplex, 1 (7.5kD, MWFE)	
				NADH dehydrogenase (ubiquinone) 1	NADH-ubiquinone oxidoreductase subunit Cit
1636	1636 40546_s_at	NDUFA2	AF047185	alpha subcomplex, 2 (8kD, B8)	88
				NADH dehydrogenase (ubiquinone) 1	NADPH:ubiquinone oxidoreductase subunit
1637	38462_at	NDUFA5	U64028	alpha subcomplex, 5 (13KD, B13)	813
				NADH dehydrogenase (ubiquinone) 1	
1638	32752_at	NDUFA7	W72440	alpha subcomplex, 7 (14.5kD, B14.5a)	
				NADH dehydrogenase (ubiquinone) 1 beta	
1639	38605_at	NDUFB1	AI345944	subcomplex, 1 (/KD, MINLL)	
				NADH dehydrogenase (ubiquinone) 1 beta	
1640	1640 38981 at	NDUFB3	AA203354	subcomplex, 3 (12kD, B12)	
				NADH dehydrogenase (ubiquinone) 1 beta	NADH dehydrogenase (ubiquinone) 1 beta NADH-ubiquinone oxidoreductase subunit CI
1641	1641 32232_at	NDUFBS	AF047181	subcomplex, 5 (16kD, SGDH)	SGDH
				NADH dehydrogenase (ubiquinone) 1 beta	
1642	32774 at	NDUFB8	AI541050	subcomplex, 8 (19kD, ASHI)	
				NADH dehydrogenase (ubiquinone) 1,	
1643	38485 at	NDUFC1	AA760866	subcomplex unknown, 1 (6kD, KFYI)	
	1			NADH dehydrogenase (ubiquinone) Fe-S	
				protein 1 (75kD) (NADH-coenzyme Q	75 kDa subunit NADH dehydrogenase
1644	1644 38395 at	NDUFS1	X61100	reductase)	precursor
				NADH dehydrogenase (ubiquinone) Fe-S	
1645	1645 38695 at	NDUES4	AA203303	reductase)	
		10010	200000		

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				NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q	
1646	1646 38060_at	NDUFS5	AI541336	reductase)	٠
1647	1647 34893_at	NDUFV2	A1557064	NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD)	
				natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor	
1648	1648 34519_at	NPR3	M59305		atrial natriuretic peptide clearance receptor
1649	1649 34234 f at	NKTR	AI688640	natural killer-tumor recognition sequence	
1650	1650 41795_at	NCK1	X17576		NCK adaptor protein 1
1651	1651 33357_at	NCKAP1	AB011159	NCK-associated protein 1	KIAA0587 protein
1652	1652 36073_at	NON	U35139·	necdin homolog (mouse)	NECDIN related protein
1653	1653 34202_at	DKFZP566B0846	6 AL050071	nectin 3	hypothetical protein
1654	1654 34264_at	NESCA	AB026894	nesca protein	NESCA
1655	1655 38719_at	NSF	U03985	N-ethylmaleimide-sensitive factor	N-ethylmaleimide-sensitive factor
1656	1656 39356_at	NEDD4L	AB007899	d 4-like	ubiquitin-protein ligase NEDD4-like
				neural precursor cell expressed,	neural precursor cell expressed,
1657	1657 40281_at	NEDDS	D63878	developmentally down-regulated 5	developmentally down-regulated 5
				neural precursor cell expressed,	
1658	1658 1695_at	NEDD8	D23662	developmentally down-regulated 8	ubiquitin-like protein
				neuroblastoma, suppression of	neuroblastoma, suppression of
1659	1659 37005_at	NBL1	D28124		fumorigenicity 1
1660	1660 31896_at	NAG.	AL050281	neuroblastoma-amplified protein	hypothetical protein
1661	1661]37286_at	NRCAM	AB002341	neuronal cell adhesion molecule	neuronal cell adhesion molecule
				neutral sphingomyelinase (N-SMase)	
1662	1662 37673_at	NSMAF	X96586	activation associated factor	FAN protein
1663	1663 38692 at	NAB1	AF045451	protein 1)	transcriptional regulatory protein p54
1664	1664 34835_at	NCSTN	D87442	nicastrin	
1665	1665 37032_at	NNMT	U08021	nicotinamide N-methyltransferase	nicotinamide N-methyltransferase
1666	1666 41722 at	LVN	U40490	nicotinamide nucleotide transhydrogenase	nicotinamide nucleotide transhydrogenase nicotinamide nucleotide transhydrogenase
1667	1667 35366_at	QN	M30269	nidogen (enactin)	nidogen
1668	1668 753_at	NID2	D86425		osteonidogen

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1669	37047_at	NPC1	AF002020 .	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1670 980	at	NPC1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1671	39345_at	NPC2	AI525834	Niemann-Pick disease, type C2	
1672	1672 35153_at	NBS1	AF058696	Nijmegen breakage syndrome 1 (nibrin)	cell cycle regulatory protein p95
				NIMA (never in mitosis gene a)-related	
1673	1673 36047_at	NEK1	AL050385	kinase 1	*
1674	1674 35843_at	Nek8	L40402	NIMA-related kinase Nek8	
1675	1675 40866_at	NIPSNAP1	AJ001258	nipsnap homolog 1 (C. elegans)	NIPSNAP1 protein
1676	1676 33916_at	NISCH	AB023192	nischarin	KIAA0975 protein
1677	1677 39165_at	NIFU	U47101	nitrogen fixation cluster-like	NifU-like protein
1678	1678 36472_at	NMI	U32849	N-myc (and STAT) interactor	Nmi
1679	1679 36933_at	NDRG1	D87953	N-myc downstream regulated gene 1	RTP
1680	1680 41656_at	NMT2	AF043325	N-myristoyltransferase 2	N-myristoyltransferase 2
		-		non-canonical ubquitin conjugating	
1681	1681 39040_at	NCUBE1	W28360	enzyme 1	
				non-canonical ubquitin conjugating	
1682	39039_s_at	NCUBE1	AI557497	enzyme 1	
				non-metastatic cells 1, protein (NM23A)	
1683	1683 1521_at	NME1	X17620	expressed in	Nm23 protein
				non-metastatic cells 2, protein (NM23B)	
1684	1684 33415_at	NME2	X58965	expressed in	NM23-H2 protein
				non-metastatic cells 2, protein (NM23B)	
1685	1685 1980_s_at	NME2	X58965	expressed in	NM23-H2 protein
				non-POU domain containing, octamer-	
1686	1686 38527_at	ONON	U02493	binding	54 kDa protein
1687	38750_at	NOTCH3	N97669	Notch homolog 3 (Drosophila)	Notch3
1688	1688 34781_at	WS-3	D84145	novel RGD-containing protein	novel RGD-containing protein
1689	1689 40122_at	NSAP1	AF037448	NS1-associated protein 1	Gry-rbp
1690	33752_at	NS1-BP	AB020657	NS1-binding protein	KIAA0850 protein
				N-sulfoglucosamine sulfohydrolase	
1691	35626_at	SGSH	U30894	(suffamidase)	N-sulphoglucosamine sulphohydrolase
1692	1692 37352_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1693	1693 37353_g_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1694	1694 40901_at	GSZNA	U17989	nuclear autoantigen	GS2NA
1004	1605 20780 24	COBON	A A 1 40 4 2 9	nuclear cap binding protein subunit 2,	
1090	132103_al	NCBFZ	AA143420	COND	

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1696	1696 35836 at	CCIE	AB019408	nuclear distribution gene C homolog (A. niqulans)	nuclear distribution gene C (A.nidulans) homolog
1697	1697 39782 at			NA-binding protein	C1D protein
1698	1698 40063_at	52			NDP52
1699 853	853 at	NFE2L2	S74017	nuclear factor (erythroid-derived 2)-like 2	Nf2
,	000	0 4	V52560		CCAAT/enhancer binding protein (C/EBP),
3	30334_ai			lls,	nuclear factor of activated T-cells,
1701	1701 40822_at	NFATC3	L41067	cytoplasmic, calcineurin-dependent 3	cytoplasmic, calcineurin-dependent 3
1702	1702 38438 at	NEKR1	M58603	nuclear factor of kappa light polypeptide	nuclear factor kappa-B DNA binding subunit
	3			nuclear factor of kappa light polypeptide	
1703	1703 1377_at	NFKB1	M58603	gene enhancer in B-cells 1 (p105)	nuclear factor kappa-B DNA binding subunit
				nuclear factor of kappa light polypeptide	nuclear factor of kappa light polypeptide
1704	1704 1461_at	NFKBIA	M69043	gene enhancer in B-cells inhibitor, alpha	gene enhancer in B-cells inhibitor, alpha
1705	37544_at	NFIL3	X64318	nuclear factor, interleukin 3 regulated	nuclear factor, interleukin 3 regulated
1706	1706 38648_at	CIZ	U80760	nuclear matrix transcription factor 4	CAGH1 alternate open reading frame
				nuclear phosphoprotein similar to S.	
1707	1707 40816_at	PWP1	L07758	cerevisiae PWP1	IEF SSP 9502
1708	1708 34312_at	NCOA2	A1040324	nuclear receptor coactivator 2	
1709	1709 33381_at	NCOA3	AF012108	nuclear receptor coactivator 3	Amplified in Breast Cancer
1710	1710 39174_at	NCOA4	X77548	nuclear receptor coactivator 4	Ret fused gene
1711	1711 40088_at	NRIP1	X84373	nuclear receptor interacting protein 1	nuclear factor RIP140
				nuclear receptor subfamily 2, group F,	
1712	1712 39397_at	NR2F2	M64497	member 2	apolipoprotein Al regulatory protein-1
				nuclear receptor subfamily 3, group C,	nuclear receptor subfamily 3, group C,
1713	1713 36690_at	NR3C1	M10901	member 1	member 1
1714	1714 35302_at	NXF1	AJ132712	nuclear RNA export factor 1	nuclear RNA export factor 1
1715	1715 37928_at	NFYB	AA621555	nuclear transcription factor Y, beta	
				nuclear transcription factor, X-box binding	
1716	1716 34667_at	NFX1	U15306		NFX1
1717	1747	100	AE061160	nuclear; Homo sapiens tyrosine	tyrocine phocohatace
	33413_al	rnL-1	Aros 1 100	prospriatase (1 nr-1) gene, comprete cus.	igiosina priospriatase

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				nuclease sensitive element binding protein	:
718	1718 32340_s_at	NSEP1	M85234		nuclease sensitive element binding protein-1
719	1719 35643_at	NUCB2	X76732	nucleobindin 2	NEFA protein
9	1000	Č	021262	miclostar and coiled-body phoenhorotein 1	
3	1/20 30391_at	NOLO!	A 1000E04	material and compared process	cyctaine-rich protein
1/2/	1/21 3/520_at	HSA6591	1.05425		nucleolar GTPase
77/	1722 35930_at	חטואואסרון היי	A FOED400		
1723	1723 39390_at	NUP133	AFU52123		niclost pore complex protein humin153
1724	32850_at	NUP153	725535		nacieal pole complex protein map 130
1725	1725 39024_at	NUP98	AF042357		
1726	1726 571_at	NAP1L1	M86667		nucleosome assembly protein 1-like 1
1727	1727 743 at	NAP1L3	D50370		nucleosome assembly protein
1728	1728 32575 at	NAP1L4	U77456	nucleosome assembly protein 1-like 4	nucleosome assembly protein 2
1729	1729 36127 g at	NBP	U18919	nucleotide binding protein	nucleotide binding protein
				nudix (nucleoside diphosphate linked	diphosphoinositof polyphosphate
1730	1730 41584 at	NUDT3	AF062529	moiety X)-type motif 3	phosphohydrolase
1731	1731 37693 at	NUMB	L40393	numb homolog (Drosophila)	numb homolog
				ob15e02.s1 NCI_CGAP_Kid3 Homo	
				sapiens cDNA clone IMAGE:1323770 3'	
				similar to SW:ROA3_HUMAN P51991	·
				HETEROGENEOUS NUCLEAR	
				RIBONUCLEOPROTEIN A3; mRNA	
1732	1732 35916 s at	INHBC	AA877215	sequence.	
173	1733 34169 s at	OCRL	U57627	oculocerebrorenal syndrome of Lowe	ocrl1
				olfactory receptor; Human olfactory	
1734	1734 31921 at	OLF3	U56421	receptor (OLF3) gene, complete cds.	HsOLF3
				O-linked N-acetylglucosamine (GlcNAc)	
				transferase (UDP-N-	
				acetylglucosamine:polypeptide-N-	
173	1735 39507 at	OGT	AL050366	acetylglucosaminyl transferase)	hypothetical protein
1736	1736 40332 at	OGFR	AF109134	opioid growth factor receptor	09-InC
173	1737 39745_at	OPA1	AB011139	optic atrophy 1 (autosomal dominant)	KIAA0567 protein
173	1738 41744_at	OPTN	AF070533	optineurin	optineurin
			:	OR11-3; olfactory receptor; Homo sapiens	
	-	1		OR7E12P pseudogene, complete	
2	1739 34539_at	OR/EIZP	Ar003834	sednerice.	

Fig.2

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1			,		7 8-diamino-pelardonic acid
1740	1740 AFFX-BioC-3 at bioA	bioA	J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1741	1741 AFFX-BioB-M atbioA		J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1742	1742 AFFX-BioDn-5 abioA	bioA	J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1743	1743 AFFX-BioDn-3_abioA	bioA	J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1744	1744 AFFX-BioC-5_at bioA	bioA	J04423	ORF 1	aminotransferase
				ORF; putative; Human ribosomal protein	
1745	1745 32412_at	RPS14	M13934	S14 gene, complete cds.	unknown protein; ribosomal protein S14
				ORF1; ORF 2; no start codon; Human	
				mRNA for ornithine decarboxylase	
1746	1746 1315_at	OAZ1	D78361	antizyme, ORF 1 and ORF 2.	ornithine decarboxylase antizyme 1
				OBE-2: OBE-3: Human retinoid X receptor	
1747	1747 32800 at	BXBA: NR2R1	1,166306	alpha mRNA 3' UTB partial seguence.	retinoid X receptor, alpha
	35000 at	1971 171 171	2000	origin recognition complex subunit 5-like	origin recognition complex subunit 5
1748	1748 38155_at	ORCSL	U92538	(yeast)	homolog
				ornithine aminotransferase (gyrate	
1749	1749 36636_at	OAT	M12267	atrophy)	ornithine aminotransferase
1750	1750 1959 at	OAZIN	D88674	ornithine decarboxylase antizyme inhibitor	antizyme inhibitor
					-
1751	1751 33367_s_at	OAZIN	D88674	ornithine decarboxylase antizyme inhibitor antizyme inhibitor	antizyme inhibitor
	:		-	ornithine decarboxylase; Human ornithine	
1752	1752 1081_at	ODC1	M33764	decarboxylase gene, complete cds.	ornithine decarboxylase 1
				orphan G protein-coupled receptor; Homo	
				sapiens G protein-coupled receptor	
1750	1753 31700_at	GPR35	AF027957	(GPR35) gene, complete cds.	G protein-coupled receptor
1754	1754 1451_s_at	OSF-2	D13666	osteoblast specific factor 2 (fasciclin I-like) osteoblast specific factor 2	osteoblast specific factor 2
1756	1755 30774 31	OXA1	XAOG95	oxidase (cytochrome c) assembly 1-like	oxidase (cytochrome c) assembly 1-like
2	103114 at	סיייור	CCCCC	com i (composito composito) composito	

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17563	39136_at	OSR1	AB017642		oxidative-stress responsive 1
17574	1438 at		AL049923		oxysterol-binding protein-like protein 8
17583	4329 at	PAK2	N25547	p21 (CDKN1A)-activated kinase 2	
17593	1759 39710 at		U30521	P311 protein	P311 HUM
17603	1760 36136 at	-	AF010315	p53-induced protein	Pig11
17614	1761 40441 a at			PAI-1 mRNA-binding protein	hypothetical protein
17624	1762 40440_at	PAI-RBP1			hypothetical protein
17633	1763 32001 s at	PACE4	M80482	paired basic amino acid cleaving system 4 subtilisin-like protease	subtilisin-like protease
	m_0_1007				paired box gene 8, isoform PAX8A; paired
	-				box gene 8, isoform PAX8B; paired box
					gene 8, isoform PAX8C; paired box gene 8,
_					isoform PAX8D; paired box gene 8, isoform
1764	1764 121 at	PAX8	66969X	paired box gene 8	PAX8E
1765 40127	40127 at	PMX1	M95929	paired mesoderm homeo box 1	homeobox protein
1766	11	KIAA0992	AB023209	palladin	KIAA0992 protein
1767	1767 40504 at	PONZ	AF001601	paraoxonase 2	paraoxonase
	1			partially supported by FGENES and	
1768	1768 36032 at	dJ167A19.1	AL031427 ·		hypothetical protein
1769	1769 39243 s at	PSIP2	U94319	PC4 and SFRS1 interacting protein 2	DFS70
1770	41665 at	PCF11	AB020631	PCF11p homolog	KIAA0824 protein
1771	38758 at	PDAP1	R98910	PDGFA associated protein 1	
1772	1772 36937 s at	PDLIM1	U90878	PDZ and LIM domain 1 (elfin)	carboxyl terminal LIM domain protein
				PDZ domain containing guanine	PDZ domain containing guanine nucleotide
1773	1773 32026 s_at	PDZ-GEF1	AB002311	nucleotide exchange factor(GEF)1	exchange factor(GEF)1
				PDZ domain containing guanine	
1774	1774 34745 at	PDZ-GEF1	AF070570	nucleotide exchange factor(GEF)1	
				PEDF; Human pigment epithelium-derived	
1775	1775 40856 at	SERPINF1; PEDF	2F U29953	factor gene, complete cds.	pigment epithelium-derived factor
				pentaxin-related gene, rapidly induced by	
1776	1776 1491 at	PTX3	M31166	IL-1 beta	tumor necrosis factor
	3		-	peptidylglycine alpha-amidating	peptidylglycine alpha-amidating
1777	1777 38465_at	PAM	M37721	топоохудепаѕе	monooxygenase
1770	1778 25822 24	BIGG	M63573	neptidylorolyl isomerase B (cyclophilin B)	secreted cyclophilin-like protein
0//	33623_at	Irrib	O COOM	/	

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1779	1779 37422 at	PPIC	S71018	peptidylprolyl isomerase C (cyclophilin C)	cyclophilin C
1780	1780 37385_at	PPIG	U40763	/clophilin G)	CARS-Cyp
1781	1781 36829_at	PER1	AF022991	period homolog 1 (Drosophila)	Rigui
1782	1782 35835_at	PDL-108	AB019409	periodontal ligament fibroblast protein	
				peripheral benzodiazepine receptor;	peripheral benzodiazapine receptor;
				Human peripheral benzodiazepine	peripheral benzodiazapine receptor short
1783	1783 32806_at	MBR; PI	BR M36035	receptor (hpbs) mRNA, complete cds.	form
1784	784 38653_at	PMP22	D11428	peripheral myelin protein 22	PMP-22(PAS-II/SR13/Gas-3)
1785	41213	PRDX1	X67951	peroxiredoxin 1	peroxiredoxin 1
	II.				Aop1_Human, MER5(Aop1_Mouse)-like
1786	1786 36631_at	PRDX3	D49396	peroxiredoxin 3	protein
1787	1787 38435 at	PRDX4	U25182	peroxiredoxin 4	antioxidant enzyme AOE37-2
1788	1788 37900_at	PEX11B	AF093670	peroxisomal biogenesis factor 11B	peroxisomal biogenesis factor
1789	1789 36864 at	PEX3	AJ001625	peroxisomal biogenesis factor 3	Pex3 protein
				peroxisomal long-chain acyl-coA	peroxisomal long-chain acyl-coA
1790	1790 36625_at	ZAP128	L40401	thioesterase	thioesterase
				peroxisomal membrane protein 3 (35kD,	
1791	1791 33265_at	PXMP3	M86852	Zellweger syndrome)	peroxisome assembly factor-1
1792	1792 36502_at	PFTK1	AB020641	PFTAIRE protein kinase 1	KIAA0834 protein
1793	1793 37694_at	PHF3	D87685	PHD finger protein 3	PHD finger protein 3
					PHD zinc finder protein XAP135, isoform a:
1794	1794 39381_at	XAP135	AF055030	PHD zinc finger protein XAP135	PHD zinc finger protein XAP135, isoform b
				, hosphatase and tensin homolog	
1795	1795 1434 at	PTEN	U92436	(mutated in multiple advanced cancers 1)	MMAC1
					type-2 phosphatidic acid phosphatase alpha-
1796	1796 34797_at	PPAP2A	AF014402	phosphatidic acid phosphatase type 2A	
					phosphatidic acid phosphohydrolase
1797	1797 33862_at	PPAP2B	AF017786	phosphatidic acid phosphatase type 2B	nomolog
,	10000	() () () () () () () () () ()	2001	phosphatidylinositol 4-kinase, catalytic,	nhoenhatidylinositol 4-kinaso
2	1/30 40/65_s_at	7174CA	L30131		
1799	1799 37685_at	PICALM	U45976	phosphatidylinositol binding clathrin lassembly protein	CALM

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		2		phosphatidylinositol glycan, class A	
1800	1800 39993 at	PIGA	D11466	ıria)	PIG-A protein
1801	801 314_at		D42138		PIG-B
1802 751	751_at	PIGC	D85418		phosphatidylinositol-glycan-class C (PIG-C)
1803	776 at	PIGF	D13435	phosphatidylinositol glycan, class F	PIG-F
1804	1804 40629 at	PIGH	L19783	phosphatidylinositol glycan, class H	phosphatidylinositol glycan, class H
				nsfer protein,	homologue of Drosphila retinal degeneration
1805	1805 38297_at	PITPNM	X98654		B gene
				phosphatidylinositol-4-phosphate 5-	phosphatidylinositol-4-phosphate 5-kinase
1806	1806 35741_at	PIP5K2B	U85245	kinase, type II, beta	type II beta
1807	37320_at	PTDSS1	D14694	phosphatidylserine synthase 1	phosphatidylserine synthase 1
				phosphodiesterase 4B, cAMP-specific	
				(phosphodiesterase E4 dunce homolog,	
1808	1808 33705_at	PDE4B	L20971	Drosophila)	phosphodiesterase
				phosphodiesterase 4D interacting protein	
1809	1809 39422 at	PDE4DIP	AB007923	(myomegalin)	KIAA0454 protein
1810	1810 37676 at	PDE8A	AF056490	phosphodiesterase 8A	cAMP-specific phosphodiesterase 8A
				phosphoenolpyruvate carboxykinase 2	
1811	1811 37188 at	PCK2	X92720	(mitochondrial)	phosphoenolpyruvate carboxykinase (GTP)
1812	1812 39175 at	PFKP	D25328	phosphofructokinase, platelet	platelet-type phosphofructokinase
1813	1813 32210 at	PGM1	M83088	phosphoglucomutase 1	phosphoglucomutase 1
1814	1814 36963 at	PGD	U30255	phosphogluconate dehydrogenase	phosphogluconate dehydrogenase
1815	1815 37677 at	PGK1	V00572	phosphoglycerate kinase 1	phosphoglycerate kinase 1
1816	1816 41221 at	PGAM1	J04173	phosphoglycerate mutase 1 (brain)	phosphoglycerate mutase 2
1817	1817 35665_at	PIK3C3	Z46973	phosphoinositide-3-kinase, class 3	phosphatidylinositol 3-kinase
				phosphoinositide-3-kinase, regulatory	
1818	1818 1269_at	PIK3R1	M61906	subunit, polypeptide 1 (p85 alpha)	
				phosphoinositide-3-kinase, regulatory	
1815	1819 37961_at	PIK3R3	U90907	subunit, polypeptide 3 (p55, gamma)	
1820	1820 32775_r_at	PLSCR1	AB006746	phospholipid scramblase 1	phospholipid scramblase 1
182	1821 32260 at	PEA15	ХВЕВПЭ	phosphoprotein enriched in astrocytes 15	
	200-20			phosphoribosyl pyrophosphate synthetase	phosphoribosyl pyrophosphate synthetase
182;	1822 36489_at	PRPS1	D00860		subunit I

Fig. 2

						_
PAPSAP1 C PAICS >> PHKB >> PHK		4	В	ပ	O	u
PAICS PHKB PYGB I PHYH at PNN I PTG1IP at PLS3 I PCD1 I PCD2 II PSCD1 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II PSCD1 II PSCD2 II II PSCD2 II II PSCD3 II II PSCD3 II II PSCD3 II II PSCD4 II II PSCD4 II II PSCD5 II II PSCD6 II II PSCD6 III II PSCD7 II II PSCD6 II II PSCD7 II II II PSCD7 II II II II II II II II II II II II II	103 37	338 at	PRPSAP1	D61391	phosphoribosyl pyrophosphate synthetase-phosphoribosypyrophosphate synthetase- associated protein 1	phosphoribosypyrophospnate synthetase- associated protein 39
PAICS >> PHKB 1 1 1 1 1 1 1 1 1		j5_			oimidazole	
PAICS PHKB PYGB U PYGB U PYGB U PHYH U PHY	·				•	phosphoribosylaminoimidazole carboxylase,
PAICS PHKB PYGB I PHYH AI PHYH I AI PAFAH1B1 I PAFAH1B1 I PACD1 I PSCD1 II PSCD2 AI PLSGL1 II PSCD2 AI PLSGL1 II PSCD2 AI PABPC1 III PABPC1					phosphoribosylaminoimidazole	phosphoribosylaminoribosylaminoimidazole
## PHKB	324 390	056 at	PAICS	X53793	succinocarboxamide synthetase	succinocarboxamide synthetase
PYGB (L at PNYH (L at PTG1IP (L at PCD1 at PCD1 at PCD2 at PCD2 at PARG at PARG at PARG at PARG at PARC at PARC at PARC at PARC at PARC at PARC at PARC at PARC at PARC	325 37:	392 at	PHKB	X84908	phosphorylase kinase, beta	phosphorylase kinase
at PHYH (1 2 2 2 2 2 2 2 2 2	326 36	667 at	PYGB	U47025	phosphorylase, glycogen; brain	glycogen phosphorylase B
PHYH PINN PTG1IP PLS3 PLS3 PSCD1 PSCD1 PSCD2 PSCD2 PSCD2 PSCD2 PSCD2 PSCD2 PSCD2 PSCD2 PSCD2 PSCD1 PSCD1 PSCD1 PSCD1 PSCD1 PSCD2 PSCD2 PSCD1 PSCD1 PSCD1 PSCD2 PSCD2 PSCD2 PSCD2 PSCD2 PSCD2 PSCD2 PSCD1 PSCD2 PSCD3 PSC	-	1			phytanoyl-CoA hydroxylase (Refsum	peroxisomal phytanoyl-CoA alpha-
PTTG1IP ; PLS3 I PAFAH1B1 PAFAH1B1 PDGFRA PSCD1 PSCD2 PSCD2 PSCD2 PSCD2 PSCD2 PSCD4 PSCD4 PSCD6 PSCD	327 32	724 at	РНҮН	AF023462	disease)	hydroxylase
PTTG1IP 2 PLS3 1 PAFAH1B1 1 PDGFRA PSCD1 PSCD2 PLXNB2 PLXNB2 PLXNC1 PARG IT PABPC1 PAB	328 33	543 s at	NNd	U77718	pinin, desmosome associated protein	pinin
at PLS3 PAFAH1B1 PAFAH1B1 PDGFRA PSCD1 PSCD2 at PLXNB2 PLXNB2 PLXNB2 PLXNB2 T PLXNC1 PARG at PABPC1 T PARG at PABPC1 T PARN T PARN	-				pituitary tumor-transforming 1 interacting	
PAFAH1B1 PAFAH1B1 PDGFRA PSCD1 PSCD2 at PLXNB2 TPLXNB2 TPLXNC1 TPARG at PABPC1 TPABPC1	829 39	003_at	PTTG11P	Z50022	protein	putative surface glycoprotein
PAFAH1B1 PDGFRA PSCD1 PSCD2 IT PLXNC1 PLXNC1 PARG IT PABPC1 PABPC1 PABPC1 PABPC1 PABPC1 PABPC1	830 34	793_s_at	PLS3	M22299	plastin 3 (T isoform)	T-plastin polypeptide
PAFAH1B1 PDGFRA PSCD1 PSCD2 IT PLAGL1 PLXNB2 PLXNC1 PLXNC1 PARG at PABPC1 PABPC1 PABPC1 PABPC1 PABPC1	-					
PDGFRA PSCD1 PSCD2 It PLXNB2 PLXNC1 PARG PARG PABPC1 PABPC1 PABPC1 PABPC1 PABPC1	831 33	יקקט at	PAFAH1R1	13385	piatelet-activating lactor acetylitydrolase, lisoform Ib. alpha subunit (45kD)	Miller-Dieker lissencephaly protein
PDGFRA PSCD1 PSCD2 It PLXNB2 PLXNC1 PARG IT PABPC1 PABPC1 PABPC1 PABPC1 PABPC1 PABPC1	<u>;</u>				platelet-derived growth factor receptor,	platelet-derived growth factor receptor A
PSCD1 PSCD2 II PLAGL1 PLXNB2 PLXNC1 PARG BI PABPC1 PABPC1 PABPC1 PABPC1 PABPC1	832 17	/31 at	PDGFRA	M21574	alpha polypeptide	chain
PSCD1 PSCD2 It PLAGL1 PLXNB2 PLXNC1 PARG at PABPC1 PABPC1 PABPC1 PARN PARN PCRP1					pleckstrin homology, Sec7 and coiled/coil	cytohesin 1, isoform 1; cytohesin 1, isoform
PSCD2 It PLAGL1 PLXNB2 PLXNC1 PARG at PABPC1 PABPC1 PABPC1 PARN PARN PCRP1	833 38	3666 at	PSCD1	M85169	domains 1(cytohesin 1)	2
PSCD2 It PLAGL1 PLXNB2 PLXNC1 PARG at PABPC1 PABPC1 PABPC1 PABPC1	-	ı			pleckstrin homology, Sec7 and coiled/coil	
PLXNG1 PLXNB2 PLXNB2 PLXNC1 PARG at PABPC1 PABPC1 PABPC1 PABPC1	834 38	3741 at	PSCD2	U70728	domains 2 (cytohesin-2)	cytohesin-2
PLXNB2 PLXNC1 PARG at PABPC1 PABPC1 PABPC1 PARN PARN	835 36	3943 r at	PLAGL1	U81992	pleiomorphic adenoma gene-like 1	C2H2 zinc finger protein PLAGL1
PLXNC1 PARG PABPC1 PABPC1 PABPC1 PARN PARN	836 34	1780 at	PLXNB2	AB002313	plexin B2	plexin B2
PARG PABPC1 PABPC1 PABPC1 PARN PARN PCRP1	837 32	2193 at	PLXNC1	AF030339	plexin C1	VESPR
PABPC1 PABPC1 PABPC1 PARN PCRP1	838 38	3270 at	PARG	AF005043	poly (ADP-ribose) glycohydrolase	poly(ADP-ribose) glycohydrolase
PABPC1 PARN PCRP1	839 31	1951 s at	PABPC1	Z48501	poly(A) binding protein, cytoplasmic 1	polyadenylate binding protein II
PARN PCRP1	84031	1950 at	PABPC1	Y00345	poly(A) binding protein, cytoplasmic 1	poly(A) binding protein, cytoplasmic 1
PARN PCRP1					poly(A)-specific ribonuclease	:
PCRP1	841 36	5003_at	PARN	AJ005698	(deadenylation nuclease)	poly(A)-specific ribonuclease
1001	842 34	4305_at	PCBP1	Z29505	poly(rC) binding protein 1	sub2.3
at PCBP2	843 3	5746_r_at	PCBP2	X78136	poly(rC) binding protein 2	hnRNP-E2
PCBP2	844 3	5745_f_at	PCBP2	X78136	poly(rC) binding protein 2	hn KN F-E2
1845 39868_at PCBP3 AL046394	1845 3	9868_at	PCBP3	AL046394	poly(rC) binding protein 3	

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3				polycystic kidney disease 2 (autosomal	on houselin 2
1846				dominant)	polycysum z
1847	1847 33380_at	POLS	AB005754	polymerase (DNA directed) sigma	LAK-1
				DNA directed), epsilon 3	polymerase (DNA directed), epsilon 3 (p17
1848	1848 38702_at F	POLE3	AF070640	(p17 subunit)	subunit)
				polymerase (RNA) II (DNA directed)	
1849	1849 40791_at	POLR2A	X63564	polypeptide A (220kD)	RNA polymerase II largest subunit
				polymerase (RNA) II (DNA directed)	
1850	1850 39746_at	POLR2B	X63563	polypeptide B (140kD)	HNA polymerase II 140 KDa subunit
			- 1 - 1	polymerase (RNA) II (DNA directed)	
1851	1851 36027_at	POLR2F	AA418779	polypeptide F	
				polymerase (RNA) II (DNA directed)	
1852	1852 35631_at	POLR2H	U37689	polypeptide H	RNA polymerase II subunit
				polymerase (RNA) II (DNA directed)	
1853	1853 1248_at	POLRZH	U37689	polypeptide H	RNA polymerase II subunit
				polymerase (RNA) II (DNA directed)	
1854	1854 503_at	POLRZL	U37690	polypeptide L (7.6kD)	RNA polymerase II subunit
				polymerase (RNA) II (DNA directed)	
1855	1855 35841_at	POLR2L	N24355	polypeptide L (7.6kD)	
1856		PTRF	AL050224	polymerase I and transcript release factor	
1857		PIGR	X73079	polymeric immunoglobulin receptor	Polymeric immunoglobulin receptor
1858	1858 40593_at	PTBP1	X66975	polypyrimidine tract binding protein 1	nuclear ribonucleoprotein
1050	1050 31600 6 24	DMC214	D38435	1 - Section increased 2-like	
	5-00010	13001	2000	not OBE1 (as 1-73) OBE2 nut cre	
				protein (aa 1-343); Bacteriophage P1 cre	
1860	1860 AFFX-CreX-5 at		X03453	gene for recombinase protein.	
				pot. ORF1 (aa 1-73); ORF2, put. cre	
				protein (aa 1-343); Bacteriophage P1 cre	
1861	1861 AFFX-CreX-3_at		X03453	gene for recombinase protein.	
1862	1862 315 at	PRDM2	D45132	PR domain containing 2, with ZNF domain zinc-finger DNA-binding protein	zinc-finger DNA-binding protein
1863	1863 32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3	homeobox protein

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				precursor; Human prolyl 4-hydroxylase	
-			•	beta-subunit and disulfide isomerase	
				(P4HB) gene, exon 11, clones 6B-	
1864	1864 36666 at	P4HB	M22806	(1,3,5,6).	prolyl 4-hydroxylase beta-subunit
1865	1865 34321 i at	GS3786	D87120	predicted osteoblast protein	GS3786
1866		PFDN4	U41816	prefoldin 4	C-1
1867	1867 38698 at	PREI3	AL080070	preimplantation protein 3	hypothetical protein
1868	1868 40269 at	PRP18	U51990	ctor 18	hPrp18
				an enkephalin	
1869	1869 38291_at	PENK	J00123	gene: exon 3 and 3'flank.	proenkephalin
1870	1870 641_at	PSEN1	L76517	presenilin 1 (Alzheimer disease 3)	presenilin 1
1871	1871 40621_at	PAWR	U63809		prostate apoptosis response protein par-4
1872	1872 41773 at	PCOLN3	U58048		PRSM1
1873	1873 31609_s_at	PCOLCE	L33799	procollagen C-endopeptidase enhancer	procollagen C-proteinase enhancer protein
1874	1874 34795_at	PLOD2	U84573	dioxygenase (lysine hydroxylase) 2	lysyl hydroxylase isoform 2
				procollagen-lysine, 2-oxoglutarate 5-	
				dioxygenase (lysine hydroxylase, Ehlers-	
1875	1875 36184_at	PLOD	L06419	Danlos syndrome type VI)	lysyl hydroxylase
				procollagen-proline, 2-oxoglutarate 4-	procollagen-proline, 2-oxoglutarate 4-
				dioxygenase (proline 4-hydroxylase),	dioxygenase (proline 4-hydroxylase), alpha
1876	1876 37037 at	P4HA1	M24486	alpha polypeptide I	polypeptide l
				procollagen-proline, 2-oxoglutarate 4-	
				dioxygenase (proline 4-hydroxylase),	
1877	1877 34390_at	P4HA2	U90441	alpha polypeptide II	prolyl 4-hydroxylase alpha (II) subunit
				-	
				procollagen-proline, 2-oxoglutarate 4-	procollagen-proline, 2-oxoglutarate 4-
				dioxygenase (proline 4-hydroxylase), beta	dioxygenase (proline 4-hydroxylase), beta
				polypeptide (protein disulfide isomerase;	polypeptide (protein disulfide isomerase;
1878	1878 691 g at	P4HB	J02783	thyroid hormone binding protein p55)	thyroid hormone binding protein p55)
1879	1879 38840 s at	PFN2	L10678	profilin 2	profilin II
1880	1880 38839_at	PFN2	AL096719	profilin 2	profilin 2 isoform b; profilin 2 isoform a
				progesterone receptor membrane	
1881	38802_at	PGRMC1	Y12711	component 1	putative progesterone binding protein
1882	1882 38821 at	PGRMC2	AJ002030	progesterone receptor membrane component 2	progresterone binding protein
	12000				

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1883	1883 39035_at	500	AF006010		progestin induced protein
1884	1884 39036 g at	005	AF006010	progestin induced protein	progestin induced protein
1885	II	PDCD10	AF022385	programmed cell death 10	TFAR15
1886	1886 37569 at	PDCD6	AF035606	programmed cell death 6	calcium binding protein
				programmed cell death 8 (apoptosis-	
1887	1887 32212_at	PDCD8	AL049703	inducing factor)	hypothetical protein
1888	1888 36592_at	PHB	S85655	prohibitin	prohibitin
1889	1889 1884 s at	PCNA	M15796	proliferating cell nuclear antigen	proliferating cell nuclear antigen
1890	1890 41600_at	PA2G4	U59435	proliferation-associated 2G4, 38kD	cell cycle protein p38-2G4 homolog
				proline-rich Gla (G-carboxyglutamic acid)	
1891	1891 35978_at	PRRG1	AF009242	polypeptide 1	proline-rich Gla protein 1
1892	1892 36023_at	PRH1	AI864120	proline-rich protein Haelll subfamily 1	,
				pro-oncosis receptor inducing membrane	pro-oncosis receptor inducing membrane
1893	1893 40803_at	PORIMIN	AL050161	injury gene	injury gene
				propionyl Coenzyme A carboxylase, alpha	Propionyl-Coenzyme A carboxylase, alpha
1894	1894 1348_s_at	PCCA	S79219	polypeptide	polypeptide precursor
				propionyl Coenzyme A carboxylase, beta	
1895	1895 36561_at	PCCB	X73424	polypeptide	propionyl-CoA carboxylase
		1,700	10001	proprotein convertase subtilisin/kexin type	DCS isoform A
1896	1896/41032_at	PCSK3	020387	C	piotegra of isologia
		-		prosaposin (variant Gaucher disease and	prosaposin (variant Gaucher disease and
1897	1897 36795_at	PSAP	J03077	variant metachromatic leukodystrophy)	variant metachromatic leukodystrophy)
1898	1898 38406 f at	PTGDS	A1207842	prostaglandin D2 synthase (21kD, brain)	
	1			prostaglandin E receptor 2 (subtype EP2),	
1899	1899 828_at	PTGER2	U19487	53kD	prostaglandin E2 receptor
190	1900 1890 at	PLAB	AB000584	prostate differentiation factor	TGF-beta superfamily protein
190	1901 32611_at	PBP	X75252	prostatic binding protein	phosphatidylethanolamine binding protein
1902	719 g at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
199	1903 718 at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
190	1904 33368 at	PRSS15	X76040	protease, serine, 15	Lon protease-like protein
190	1905 40078 at	SPUVE	AF015287	protease, serine, 23	serine protease
190	1906 39845_at	PRSS25	AF020760	protease, serine, 25	serine protease
190,	1907 688 at	PSMC1	L02426	proteasome (prosome, macropain) 26S subunit, ATPase, 1	26S protease (S4) regulatory subunit

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				proteasome (prosome, macropain) 26S	
1908	1908 35353_at	PSMC2	D11094		MSS1 protein
Γ				ne, macropain) 26S	proteasome (prosome, macropain) 26S
1909	1909 592_at	PSMC3	M34079	subunit, ATPase, 3	subunit, ATPase, 3
				proteasome (prosome, macropain) 26S	
1910	1910 37766_s_at	PSMC5	AF035309	subunit, ATPase, 5	
				proteasome (prosome, macropain) 26S	
1911	1911 949_s_at	PSMC6	D78275	subunit, ATPase, 6	proteasome subunit p42
				proteasome (prosome, macropain) 26S	
1912	912 1314_at	PSMD1	D44466	subunit, non-ATPase, 1	proteasome subunit p112
				proteasome (prosome, macropain) 26S	
1913	1913 1192 at	PSMD12	AB003103	subunit, non-A1Pase, 12	Zos proteasorne suburni pos
			_	proteasome (prosome, macropain) 26S	proteasome (prosome, macropain) 265
1914	1914 32240_at	PSMD5	D31889	subunit, non-ATPase, 5	subunit, non-ATPase, 5
				SHS (niscone macronal DRS	
1915	1915 945 at	PSMD7	D50063	subunit, non-ATPase, 7 (Mov34 homolog) proteasome subunit p40 / Mov34 protein	proteasome subunit p40 / Mov34 protein
			i	proteasome (prosome, macropain) 26S	
1916	1916 40276_at	PSMD7	D50063	subunit, non-A l Pase, 7 (Mov34 homolog)	proteasome subunit p40 / Mov34 protein
				proteasome (prosome, macropain) 26S	_
1917	1917 32584_at	PSMD8	D38047	subunit, non-ATPase, 8	26S proteasome subunit p31
				proteasome (prosome, macropain) 26S	
1918	1918 36492_at	PSMD9	Al347155	subunit, non-ATPase, 9	
				proteasome (prosome, macropain)	
1919	1919 41171_at	PSME2	D45248	activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
				proteasome (prosome, macropain)	
1920	1920 1184_at	PSME2	D45248	activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
				proteasome (prosome, macropain)	
1921	1921 36974 at	PSMF1	D88378	inhibitor subunit 1 (PI31)	proteasome inhibitor hPI31 subunit
				proteasome (prosome, macropain)	
1922	1922 38371_at	PSMA1	M64992	subunit, alpha type, 1	prosomal protein P30-33K
				proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit;
1923	1923 1446_at	PSMA2	D00760	subunit, alpha type, 2	alpha type, 2
				proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
1924	1924 1448 at	PSMA3	D00762	subunit, alpha type, 3	laipna type, 3



PSMA4 D00763 subunit, alpha type, 4						
PSMA4 D00763 Subunit, alpha type, 4		¥	മ	ပ		LJ.
PSMA4 D00763 Stubunit, alpha type, 4 proteasome (prosome, macropain) PSMA4 D00763 subunit, alpha type, 5 proteasome (prosome, macropain) PSMA5 A1246726 subunit, alpha type, 5 proteasome (prosome, macropain) PSMB1 D00761 subunit, alpha type, 6 proteasome (prosome, macropain) PSMB2 D26599 subunit, beta type, 1 proteasome (prosome, macropain) PSMB4 D26600 subunit, beta type, 4 macropain) PSMB4 D26600 subunit, beta type, 4 macropain) PSMB5 D29011 subunit, beta type, 6 proteasome (prosome, macropain) PSMB6 D29011 subunit, beta type, 6 proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 6 proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) PSMB9 A4808961 proteasome (prosome, macropain	100,	0.47	7 4 7 4 7	202000		proteasome (prosome, macropain) subunit,
PSMA4 D00763 subunit, alpha type, 4 subunit, alpha type, 4 subunit, alpha type, 5 proteasome (prosome, macropain) str PSMA6 X59417 subunit, alpha type, 6 proteasome (prosome, macropain) subunit, alpha type, 6 proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 4 proteasome (prosome, macropain) subunit, beta type, 4 proteasome (prosome, macropain) subunit, beta type, 5 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional subunit, beta type, 7 subunit, beta type, 7 subunit, beta t	1925	1450_g_at	PSMA4	D00/63		alpina type, 4
PSMA4 D00763 subunit, alpha type, 4						proteasome (prosome, macropain) subunit,
proteasome (prosome, macropain) at PSMA6 X59417 subunit, alpha type, 5 proteasome (prosome, macropain) PSMB1 D00761 subunit, alpha type, 5 proteasome (prosome, macropain) PSMB1 D00761 subunit, beta type, 1 proteasome (prosome, macropain) PSMB4 D26600 subunit, beta type, 4 proteasome (prosome, macropain) PSMB4 D26600 subunit, beta type, 4 proteasome (prosome, macropain) PSMB4 D26600 subunit, beta type, 4 proteasome (prosome, macropain) at PSMB5 D29011 subunit, beta type, 6 proteasome (prosome, macropain) at PSMB7 D38048 subunit, beta type, 6 proteasome (prosome, macropain) at PSMB7 D38048 subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (pros	1926	1449_at	PSMA4	D00763		alpha type, 4
PSMA5 Al246726 Subunit, alpha type, 5					proteasome (prosome, macropain)	
PSMA6 X59417 Subunit, alpha type, 6	1927	37046_at	PSMA5	AI246726	subunit, alpha type, 5	
PSMA6 X59417 Subunit, alpha type, 6					proteasome (prosome, macropain)	
PSMB1 D00761 Subunit, beta type, 1	1928	36122_at	PSMA6	X59417		prosomal P27K protein
PSMB1 D00761 Subunit, beta type, 1 PSMB2 D26599 Subunit, beta type, 2 Proteasome (prosome, macropain) PSMB4 D26600 Subunit, beta type, 4 PSMB4 D26600 Subunit, beta type, 4 PSMB4 D29011 Subunit, beta type, 6 Proteasome (prosome, macropain) PSMB5 D29012 Subunit, beta type, 6 Proteasome (prosome, macropain) PSMB5 D29012 Subunit, beta type, 6 Proteasome (prosome, macropain) PSMB7 D38048 Subunit, beta type, 7 PSMB7 D38048 Subunit, beta type, 9 (large multifunctional at PIAS3 A8021868 Protein calcivated STAT3 PRKCBP1 W22296 Protein inhibitor of activated STAT3 PRKCBP1 W32296 Protein kinase (cAMP-dependent, at PRKC1 L33881 Protein kinase C binding protein 1 PRKC1 L33881 Protein kinase C like 2 Protein kinase C like 2 PRKC1 L33881 Protein kinase C like 2 Protein kinase C like 2 PRKC1 L33881 Protein kinase C like 2 Protein kinase C like 2 PRKC1 L33881 Protein kinase C like 2 Protein kinase C like 2 PRKC1 PRKC1 L33881 Protein kinase C like 2 Protein kinase C like 2 PRKC1 L33881 Protein kinase C like 2 Protein kinase C like 2 PRKC1 L33881 Protein kinase C like 2 Protein kinase C like 2 PRKC1 L33881 Protein kinase C like 2 Protein kinase C like 2 PRKC1 L33881 Protein kinase C like 2 PRKC1 PR						proteasome (prosome, macropain) subunit,
PSMB2 D26599 Subunit, beta type, 2	1929	1447_at	PSMB1	D00761		beta type, 1
PSMB2 D26599 Subunit, beta type, 2 PSMB4 D26600 Subunit, beta type, 4					ne, macropain)	
PSMB4 D26600 subunit, beta type, 4 proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional proteasome) protein disultide isomerase-related protein the protein protein inhibitor of activated STAT3 protein inhibitor of activated STAT3 protein inhibitor of activated STAT3 protein kinase (cAMP-dependent, catalytic) inhibitor gamma protein kinase (cital protein kinase C, iota prote	1930	1310_at	PSMB2	D26599		proteasome subunit HsC7-I
PSMB4 D26600 Subunit, beta type, 4					ie, macropain)	
PSMB4 D26600 subunit, beta type, 4 PSMB5 D29011 subunit, beta type, 5 PSMB5 D29011 subunit, beta type, 5 PSMB6 D29012 subunit, beta type, 6 PSMB7 D38048 subunit, beta type, 6 PSMB7 D38048 subunit, beta type, 7 PTOTE SUBUNIT, beta type, 7 PTOTE SUBUNIT, beta type, 7 PTOTE SUBUNIT, beta type, 7 PTOTE SUBUNIT, beta type, 7 PTOTE SUBUNIT, beta type, 7 PTOTE SUBUNIT, beta type, 7 PTOTE SUBUNIT, beta type, 7 PTOTE SUBUNIT, beta type, 7 PTOTE SUBUNIT, beta type, 7 PTOTE SUBUNIT, beta type, 7 PTOTE SUBUNIT, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional protease 2) at PSMB9 AA808961 protein disulfide isomerase-related protein at PRKCBP1 W22296 protein inhibitor of activated STAT3 AB019517 catalytic) inhibitor gamma at PRKCI L33881 protein kinase C binding protein 1 THE PRKCI L33881 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota PRKCI L33881 protein kinase C-like 2	1931	33154_at	PSMB4	D26600		proteasome subunit HsN3
PSMB4 D26600 Subunit, beta type, 4						
PSMB5 D29011 subunit, beta type, 5 proteasome (prosome, macropain) PSMB6 D29012 subunit, beta type, 6 proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) PSMB9 AA808961 protein disultide isomerase-related protein PHXG8 AB021868 protein inhibitor of activated STAT3 PRKCBP1 W22296 protein kinase (CAMP-dependent, protein kinase (CAMP-dependent, protein kinase C binding protein 1 PRKC1 L33881 protein kinase C, iota PRKC1 L33881 protein kinase C, iota PRKC12 U33052 protein kinase C- like 2	1932	1311_at	PSMB4	D26600		proteasome subunit HsN3
PSMB5 D29011 subunit, beta type, 5 PSMB6 D29012 subunit, beta type, 6 PSMB7 D38048 proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) protein disultide isomerase-related protein protein disultide isomerase-related protein protein kinase (cAMP-dependent, macropain) protein kinase C binding protein 1 protein kinase C binding protein 1 protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota					proteasome (prosome, macropain)	•
PSMB6 D29012 subunit, beta type, 6 proteasome (prosome, macropain) tr PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropai	1933	37666_at	PSMB5	D29011	subunit, beta type, 5	proteasome subunit X
PSMB6 D29012 Subunit, beta type, 6					proteasome (prosome, macropain)	
proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropa	1934	941_at	PSMB6	D29012	subunit, beta type, 6	proteasome subunit Y
PSMB7 D38048 Subunit, beta type, 7				-	proteasome (prosome, macropain)	
PSMB7 D38048 Subunit, beta type, 7	1935	39060_at	PSMB7	D38048	subunit, beta type, 7	proteasome subunit z
PSMB7 D38048 Subunit, beta type, 7					proteasome (prosome, macropain)	
Proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional protease 2)	1936	1313_at	PSMB7	D38048	subunit, beta type, 7	proteasome subunit z
PSMB9 AA808961 protease 2) , orden disulfide isomerase-related protein PIAS3 AB021868 protein inhibitor of activated STAT3 protein kinase (cAMP-dependent, AB019517 catalytic) inhibitor gamma pRKCBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C-like 2					proteasome (prosome, macropain)	
PSMB9 AA808961 protease 2) , P5 D49489 protein disulfide isomerase-related protein PIAS3 AB021868 protein inhibitor of activated STAT3 PKIG AB019517 catalytic) inhibitor gamma PRKCBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota					subunit, beta type, 9 (large multifunctional	
P5 D49489 protein disulfide isomerase-related protein PIAS3 AB021868 protein inhibitor of activated STAT3 PRICG AB019517 catalytic) inhibitor gamma PRKCBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota PRKCI L33881 protein kinase C, iota PRKCI L33881 protein kinase C, iota PRKCI L33881 protein kinase C, iota	1937	38287_at	PSMB9	AA808961	protease 2)	
PIAS3 AB021868 protein inhibitor of activated STAT3 PKIG AB019517 catalytic) inhibitor gamma PRKCBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota at PRKCI L33881 protein kinase C, iota PRKCI L33881 protein kinase C, iota protein kinase C, iota	1938	41750 at	P.5	D49489	protein disulfide isomerase-related protein	human P5
at PKIG AB019517 catalytic) inhibitor gamma at PRKCBP1 W22296 protein kinase C binding protein 1 at PRKCI L33881 protein kinase C, iota at PRKCI L33881 protein kinase C, iota at PRKCI U33052 protein kinase C-like 2	1939	32558 at	PIAS3	AB021868	protein inhibitor of activated STAT3	protein inhibitor of activatied STAT3
PKIG AB019517 catalytic) inhibitor gamma PRKCBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota II PRKCI L33881 protein kinase C, iota PRKCI 2 U33052 protein kinase C-like 2					protein kinase (cAMP-dependent,	
at PRKCBP1 W22296 protein kinase C binding protein 1 at PRKCI L33881 protein kinase C, iota at PRKCI L33881 protein kinase C, iota at PRKCI U33052 protein kinase C-like 2	1940	34376_at	PKIG	AB019517	catalytic) inhibitor gamma	protein kinase inhibitor gamma
at PRKCI L33881 protein kinase C, iota 1 at PRKCI L33881 protein kinase C, iota at PRKCI U33052 protein kinase C-like 2	1941	36957_at	PRKC8P1	W22296	protein kinase C binding protein 1	
at PRKCI L33881 protein kinase C, iota	1942	1602_at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
at PRKCL2 U33052 brotein kinase C-like 2	1943	1603_g_at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
	1944	36835 at	PRKCL2	U33052	protein kinase C-like 2	PRK2



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!				e I, alpha (tissue specific	cAMP-dependent protein kinase type I-alpha
1945	1945 41768_at	PHKAH1A	M33336		SUDULIR
				e I, alpha (tissue specific	cAMP-dependent protein kinase type I-alpha
1946	1946 227_g_at	PRKAR1A	M33336		subunit
Γ				protein kinase, cAMP-dependent,	
				I, alpha (tissue specific	cAMP-dependent protein kinase type I-alpha
1947	1947 226_at	PRKAR1A	M33336		subunit
				notain kinasa interferon-induciple duuble	protein activator of the interferon-induced
194R	1948 32205 at	PRKRA	AF072860	stranded RNA dependent activator	protein kinase
				bunit,	serine /threonine specific protein
1949	1949 37725_at	PPP1CC	X74008		phosphatase
				protein phosphatase 1, regulatory	
1950	1950 40438_at	PPP1R12A	D87930	(inhibitor) subunit 12A	myosin phosphatase target subunit 1
				protein phosphatase 1, regulatory	
1951	1951 39366_at	PPP1R3C	N36638	(inhibitor) subunit 3C	
				protein phosphatase 1, regulatory subunit	
1952	1952 41540_at	PPP1R7	250749	7	yeast sds22 homolog
				protein phosphatase 1A (formerly 2C),	
1953	1953 857_at	PPM1A	S87759	magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
				protein phosphatase 1A (formerly 2C),	
1954	1954 36501_at	PPM1A	S87759	magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
				protein phosphatase 1D magnesium-	
1955	1955 37107_at	PPM1D	U78305	dependent, delta isoform	Wip1
				protein phosphatase 2 (formerly 2A),	
1956	1956 924_s_at	PPP2CB	J03805	catalytic subunit, beta isoform	
				protein phosphatase 2 (formerly 2A),	•
				regulatory subunit B (PR 52), alpha	
1957	1957 41167_at	PPP2R2A	M64929	isoform	protein phosphatase-2A subunit-alpha
				protein phosphatase 2 (formerly 2A),	
				regulatory subunit B (PR 52), alpha	
1958	1958 1383_at	PPP2R2A	M64929	isoform	protein phosphatase-2A subunit-alpha
1959	1959 32734 at	PPP2R5E	L76703	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	protein phosphatase B56-epsilon



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				egulatory subunit	protein phosphatase 2A Balpha1 regulatory
1960	960 40786_at	PPP2R5C	U37352		subunit
				protein phosphatase 2, regulatory subunit	protein phosphatase 2A B'alpha1 regulatory
1961	176 at	PPP2R5C	U37352	B (B56), gamma isoform	subunit
	1			protein phosphatase 2A, regulatory	
1962	1962 39127 f at	PPP2R4	X73478	subunit B' (PR 53)	phosphotyrosyl phosphatase activator
	∦ .			protein phosphatase 3 (formerly 2B),	protein phosphatase 3 (formerly 2B),
				catalytic subunit, beta isoform (calcineurin	catalytic subunit, beta isoform (calcineurin catalytic subunit, beta isoform (calcineurin A
1963	38277 at	PPP3CB	M29550	A beta)	beta)
				protein phosphatase 3 (formerly 2B),	
				catalytic subunit, gamma isoform	
1964	1964 32541 at	PPP3CC	S46622	(calcineurin A gamma)	calcineurin A catalytic subunit
	u			protein phosphatase 4, regulatory subunit	
1965	1965 34371_at	PPP4R1	U79267	-	
		0	70007	anotoin phoenhataea & catalytic cubunit	protein phosphatase 6
1966	1966 37581_at	rrrec	735312	plotelli pilospilatase e, catalytis casalini	Colpbs)
1967	1967 35752_s_at	PROS1	M15036	protein S (alpha)	protein S (alpha)
1968	1968 32564 at	SEC61B	AA083129	protein translocation complex beta	
1969	1969 1064 at	PTK9	U02680	protein tyrosine kinase 9	protein tyrosine kinase
				protein tyrosine phosphatase type IVA,	
1970	1970 843 at	PTP4A1	U48296	member 1	protein tyrosine phosphatase PTPCAAX1
	1			protein tyrosine phosphatase type IVA,	
1971	38415 at	PTP4A2	U14603	member 2	protein-tyrosine phosphatase
				protein tyrosine phosphatase type IVA,	
1972	1972 1241 at	PTP4A2	U14603	member 2	protein-tyrosine phosphatase
				protein tyrosine phosphatase, non-	protein tyrosine phosphatase, non-receptor
1973	1973 40137 at	PTPN1	M31724	receptor type 1	type 1
	i			protein tyrosine phosphatase, non-	
1974	1974 1463 at	PTPN12	M93425	receptor type 12	protein tyrosine phosphatase
	1			protein tyrosine phosphatase, non-	
1075	1075 94100 01	DTDN13	1112128	associated phosphatase)	protein tyrosine phosphatase 1E
	04130 at		221212		protein tyrosine phosphatase, receptor type,
					A, isoform 1 precursor; protein tyrosine
			٠	protein tyrosine phosphatase, receptor	phosphatase, receptor type, A, isoform 2
1976	1976 1496_at	PTPRA	M34668	type, A	precursor

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				tyrosine phosphatase, receptor	
1977	36204_at	PTPRF	Y00815		put. LAR preprotein (AA -16 to 1881)
				protein tyrosine phosphatase, receptor	
	000	i i	0,000	type, f polypeptide (PTPRF), interacting	Ab disconsisted and a second s
19/8	19/8 41/80_at	PFFIAI	022816	protein (liptili), alpha i	מו ווופוסול (פווויסופוווי-חאר)
				lyrosine phosphatase, receptor	
1979	1488_at	PTPRK	L77886	type, K	protein tyrosine phosphatase
				protein tyrosine phosphatase, receptor	
1980	995_g_at	PTPRM	X58288	type, M	protein-tyrosine phosphatase
				protein tyrosine phosphatase, receptor	
1981	31892_at	PTPRM	X58288	type, M	protein-tyrosine phosphatase
				protein-kinase, interferon-inducible double	
				stranded RNA dependent inhibitor,	
1982	1982 41141_at	PRKRIR	AL049970	repressor of (P58 repressor)	hypothetical protein
				protein-L-isoaspartate (D-aspartate) O-	
1983	983 37737_at	PCMT1	D25547	methyltransferase	PIMT isozyme I
				protein-L-isoaspartate (D-aspartate) O-	
1984	1984 37736_at	PCMT1	D13892	methyltransferase	carboxyl methyltransferase
1985	32227_at	PRG1	X17042	proteoglycan 1, secretory granule	proteoglycan 1, secretory granule
1986	38590_r_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1987	38589_i_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1988	37936_at	HPRP4P	AI184802	PRP4/STK/WD splicing factor	
				pseudoferritin H protein; Human ferritin H	
1989	1989 31697_s_at	FTHP1	J04755	processed pseudogene, complete cds.	
1990	1990 36117_at	PTK2	L13616	PTK2 protein tyrosine kinase 2	focal adhesion kinase
1991	1991 40048_at	PUM1	D43951	pumilio homolog 1 (Drosophila)	KIAA0099 protein
1992	1992 35359_at	PUM2	D87078	pumilio homolog 2 (Drosophila)	KIAA0235 protein
1993	1993 35221_at	PURA	X91648	purine-rich element binding protein A	
				put. ORFX (AA 1-75); beta subunit (AA 1-	
				340); Human liver mHNA for beta-subunit	
				signal transducing proteins Gs/Gi (beta-	guanine nucleotide-binding protein, beta-1
1994	1994 33341_at	GNB1	X04526	(G).	subunit
1995	995 33720_at	LOC56902	L48692	putatative 28 kDa protein	
1996	1996 39363 at	BC-2	AF042384	putative breast adenocarcinoma marker (32kD)	BC-2 protein

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1997	1997 39884 g at	HSA9761	AF091078	putative dimethyladenosine transferase	putative dimethyladenosine transferase
				putative glialblastoma cell differentiation-	putative glialblastoma cell differentiation-
1998	1998 38841_at	GDBR1	AF068195	related	related protein
1999	1999 41188 at	LC27	W28186	putative integral membrane transporter	
				putative L-type neutral amino acid	
2000	2000 38984_at	KIAA0436	AB007896	transporter	
2001	2001 39116_at	LOC54499	AF070626	putative membrane protein	
000				mutativa mudaic acid hinding protein BY-1 pucleic acid binding protein	nucleic acid binding protein
2002	2002 33200 I al	- 10	70001	Putative prostate cancer tumor	
2003	2003 36852 at	N33	U42349	suppressor	
				putative protein similar to nessy	
2004	2004 33710_at	C3F	U72515		C3f
2005	40203 at	SUIT	AJ012375	or	putative translation initiation factor
2006	2006 37678 at	NMA	U23070	putative transmembrane protein	putative transmembrane protein
				putative transmembrane protein; homolog	
				of yeast Golgi membrane protein Yil1p	
2007	2007 35326_at	54TM	AF004876	(Yip1p-interacting factor)	54 I Mp
				putative; Homo sapiens PTS gene,	
2008	2008 35697 at	PTS	L76259		6-pyruvoyltetrahydropterin synthase
				putative; originaly identified as an	
				oncogene', product renamed by NCBI	
			-	staff; Homo sapiens longation factor 1-	
2005	2009 40887 q at	PTI-1	L41498	alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
				putative; originaly identified as an	
				oncogene', product renamed by NCBI	
				staff; Homo sapiens longation factor 1-	
2010	2010 40886 at	PTI-1	L41498	alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
				pVHL-interacting deubiquitinating enzyme	
2011	2011 33219 at	VDU1	AB029020		KIAA1097 protein
				Pyruvate dehydrogenase complex, lipoyl- containing component X: E3-binding	pyruvate dehydrogenase complex protein X
201;	2012 36164 at	PDX1	U82328	protein	subunit precursor
Š	2013 32378 at	PKM2	M26252	pyruvate kinase, muscle	pyruvate kinase, muscle
۲	2014 260 at	ODPR	M16447	quinoid dihydropteridine reductase	quinoid dihydropteridine reductase

Fig. 21

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1	10000	ВЗНОМ	N21852	R3H domain (binds single-stranded	KIAAC029 protein
	20010_al	NO LONG	A 1400E94	Pa	prenylated Rab acceptor 1 (PRA1)
	2016 39030_at	HABACI	AU 135354		to the second and second and the sec
- 12	2017 37703 at	BABGGTB	708201	Rab geranyigeranyiransi erase, beta subunit	rab geranylgeranyl transferase
180	2018 38264 at	RABIF	U74324	eracting factor	guanine nucleotide exchange factor mss4
					100 P
019	2019 36660_at	RAB11A	AF000231	<u>_</u>	rabila
020	2020 35325_at	RAB14	AF052113		
120	2021 34393 r at	RAB1A	AL050268	ヿ	hypothetical protein
022	2022 34392_s_at	RAB1A	AL050268		hypothetical protein
023	2023 33326_at	RAB21	D42087	RAB21, member RAS oncogene family	RAB21, member RAS oncogene family
1004	2024 809 at	RAB27A	U57094	BAB27A. member RAS oncogene family	Rab27a
25.5	2025 33371 s at	RAB31	U59877	RAB31, member RAS oncogene family	low-Mr GTP-binding protein Rab31
026	ĕ	RABSA	M28215	RAB5A, member RAS oncogene family	GTP-binding protein
				rab6 GTPase activating protein (GAP and	
027	2027 35289 at	GAPCENA	AJ011679	centrosome-associated)	Rabe GTPase activating protein, GAPCenA
2028	2028 35304 at	RABGA	AF052130	RAB6A, member RAS oncogene family	
2029	2029 39628 at	RAB9A	AI671547	RAB9A, member RAS oncogene family	
2030	2030 41716 at	RC3	AB020663	rabconnectin-3	KIAA0856 protein
				Rac/Cdc42 guanine nucleotide exchange	
2031	2031 37543_at	ARHGEF6	D25304	factor (GEF) 6	
2032	2032 36857_at	RAD1	AF084513	RAD1 homolog (S. pombe)	DNA repair exonuclease
2033	2033 38114 at	RAD21	D38551	RAD21 homolog (S. pombe)	RAD21 homolog
2034	2034 1874 at	RAD23B	D21090	RAD23 homolog B (S. cerevisiae)	XP-C repair complementing protein (p58/HHR23B)
2035	2035 32757 at	RAE1	U84720	RAE1 RNA export 1 homolog (S. pombe)	mRNA export protein
				RAGE-4 ORF2; one of 2 possible coding regions; RAGE-4 ORF3; one of 2 possible	
				carcinoma antigen RAGE-4 mRNA,	
2036	2036 1524_at		U46194	complete putative cds.	
2037	2037 36628_at	RALBP1	L42542	ralA binding protein 1	RLIP76 protein
2038	2038 37539_at	RGL	AB023176	RalGDS-like gene	KIAA0959 protein

Fig :31

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	A	В	C	_	П
2039	2039 41342_at	RANBP1	D38076		Ran-BP1(Ran-binding protein 1)
2040	2040 40824 at	RANBP16	AB018288		KIAA0745 protein
2041	2041 41174 at	RANBP2L1	AF012086	ike 1	Ran binding protein 2
2042	2042 35255_at	RANBP7	AF098799		RanBP7/importin 7
2043	2043 32602 at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1 smg GDS	smg GDS
2044	2044 1848 at	RAP1A	M22995	RAP1A. member of RAS oncogene family ras-related protein	ras-related protein
					in standard and a second
2043	2045 40146_at	HAPIB	ALUGUZ 12	Ras association (BalGDS/AF-6) domain	Ilyportieneal Process
2046	2046 39601 at	RASSF1	AF061836		putative tumor suppressor protein
				Ras association (RalGDS/AF-6) domain	Ras association (RaIGDS/AF-6) domain
2047	2047 37598_at	RASSF2	D79990	family 2	family 2
2048	2048 1659_s_at	RHEB2	D78132	Ras homolog enriched in brain 2	ras-related GTP-binding protein
2049	2049 37309_at	ARHA	L09159	ras homolog gene family, member A	multidrug resistance protein
2050	2050 1394_at	ARHA	L25080	ras homolog gene family, member A	GTP-binding protein
2051	2051 35803_at	ARHE	S82240	ras homolog gene family, member E	RhoE
				RAS p21 protein activator (GTPase	
2052	2052 36935_at	RASA1	M23379	activating protein) 1	GTPase-activating protein
				RAS p21 protein activator (GTPase	
2053	2053 1675_at	RASA1	M23379	activating protein) 1	GTPase-activating protein
				Ras-GTPase activating protein SH3	
2054	2054 35793_at	G3BP2	AB014560	domain-binding protein 2	KIAA0660 protein
				ras-related C3 botulinum toxin substrate 1	
				(rho family, small GTP binding protein	
2055	2055 40864_at	RAC1	D25274	Rac1)	
				ras-related C3 botulinum toxin substrate 1	ras-related C3 botulinum toxin substrate 1
				(rho family, small GTP binding protein	isoform Rac1; ras-related C3 botulinum toxin
2056	2056 2050 s_at	RAC1	M29870	Rac1)	substrate 1 isoform Rac1b
2057	2057 35316_at	RAGA	U41654	Ras-related GTP-binding protein	adenovirus E3-14.7K interacting protein 1
2058	2058 33234_at	BCAA	AA887480	RBP1-like protein	
2059	2059 41407_at	RDBP	L03411	RD RNA-binding protein	RD protein
2060	2060 34684 at	BECO	136140	Beco protein-like (DNA helicase Q1-like) DNA helicase	DNA helicase
3	100to	וורספני	1000		

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	RECOL	AI685944	RecQ protein-like (DNA helicase Q1-like)	
1			regulated at the translational level; contains I-mfa domain; untilizes unique GTG start codon; Homo sapiens HIC	HIC protein isoform p40: HIC protein isoform
	H	AF054589	isoform p32 mRNAs, complete cds.	p32
l	70000	0 F C C C C C	regulator of G-protein signalling 19	
	RGS2	1 13463	regulator of G-protein signalling 2, 24kD	helix-loop-helix phosphoprotein
1	RENT2	AL080198	regulator of nonsense transcripts 2	hypothetical protein
	RRAS2	Al365215	related RAS viral (r-ras) oncogene homolog 2	
ŀ	1 1 2001 7	000	remainder of gene in clone 549K18	COLET Profesio
	t: / 106 / CD	ALCCCCC	(100001)	
	RFC4	M87339	replication factor C (activator 1) 4 (37kD)	replication factor C, 37-kDa subunit
	RPA1	M63488	replication protein A1 (70kD)	replication protein A, 70-kDa subunit
	RPA3	L07493	replication protein A3 (14kD)	replication protein A 14kDa subunit
	RCOR	D31888	REST corepressor	REST corepressor
			restin (Reed-Steinberg cell-expressed	-
	RSN	X64838	intermediate filament-associated protein)	restin
	RFP2	AJ224819	ret finger protein 2	tumor suppressor
İ	1	010010	reticulocalbin 1, EF-hand calcium binding	rid cooling
		0,4557.0	reticulocalbin 2, EF-hand calcium binding	
	RCN2	X78669	domain	EF-hand protein
			reticulocalbin 2, EF-hand calcium binding	
	RCN2	X78669	domain	EF-hand protein
	RTN4	AB020693	reticulon 4	KIAA0886 protein
	RP2	AJ007590	retinitis pigmentosa 2 (X-linked recessive)	
	RPGR	U57629	retinitis pigmentosa GTPase regulator	retinitis pigmentosa GTPase regulator
	R81	M15400	retinoblastoma 1 (including osteosarcoma)	retinoblastoma 1 (including osteosarcoma)
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2081	2081 35227_at	RBBP8	U72066		CtBP interacting protein CtIP
2082	33860_at	RBAF600	AB007931	retinoblastoma-associated factor 600	KIAA0462 protein
2083	2083 32597_at		X76061	retinoblastoma-like 2 (p130)	130K protein
2084	2084 35848_at	RAI17	AL049432	retinoic acid induced 17	
				retropseudogene, Human retropseudogene MSSP-1 DNA, complete	
2085	2085 31672 g at	RBMS1P; MSSP1	1 D82351	cds.	MSSP-1
				REV3-like, catalytic subunit of DNA	
2086	2086 38908_s_at	REV3L	AL096744	polymerase zeta (yeast)	hypothetical protein
				reversion-inducing-cysteine-rich protein	
2087	2087 35236_g_at	RECK	AA099265	with kazal motifs	
				reversion-inducing-cysteine-rich protein	
2088	2088 35235_at	RECK	AA099265	with kazal motifs	
				reversion-inducing-cysteine-rich protein	
2089	2089 35234_at	RECK	D50406	with kazal motifs	RECK protein precursor
2090	2090 553_g_at	ARHGAP1	U02570	Rho GTPase activating protein 1	CDC42 GTPase-activating protein
2091	39700_at	ARHGAP1	Al961929	Rho GTPase activating protein 1	
				Rho guanine nucleotide exchange factor	
2092	2092 34180_at	ARHGEF10	AB002292	(GEF) 10	Rho guanine nucleotide exchange factor 10
				Rho guanine nucleotide exchange factor	
2093	2093 40828_at	ARHGEF7	D63476	(GEF) 7	PAK-interacting exchange factor beta
				rho/rac guanine nucleotide exchange	
2094	2094 40100_at	ARHGEF2	U72206	factor (GEF) 2	guanine nucleotide regulatory factor
				Rho-specific guanine nucleotide exchange	
2095	2095 36537_at	P114-RHO-GEF	AB011093	factor p114	KIAA0521 protein
2096	2096 41040_at	RPP38	U77664	ribonuclease P (38kD)	RNaseP protein P38
2097	2097 32664_at	RNASE4	D37931	ribonuclease, RNase A family, 4	RNase 4
209	2098 36187_at	RNH	X13973	ribonuclease/angiogenin inhibitor	ribonuclease/angiogenin inhibitor
2095	2099 34314 at	BRM1	X59543	ribonucleotide reductase M1 polypeptide	M1 subunit of ribonucleotide reductase
2100	2100 2016 s at	RPL10	M64241	ribosomal protein L10	Wilm's tumor-related protein
2101	2101 41178 at	RPL11	X79234	ribosomal protein L11	ribosomal protein L11
2102	2102 33668_at	RPL12	AF037643	ribosomal protein L12	
210	2103 31509_at	RPL13	X64707	ribosomal protein L13	ribosomal protein L13
5 10 10	2104 35119_at	RPL13A	X56932	ribosomal protein L13a	23 kD highly basic protein
2 10 10 10	2105 31907_at	RPL14	D87735	ribosomal protein L14	ribosomal protein L14

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2106 32432	7/-	RPI 15	1 25899	ribosomal profein L15	ribosomal protein L10
2107 32440	. 1 63	RPL17	X53777	ribosomal protein L17	ribosomal protein L17
2108 31546	46_at	RPL18	L11566	ribosomal protein L18	ribosomal protein L18
2109 33614_at	14_at	RPL18A	X80822	ribosomal protein L18a	ribosomal protein L18a
2110 32435	35_at	RPL19	X63527	ribosomal protein L19	ribosomal protein L19
2111 32337	37_at	RPL21	U25789	ribosomal protein L21	ribosomal protein L21
2112 33451_s	51_s_at	RPL22	AI526079	ribosomal protein L22	
2113 32395_r	95_r_at	RPL23	X55954	ribosomal protein L23	HL23 ribosomal protein
2114 32394_s_at	94_s_at	RPL23	X55954	ribosomal protein L23	HL23 ribosomal protein
2115 32341_f	41_f_at	RPL23A	U37230	ribosomal protein L23a	ribosomal protein L23a
2116 33677_at	77_at	RPL24	M94314	ribosomal protein L24	ribosomal protein L30
2117 32444_at	44_at	RPL26	X69392	ribosomal protein L26	ribosomal protein L26
2118 39830_at	30_at	RPL27	AA044823	ribosomal protein L27	
2119 32436_at	36_at	RPL27A	U14968	ribosomal protein L27a	ribosomal protein L27a
2120 31708_at	08_at	RPL30	L05095	ribosomal protein L30	ribosomal protein L30
2121 33676_at	76_at	RPL31	X15940	ribosomal protein L31	ribosomal protein L31
2122 32276_at	76_at	RPL32	X03342	ribosomal protein L32	ribosomal protein L32
2123 33657_at	57_at	RPL34	L38941	ribosomal protein L34	ribosomal protein L34
2124 41765_at	'65_at	RPL35	AI541285	ribosomal protein L35	
2125 41152_	52_f_at	RPL36A	T89651	ribosomal protein L36a	
2126 33656	56_at	RPL37	D23661	ribosomal protein L37	ribosomal protein L37
2127 31962	62_at	RPL37A	L06499	ribosomal protein L37a	ribosomal protein L37a
2128 34085_at	185_at	RPL38	226876	ribosomal protein L38	ribosomal protein
2129 33485_at	185_at	RPL4	D23660	ribosomal protein L4	ribosomal protein
					human homologue to yeast ribosomal
2130 32466_at	166_at	RPL41	212962	ribosomal protein L41,	protein YL41
2131 33660	360_at	RPL5	U14966	ribosomal protein L5	ribosomal protein L5
2132 319	31952_at	RPL6	X69391	ribosomal protein L6	ribosomal protein L6
2133 36333	333_at	RPL7	X57958	ribosomal protein L7	ribosomal protein L7
2134 315	31505_at	RPL8	228407	ribosomal protein L8	ribosomal protein L8
2135 315	31568_at	RPS10	U14972	ribosomal protein S10	ribosomal protein S10
2136 32330_at	330_at	RPS11	X06617	ribosomal protein S11	ribosomal protein S11
2137 33116_	116_f_at	RPS12	AA977163	ribosomal protein S12	
2138 33619_at	519_at	RPS13	L01124	ribosomal protein S13	ribosomal protein S13
2139 34317	317_g_at	RPS15A	W52024	ribosomal protein S15a	ribosomal protein S15a
2140 38061	J61_at	RPS16	AI541256	ribosomal protein S16	

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2141 34	34593_g_at	RPS17			ribosomal protein 517
2142 34592	4592_at	RPS17	M13932		ribosomal protein S17
1433	2143 31330_at	RPS19	M81757	ribosomal protein S19	S19 ribosomal protein
1443	2144 31527 at	RPS2	X17206		ribosomal protein S2
2145 32438	2438_at	RPS20	L06498	ribosomal protein S20	ribosomal protein S20
1463	2146 347_s_at	RPS23	D14530	ribosomal protein S23	ribosomal protein
147 32	2147 32315_at	RPS24	M31520	ribosomal protein S24	ribosomal protein S24
2148 31573	1573_at	RPS25	M64716	ribosomal protein S25	ribosomal protein
-				ribosomal protein S27 (metallopanstimulin	
149 3	2149 32748_at	RPS27	AI557852	1)	
1503	2150 34570_at	RPS27A	S79522	ribosomal protein S27a	ubiquitin carboxyl extension protein
21513	2151 39798_at	RPS28	R87876	ribosomal protein S28	
21523	2152 34645_at	RPS3	X55715	ribosomal protein S3	ribosomal protein S3
2153 1653 at	653_at	RPS3A	M84711	ribosomal protein S3A	v-fos transformation effector protein
21543	2154 34643_at	RPS4X	M58458	ribosomal protein S4, X-linked	ribosomal protein S4X isoform
2155 32437	2437 at	RPS5	U14970	ribosomal protein S5	ribosomal protein S5
2156 31511	1511_at	RPS9	U14971	ribosomal protein S9	ribosomal protein S9
21573	2157 31538 at	RPLP0	M17885	ribosomal protein, large, P0	ribosomal protein P0
2158 31956_1	1956_f_at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
2159 31957	1957_r_at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
				ribosome binding protein 1 homolog	
21603	33213_g_at	RRBP1	AF006751	180kD (dog)	ES/130
				Ric-like, expressed in many tissues	
21613	38331_at	RIT	Y07566	(Drosophila)	Ric-like, expressed in many tissues
21623	2162 35656_at	RNF6	AJ010346	ring finger protein (C3H2C3 type) 6	RING-H2
21633	2163 39150_at	HNF11	U69559	ring finger protein 11	
21643	2164 35811_at	RNF13	AF037204	ring finger protein 13	RING zinc finger protein
21653	2165 33343_at	RNF14	AB022663	ring finger protein 14	ring finger protein 14
21663	2166 33484_at	RNF2	Y10571	ring finger protein 2	ring finger protein 2
21673	37964 at	RNF3	W25793	ring finger protein 3	
21683	35777_at	RNF4	AB000468	ring finger protein 4	zinc finger protein
				ring zinc-finger protein; escapes X	
				finder protein (ZNF127-Xp) gene and 5'	
2169 37650	37650 at	ZNF127-Xp	U41315	flanking sequence.	ZNF127-Xp
2170 37732	m ,	RYBP	AL049940	RING1 and YY1 binding protein	
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RNMT	-			ľ		1
RBMM1	1		1.	ט :	0	T
RBM14 AF080561 RNA binding motif protein 14	2171]3		RNMT	AB007858		HNA (guanine-7-) metnyitransterase
RBM3 U28686 RNA binding motif protein 3 RBM4 U88505 RNA binding motif protein 4 RBM5 AF091263 RNA binding motif protein 5 RNA binding motif protein 5 RNA binding motif protein 6 RNA binding motif protein 6 RNA binding motif protein 6 RNA binding motif protein 9 RNA binding motif protein 7 RNA binding motif protein 7 RNA binding protein 11 RNA binding protein 11 RNA binding protein 11 RNA binding protein 12 RNA binding protein 11 RNA Binding protein 12 RNA binding protein 6 Binding RNA RNA binding protein 12 RNA Binding protein 6 Binding RNA RNA binding protein gene with multiple 12 RNA Binding protein gene with multiple 13 RNA-binding protein gene with multiple 14 RNA Binding protein gene with multiple 15 RNA-binding protein regulatory subunit 15 RNA-binding protein gene with multiple 16 RNA Binding protein gene with multiple 16 RNA Binding protein gene with multiple 17 RNA-binding protein regulatory subunit 17 RNA-binding protein gene with multiple 18 RNA-binding protein regulatory subunit 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with multiple 18 RNA-binding protein gene with mul	2172 4	1460_at	RBM14	AF080561		SYT interacting protein SIP
RBM4 U89505 RNA binding motif protein 4 PBM5 AF091263 RNA binding motif protein 5 FAF081263 RNA binding motif protein 6 FAF08256 RNA binding motif protein 6 FAF08256 RNA binding motif protein 6 FAF08256 RNA binding motif protein 7 RNA binding motif protein 7 FAF08256 RNA binding protein 1 RNA DECENTION 1 RNA DECENTION 2 RNA DECENTION 2 RNA DECENTION 2 RNA DECENTION 3 RNA DECENT	21734	1741_at	RBM3	U28686		RNPL
RBM5 AF091263 RNA binding motif protein 5 RNA binding motif protein 6 RNA binding motif protein 6 RNA binding motif protein 9 RNA binding motif protein 9 RNA binding motif protein 9 RNA binding motif single stranded 1 Interacting protein 1 RNA binding motif single stranded 1 Interacting protein 1 RNA binding protein 1 RNAHP AF025654 RNA binding protein 61 RNAHP AF083255 RNA binding protein gene with multiple 1 RNAHP AF083255 RNA binding protein gene with multiple 1 RNAHP AF083255 RNA binding protein gene with multiple 1 RNAHP AF083255 RNA binding protein gene with multiple 1 RNA-binding protein regulatory subunit 2 RNA-binding protein regulatory subunit 3 RNA-binding protein RNP1 RRM RNA-binding protein (RNP1 RRM RNA-binding protein (RNB1 RRM RNA-binding protein All (RNB1 RRM RNA-binding protein All (RNB1 RRM RNA-binding protein All (RNB1 RRM RNA-binding protein All (RNB1 RRM RNA-binding protein All (RNB1 RRM RRM RNA-binding protein All (RNB1 RRM RRM RRM RRM RRM RRM RRM RRM RRM RR	21743	5351_at	RBM4	U89505		Hlark
RBM6	21753	2804_at	RBM5	AF091263	RNA binding motif protein 5	RNA binding motif protein 5
RBMS	21764		RBM6	AF069517	RNA binding motif protein 6	RNA binding protein DEF-3
RBMX 223064 RNA binding motif protein, X chromosome I RNA binding motif, single stranded interacting protein 1 RNA binding motif, single stranded interacting protein S1, serine-rich I RNA binding protein gene with multiple splicing RNA belicase family RNA helicase family f	21774		RBM9	AL009266	RNA binding motif protein 9	hypothetical protein
RNPS1 X77494 interacting protein 1 interacting protein 1 RNPS1 L37368 domain RNA binding protein 1 RNA binding protein 1 RNA B01834 RNA helicase and 5'- RNAHH AF022654 phosphatase RNAHH AF08255 RNA helicase related protein RNAHH AF08255 RNA helicase related protein RNAHP AF083255 RNA helicase related protein RNAHP AF083255 RNA-binding protein gene with multiple splicing RNA-binding protein gene with multiple splicing RNA-binding protein regulatory subunit RNPC2 L10910 containing 2 RNA-binding protein factor 1 (acute RTCD1 Y11651 RNA-binding protein factor 1 (acute myeloid leukemia 1; aml1 oncogene) RUVBL 1 Y18418 RuvB-like 1 (E. coli) RUVBL 2 AB024301 RuvB-like 2 (E. coli) S100A10 AI201310 polypeptide (p11))	21783	19731_at	RBMX	Z23064	RNA binding motif protein, X chromosome	hnRNP G protein
RBMS1					RNA binding motif, single stranded	RNA binding motif, single stranded
RNA binding protein S1, serine-rich domain	21793	13867_s_at	RBMS1	X77494	interacting protein 1	interacting protein 1, isoform a
RNPS1 L3736B domain RNA guanylyttransferase and 5'- RNA guanylyttransferase and 5'- RNAA0801 AF025654 phosphatase KIAA0801 AB018344 RNA helicase family RNAH AJ223948 RNA helicase family RNAH AF083255 RNA helicase-related protein RNAH AF083255 RNA helicase-related protein RNA-binding protein gene with multiple splicing RNA-binding protein gene with multiple splicing RNA-binding protein regulatory subunit RNA-binding cejon (RNP1, RRM) RMP AB006572 RPB5-mediating protein RTCD1 Y11651 RTC domain containing 1 RUNX1 D43968 RVB6-mediating protein RUVBL1 Y18418 RuvB-like 1 (E. coli) RUVBL2 AB024301 RuvB-like 2 (E. coli) RUVBL2 AB024301 RuvB-like 2 (E. coli) S100 calcium binding protein 1, light (annexin II ligand, calpactin 1, light S100 calcium binding protein 1, light (annexin II ligand, calpactin 1, light					RNA binding protein S1, serine-rich	
RNA guanylytransferase and 5'- RNAA0801	21803	16186_at	RNPS1	L37368	domain	RNA-binding protein
RNGTT					RNA guanylyltransferase and 5'-	
KIAA0801 AB018344 RNA helicase family RNAH AJ223948 RNA helicase related protein RNAHP AF083255 RNA helicase-related protein RNAHP AF083255 RNA helicase-related protein BNA-binding protein gene with multiple RNA-binding protein gene with multiple RNA-binding protein gene with multiple RNA-binding protein gene with multiple RNA-binding protein regulatory subunit RNA-binding protein regulatory subunit RNMP AB006572 RNMA-binding protein regulatory subunit RNA-binding protein RNMP AB006572 RNMA-binding protein RNA-binding protein RUNX1 DA3968 RUNK1 DA3968 RUVBL1 Y18418 RUVBL2 AB024301 RUVBL2 RuvB-like 1 (E. coli) RUVBL2 AB024301 RUNA1 RuvB-like 2 (E. coli) RUNA201310 Rolypeptide (p11)	2181	35202_at	RNGTT	AF025654	phosphatase	mRNA capping enzyme
RNAH AJ223948 RNA helicase family RNAHP AF083255 RNA helicase-related protein RNA-binding protein gene with multiple RNA-binding protein gene with multiple RBPMS D84109 splicing RBPMS D84109 RNA-binding protein gene with multiple RBPMS D84109 RNA-binding protein regulatory subunit RNA-binding protein regulatory subunit RNA-binding region (RNP1, RRM) RNA-binding protein regulatory subunit RNA-binding protein RNDC2 L10910 Containing 7 Containing 7 RTCD1 Y11651 RUNX1 RPB5-mediating protein RUNX1 D43968 RUVBL1 RuvB-like 1 (E. coli) RUVBL2 AB024301 RUVBL2 RuvB-like 2 (E. coli) RuvB-like (D11) RuvB-like (D11)	2182	33237_at	KIAA0801	AB018344	RNA helicase	KIAA0801 protein
AF083255 RNA helicase-related protein at RBPMS D84110 splicing RNA-binding protein gene with multiple RNA-binding protein gene with multiple BNA-binding protein gene with multiple RNA-binding protein regulatory subunity RNA-binding protein regulatory subunity RNA-binding protein	2183	36045_at	RNAH	AJ223948	RNA helicase family	RNA helicase
at RBPMS D84110 RNA-binding protein gene with multiple RBPMS D84109 splicing DJ-1 AF021819 RNA-binding protein regulatory subunit RNPC2 L10910 containing 2 RMP AB006572 RPB5-mediating protein RMP AB006572 RPB5-mediating protein RUNPC1 Y11651 RTC domain containing 1 RUNX1 D43968 myeloid leukemia 1; aml1 oncogene) RUVBL1 Y18418 RuvB-like 1 (E. coli) RUVBL2 AB024301 RuvB-like 2 (E. coli) RUVBL2 AB024301 RuvB-like 2 (E. coli) Runexin II ligand, calpactin 1, light polypeptide (p11) Runexin II ligand, calpactin 1, light polypeptide (p11)	2184	38762_at	RNAHP	AF083255	RNA helicase-related protein	RNA helicase-related protein
RBPMS D84110 splicing RNA-binding protein gene with multiple RNA-binding protein gene with multiple DJ-1 AF021819 RNA-binding protein regulatory subunit RNA-binding protein regulatory subunit RNA-binding region (RNP1, RRM) RNPC2 L10910 containing 2 RMP AB006572 RPBS-mediating protein RTCD1 Y11651 RTC domain containing 1 RUNX1 D43968 myeloid leukemia 1; aml1 oncogene) RUVBL1 Y18418 RuvB-like 1 (E. coli) RUVBL2 AB024301 RuvB-like 2 (E. coli) RUVBL2 AB024301 RuvB-like 2 (E. coli) S100 calcium binding protein A10 (annexin II ligand, calpactin I, light S100A10 AI201310 polypeptide (p11)					RNA-binding protein gene with multiple	
RNA-binding protein gene with multiple	2185	38049_g_at	RBPMS	D84110	splicing	RBP-MS/type 4
RBPMS D84109 splicing DJ-1 AF021819 RNA-binding protein regulatory subunit RNA-binding region (RNP1, RRM) RNA-binding region (RNP1, RRM) RNPC2 L10910 containing 2 RMP AB006572 RPB5-mediating protein RMP Y11651 RTC domain containing 1 RUNX1 D43968 myeloid leukemia 1; aml1 oncogene) RUVBL1 Y18418 RuvB-like 1 (E. coli) RUVBL2 AB024301 RuvB-like 2 (E. coli) RUVBL2 AB024301 S100 calcium binding protein A10 (annexin II ligand, calpactin I, light S100A10 AI201310 polypeptide (p11))					RNA-binding protein gene with multiple	
DJ-1 AF021819 RNA-binding protein regulatory subunit RNPC2 L10910 containing 2 RMP AB006572 RPB5-mediating protein RTCD1 Y11651 RTC domain containing 1 RUNX1 D43968 myeloid leukemia 1; aml1 oncogene) RUVBL1 Y18418 RuvB-like 1 (E. coli) RUVBL2 AB024301 RuvB-like 2 (E. coli) S100 calcium binding protein A10 (annexin II ligand, calpactin 1, light S100410 Al201310 polypeptide (p11))	2186	38047_at	RBPMS	D84109	splicing	RBP-MS/type 3
RNPC2 L10910 containing 2	2187	38974_at	DJ-1	AF021819	RNA-binding protein regulatory subunit	RNA-binding protein regulatory subunit
RNPC2 L10910 containing 2 RMP AB006572 RPB5-mediating protein RTCD1 Y11651 RTC domain containing 1 RUNX1 D43968 runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) RUVBL1 Y18418 RuvB-like 1 (E. coli) RUVBL2 AB024301 RuvB-like 2 (E. coli) S100 calcium binding protein A10 (annexin II ligand, calpactin 1, light S1001310 Polypeptide (p11)) Polypeptide (p11)					RNA-binding region (RNP1, RRM)	
RMP AB006572 RPB5-mediating protein RTCD1 Y11651 RTC domain containing 1 RUNX1 D43968 runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) RUVBL1 Y18418 RuvB-like 1 (E. coli) RUVBL2 AB024301 RuvB-like 2 (E. coli) S100 calcium binding protein A10 (annexin II ligand, calpactin 1, light S100A10 AI201310 polypeptide (p11))	2188	39725_at	RNPC2	L10910	containing 2	splicing factor
RTCD1 Y11651 RTC domain containing 1	2189	38011_at	RMP	AB006572	RPB5-mediating protein	RPB5 meidating protein
RUNX1 D43968 myeloid leukemia 1; aml1 oncogene)	2190	35195_at	RTCD1	Y11651	RTC domain containing 1	phosphate cyclase
at RUVBL1 Y18418 RuvB-like 1 (E. coli) at RUVBL2 AB024301 RuvB-like 2 (E. coli) at RUVBL2 AB024301 RuvB-like 2 (E. coli) S100 calcium binding protein A10 (annexin II ligand, calpactin I, light at S100A10 AI201310 polypeptide (p11))					runt-related transcription factor 1 (acute	
at RUVBL1 Y18418 RuvB-like 1 (E. coli) at RUVBL2 AB024301 RuvB-like 2 (E. coli) S100 calcium binding protein A10 (annexin II light at S100A10 AI201310 polypeptide (p11))	2191	943_at	RUNX1	D43968	myeloid leukemia 1; aml1 oncogene)	AML1b protein
at RUVBL1 Y18418 RuvB-like 1 (E. coli) at RUVBL2 AB024301 RuvB-like 2 (E. coli) S100 calcium binding protein A10 (annexin II ligand, calpactin I, light at S100A10 AI201310 polypeptide (p11))						erythrocyte cytosolic protein of 54 kDa, ECP-
at RUVBL2 AB024301 RuvB-like 2 (E. coli) S100 calcium binding protein A10 (annexin Il ligand, calpactin I, light polypeptide (p11))	2192	40124_at	RUVBL1	Y18418	RuvB-like 1 (E. coli)	54
at S100A10 A[201310	2193	35758_at	RUVBL2	AB024301	RuvB-like 2 (E. coli)	RuvB-like DNA helicase TIP49b
at S100A10 AI201310				-	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light	
	2194	39338_at	S100A10	A1201310	polypeptide (p11))	

Fig.21

AB023183 AB023183 AB023183 AB023183 AC domain-containing inositol D87464 BAC domain-containing inositol D87464 AB020658 (yeast) AL049954 S-adenosylhomocysteine hydrolase-like 1 W63793 AL000534 Sarcoma amplified sequence AF052155 SEC13-like 1 (S. cerevisiae) AF052155 SEC13-like 1 (S. cerevisiae) D67064 SEC24 related gene family, member B (S. AJ131244 Cerevisiae) SEC3 homolog A (S. cerevisiae) SEC3 homolog A (S. cerevisiae) Cerevisiae) AD11179 SEC24 related gene family, member B (S. AJ131245 SEC34 related gene family, member D (S. SEC34 protein 1 SEC34 related gene family, member D (S. SEC34 protein 1 SEC34 related gene family, member D (S. SEC34 protein 1 SEC34 related gene family, member D (S. SEC34 protein 1 SEC34 related gene family, member D (S. SEC34 protein 1 SEC34 related gene family, member D (S. SEC34 protein 1 SEC34 related gene family, member D (S. SEC34 protein 1 SEC34 related gene family, member D (S. SEC34 protein 1 SEC34 related protein 1 (osteopontin, bone sialoprotein 1 (osteopontin, bone sialoprotein) Secreted protein, acidic, cysteine-rich J03040 Secreted protein, acidic, cysteine-rich secreted protein) Secreted protein, neuroendocrine protein 1 Secreted protein) Secreted protein, neuroendocrine protein 1 Secreted protein)						
SAC2 AB023183 Sac domain-containing inositol SAC3 D87464 phosphatase 2 SAC3 D87464 phosphatase 2 SAC3 D87464 phosphatase 3 SAC3 D87464 phosphatase 3 SAC3 D87464 phosphatase 3 SAC3 BAD20658 (yeast) AHCYL1 AL049954 S-adenosylhomocysteine hydrolase-like 1 AHCYL1 M21154 S-adenosylhomocysteine hydrolase-like 1 AMD1 M21154 S-adenosylhomocysteine hydrolase-like 1 SGCE AJ000534 sarcoglycan, epsilon SCHIP1 AF052155 SEC13like 1 (S. cerevisiae) SCHIP1 AF052155 SEC13like 1 (S. cerevisiae) SEC13L1 AF052155 SEC13like 1 (S. cerevisiae) SEC24A AJ131244 SEC23 hounding family, member B (S. SEC31BL) SEC24B AJ131245 SEC24 related gene family, member B (S. SEC31BL) ASEC3B AJ011779 SEC32 related gene family, member B (S. SEC31BL) ASEC3B AJ011779 SEC32 related gene family, member B (S. SEC31BL)		A	В	C	Q.	Ш
SAC2 AB023183 phosphatase 2 SAC3 D87464 phosphatase 2 SAC3 D87464 phosphatase 2 SAC3 D87464 phosphatase 3 SAC3 BAC1 suppressor of actin mutations 1-like 1 AHCYL1 AL049954 S-adenosylhomocysteine hydrolase-like 1 AHCYL1 R59606 S-adenosylhomocysteine hydrolase-like 1 AMD1 M21154 S-adenosylhomocysteine hydrolase-like 1 SGCE AJ00534 S-adenosylhomocysteine hydrolase-like 1 SGCE AJ006534 S-adenosylmethionine decarboxylase 1 SGCE AJ006534 Sarcoma amplified sequence SCHIP1 AF052155 SEC13-like 1 (S. cerevisiae) SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) SEC24A AJ131244 Cerevisiae) SEC24B AJ131245 Cerevisiae) ASCAB AJ11779 SEC32 related gene family, member B (S. cerevisiae) ASCAB AJ11779 SEC32 related gene family, member B (S. cerevisiae)					Sac domain-containing inositol	
at SAC3 D87464 Sac domain-containing inositol at SAC3 D87464 Sac domain-containing inositol at SACM1L AB020658 (yeast) at AHCYL1 AL049954 S-adenosylhomocysteine hydrolase-like 1 at AHCYL1 R59606 S-adenosylhomocysteine hydrolase-like 1 at AMD1 W63793 S-adenosylhomocysteine hydrolase-like 1 at AMD1 W63793 S-adenosylhomocysteine hydrolase-like 1 at SAC U01160 S-adenosylhomocysteine hydrolase-like 1 at SEC181 AF052155 SEC13-like 1 at SEC181 AF052155 SEC13-like 1 at SEC24A AJ131245 SEC24 related gene family, member B <	2195	36089_at	SAC2	AB023183	phosphatase 2	KIAA0966 protein
at SAC3 D97464 phosphatase 3 at SACM1L AB020658 (yeast) at SACM1L AL049954 S-adenosylhomocysteine hydrolase-like 1 at AHCYL1 RS9606 S-adenosylhomocysteine hydrolase-like 1 at AHCYL1 RS9606 S-adenosylhomocysteine hydrolase-like 1 at AHCYL1 RS9606 S-adenosylhomocysteine hydrolase-like 1 at AMD1 W63793 S-adenosylhomocysteine hydrolase-like 1 at AMD1 W63793 S-adenosylhomocysteine hydrolase-like 1 at SAC U01160 Sarcomen at SAC U0160 Sacdenosylmethionine decarboxylase 1 at SAC U01160 Sarcomen at SCECI AL006534 Sacrosylmethionine decarboxylase 1 at SEC131.1 AF052155 SEC13-like 1 (S. cerevisiae) at SEC141.1 AF052154 SEC13-like 1 (S. cerevisiae) at SEC24A AJ131245 Cerevisiae) at SEC34B <t< td=""><td></td><td></td><td></td><td></td><td>Sac domain-containing inositol</td><td></td></t<>					Sac domain-containing inositol	
at SACM1L AB020658 (yeast) at AHCYL1 AL049954 S-adenosylhomocysteine hydrolase-like 1 at AHCYL1 R59606 S-adenosylhomocysteine hydrolase-like 1 at AMD1 W63793 S-adenosylhomocysteine hydrolase-like 1 at AMD1 M21154 S-adenosylhomocysteine hydrolase-like 1 at SGCE AJ000634 Sarcoglycan, epsilon at SGCE AJ000634 sarcoma amplified sequence at SGCE AJ000634 sarcoglycan, epsilon at SEC13L1 AF070614 schwannomin interacting protein 1 at SEC13L1 AF070614 screwisiae) at SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) at SEC23A AJ131244 cerevisiae) at SEC24B AJ131245 cerevisiae) at SEC24B AJ131245 cerevisiae) at SEC3A AJ131245 cerevisiae) at SEC3A AJ131245 cerevisiae	2196		SAC3	D87464	phosphatase 3	KIAA0274 gene product
at SACM1L AB020658 (yeast) at AHCYL1 AL049954 S-adenosylhomocysteine hydrolase-like 1 at AHCYL1 R59606 S-adenosylhomocysteine hydrolase-like 1 at AMD1 W63793 S-adenosylhomocysteine hydrolase-like 1 at AMD1 W63793 S-adenosylmethionine decarboxylase 1 at SGCE AL000634 Sarcoglycan, epsilon at SGCE AL000634 Sarcoma amplified sequence at SCRIP1 AF070614 Scrivania at SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) at SEC23A X97064 SEC34 related gene family, member A (S. cerevisiae) at SEC24A AJ131245 Cerevisiae) at SEC24B AJ131245 Cerevisiae) at SEC24B AJ131245					SAC1 suppressor of actin mutations 1-like	
at AHCYL1 R59606 S-adenosylhomocysteine hydrolase-like 1 at AMD1 W63793 S-adenosylhomocysteine hydrolase-like 1 at AMD1 W63793 S-adenosylmethionine decarboxylase 1 at SGCE AJ000534 Sarcoma amplified sequence at SCHIP1 AF052155 SEC13-like 1 (S. cerevisiae) at SCC13L1 AF052155 SEC13-like 1 (S. cerevisiae) at SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) at SEC24A AJ131244 SEC24 related gene family, member B (S. cerevisiae) at SEC24B AJ131245 Cerevisiae) at SEC24B AJ131245 Cerevisiae) at SEC24B AJ131245 Cerevisiae) at SEC3L AB018298 Cerevisiae) at SEC3L AB018298 Cerevisiae) at SFRP1 AF052124 SEC63 protein at SFRP1 AF052124 related gene family, member D (S. SEC31 related gene famil	2197	- 11	SACM1L	AB020658	(yeast)	KIAA0851 protein
at AHCYL1 R59606 S-adenosylhomocysteine hydrolase-like 1 at AMD1 W63793 S-adenosylmethionine decarboxylase 1 at SAS AJ000534 Sarcoma amplified sequence at SGCE AJ000534 Sarcoma amplified sequence at SAS U01160 Schwannomin interacting protein 1 at SEC13L1 AF070614 Schwannomin interacting protein 1 at SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) at SEC23A X97064 SEC13-like 1 (S. cerevisiae) at SEC24A AJ131244 Cerevisiae) at SEC24A AJ131244 Cerevisiae) at SEC24A AJ131245 Cerevisiae) at SEC24B AJ131245 Cerevisiae) at SEC24B AJ131245 Cerevisiae) at SEC3B AJ11779 SEC3A related gene family, member D (S. at SERPH AF056087 Secreted firizaled protein 1 secreted firizaled gene family, member B (S. S. </td <td>2198</td> <td>34792_at</td> <td>AHCYL1</td> <td>AL049954</td> <td>S-adenosylhomocysteine hydrolase-like 1</td> <td>hypothetical protein</td>	2198	34792_at	AHCYL1	AL049954	S-adenosylhomocysteine hydrolase-like 1	hypothetical protein
at AMD1 W63793 S-adenosylmethionine decarboxylase 1 at AMD1 M21154 S-adenosylmethionine decarboxylase 1 at SGCE AJ000534 sarcoglycan, epsilon at SAS U01160 sarcoma amplified sequence at SCHIP1 AF070614 schwannomin interacting protein 1 g_at SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) at SEC23L1 AF052155 SEC13-like 1 (S. cerevisiae) at SEC24A AJ131244 Cerevisiae) at SEC24A AJ131244 Cerevisiae) at SEC24B AJ131245 Cerevisiae) at SEC24 related gene family, member B (S. cerevisiae) at SEC24B AJ131245 Cerevisiae) at SEC24B AJ131245 SEC24 related gene family, member B (S. cerevisiae) at SEC3B AB018298 Cerevisiae) at SFRP1 AF056087 Secreted protein s_at SPP1 AF056087 Secreted phosphorotein I, early	2199		AHCVI 1	R59606	S-adenosylpomocysteine hydrolase-like 1	
AMD1 M21154 S-adenosylmethionine decarboxylase 1 SGCE AJ000534 sarcoglycan, epsilon SAS U01160 sarcoma amplified sequence SCHIP1 AF070614 schwannomin interacting protein 1 SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) SEC23A X97064 SEC23 Inmolog A (S. cerevisiae) SEC24A AJ131244 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24 related gene family, member B (S. SEC3A SEC24 related gene family, member D (S. SEC3A SEC3A AJ131245 cerevisiae) SEC3A AB018298 cerevisiae) SEC3A AB018298 cerevisiae) SEC63L AJ056087 secreted frizzled-related protein 1 SPP1 AF056087 secreted protein 2 entry T-lymphocyte SPARC J03040 (osteonectin) SGNE1 Y00757 1 (7R2 protein) SEINEI Y00757	2200		AMD1	W63793	S-adenosylmethionine decarboxylase 1	
SEC24B	200		, CMA	M01154	S. adenosylmethionina decarboxylase 1	S-adenosylmethionine decarboxylase 1
SAS U01050 sarcoma amplified sequence SCHIP1 AF070614 schwannomin interacting protein 1 SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) SEC14L1 D67029 SEC13-like 1 (S. cerevisiae) SEC23A X97064 SEC23 homolog A (S. cerevisiae) SEC24A AJ131244 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24 related gene family, member B (S. SEC3B SEC24 related gene family, member D (S. SEC3B SEC3A AB01829B cerevisiae) SEC24 related gene family, member D (S. SEC3B SEC24 related gene family, member D (S. SEC3B SEC3A AF056087 secreted frizzled-related protein 1 SPP1 AF056124 activation 1, early T-lymphocyte SPARC J03040 (osteonectin) SCR Secreted protein, acidic, cysteine-rich SCR Secreted protein, acidic, cysteine-rich SCR Secr	2262	41449 at	ACE A	A.1000534	sarcodycan ensilon	epsilon-sarcoglycan
SCHIP1 AF070614 schwannomin interacting protein 1 SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) SEC14L1 D67029 SEC14-like 1 (S. cerevisiae) SEC23A X97064 SEC24 related gene family, member A (S. cerevisiae) SEC24A AJ131244 cerevisiae) SEC24 related gene family, member B (S. SEC24 related gene family, member D (S. SEC24 related gene family, member D (S. SEC3L) SEC24D AB01829B cerevisiae) SEC3L AJ011779 SEC24 related gene family, member D (S. SEC3L) SEC3L AJ011779 SEC24 related gene family, member D (S. secreted frizzled-related protein 1 (ssteopontin, secreted phosphoprotein 1 (ssteopontin, bone sialoprotein 1 (ssteopontin, bone sialoprotein 1 (ssteopontin, bone sialoprotein 1, early T-lymphocyte activation 1) SPARC J03040 (ssteonectin) SCNE1 Y00757 1 (7B2 protein) SEI FNRP1 1 (7B2 protein)	2203	36083 at	SAS	U01160		SAS
SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) SEC14L1 D67029 SEC14-like 1 (S. cerevisiae) SEC23A X97064 SEC24 related gene family, member A (S. cerevisiae) SEC24A AJ131244 cerevisiae) SEC24 related gene family, member B (S. SEC24 related gene family, member B (S. SEC24D) SEC24 related gene family, member B (S. SEC24D) SEC24D AB01829B cerevisiae) SEC3L AB01829B cerevisiae) SEC63L AJ011779 SEC63 protein SERP1 AF056087 secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte SPARC J03040 (osteonectin) SCARE1 Y00757 1 (7B2 protein) SCINE1 Y00757 1 (7B2 protein)	2204	36536 at	SCHIP1	AF070614	schwannomin interacting protein 1	schwannomin interacting protein 1
SEC13L1 AF052155 SEC13-like 1 (S. cerevisiae) SEC14L1 D67029 SEC14-like 1 (S. cerevisiae) SEC23A X97064 SEC24 homolog A (S. cerevisiae) SEC24A AJ131244 cerevisiae) SEC24 related gene family, member A (S. SEC24 related gene family, member B (S. SEC24B) SEC24 related gene family, member B (S. SEC24 related gene family, member D (S. SEC24D) SEC24D AB018298 cerevisiae) SEC3L AB018298 cerevisiae) SEC63L AJ011779 SEC63 protein SERP1 AF056087 secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte SPARC J03040 secreted protein, acidic, cysteine-rich secretory granule, neuroendocrine protein SGNE1 Y00757 1 (7B2 protein) SEI FNRP1 1 (7B2 protein)	2205	33423 g at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
SEC14L1 D67029 SEC14-like 1 (S. cerevisiae) SEC23A X97064 Sec23 homolog A (S. cerevisiae) SEC24A AJ131244 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24D AB018298 cerevisiae) SEC3D AB018298 cerevisiae) SEC63L AJ011779 SEC63 protein SEC63L AJ011779 SEC63 protein AF056087 secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte AF052124 activation 1) secreted protein, acidic, cysteine-rich secretory granule, neuroendocrine protein SPARC J03040 (osteonectin) SCNE1 Y00757 1 (7B2 protein) SEI FNRP1 Selenium binding protein	2206	33422_at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
SEC23A X97064 Sec23 homolog A (S. cerevisiae) SEC24A AJ131244 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24 related gene family, member B (S. SEC24 related gene family, member B (S. SEC24) SEC24 related gene family, member B (S. SEC24) SEC24D AB018298 cerevisiae) SEC63L AJ011779 SEC63 protein SFRP1 AF056087 secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte AF052124 activation 1) secreted protein, acidic, cysteine-rich (osteonectin) SPARC J03040 (osteonectin) SSCNE1 Y00757 1 (7B2 protein) SEI FNRP1 1 (7B2 protein)	2207	36207_at	SEC14L1	D67029	SEC14-like 1 (S. cerevisiae)	SEC14 (S. cerevisiae)-like 1
SEC24A AJ131244 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24 related gene family, member B (S. SEC24 related gene family, member D (S. SEC3L) SEC24 related gene family, member D (S. SEC3L) SEC24D AB018298 cerevisiae) SEC3L AJ011779 SEC63 protein SEC63L AJ011779 SEC63 protein AF056087 secreted frizzled-related protein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1) SPP1 AF052124 activation 1) SPARC J03040 (osteonectin) SGNE1 Y00757 1 (7B2 protein) SFI FNRP1 1/29091 secretory granule, neuroendocrine protein SFI FNRP1 1/29091 selenium binding protein	2208	39099_at	SEC23A	X97064	Sec23 homolog A (S. cerevisiae)	Sec23 protein
SEC24A AJ131244 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24B AJ131245 cerevisiae) SEC24D AB018298 cerevisiae) SEC24 related gene family, member D (S. SEC24 related gene family, member D (S. SEC3L) AB018298 SEC24 related gene family, member D (S. SEC3L) cerevisiae) SEC24D AB018298 cerevisiae) SEC3L AJ011779 SEC63 protein 1 SEC4D AF056087 secreted frizzled-related protein 1 SPR1 AF052124 activation 1) SPARC J03040 (osteonectin) SCNE1 Y00757 1 (782 protein) SFI FNRP1 1/29091 selenium binding protein 1					SEC24 related gene family, member A (S.	
SEC24 related gene family, member B (S. SEC24B) AJ131245 cerevisiae) SEC24D AB018298 cerevisiae) SEC3L AJ011779 SEC3 protein SEC63L AJ011779 SEC63 protein SFRP1 AF056087 secreted frizzled-related protein 1 secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1) secreted protein 3 SPARC J03040 (osteonectin) SGNE1 Y00757 1 (7B2 protein) SFI FNRP1 L129091 secretory granule, neuroendocrine protein 1 SFI FNRP1 L129091 selenium binding protein 1	2209	34199_at	SEC24A	AJ131244	cerevisiae)	Sec24A protein
SEC24B AJ131245 cerevisiae) SEC24D AB018298 cerevisiae) SEC63L AJ011779 SEC63 protein SFRP1 AF056087 secreted frizzled-related protein 1 at SPP1 Secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1) secreted phosphoprotein 1, early T-lymphocyte activation 1) secreted protein 3 SPARC J03040 (osteonectin) SGNE1 Y00757 1 (7B2 protein) SFI FNRP1 1/29031 selenium binding protein 1					SEC24 related gene family, member B (S.	
SEC24D AB018298 cerevisiae) SEC63L AJ011779 SEC63 protein SFRP1 AF056087 secreted frizzled-related protein 1 at SPP1 AF052124 activation 1) secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1) secreted protein 1, early T-lymphocyte activation 1) SPARC J03040 (osteonectin) SGNE1 Y00757 1 (7B2 protein) SFI FNRP1 1/29031 selenuum binding protein 1	2210	35845_at	SEC24B	AJ131245	cerevisiae)	Sec24B protein
SEC24D AB018298 cerevisiae) SEC63L AJ011779 SEC63 protein SFRP1 AF056087 secreted frizzled-related protein 1 at SPP1 Secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1) secreted protein 1, early T-lymphocyte activation 1) secreted protein, acidic, cysteine-rich secreted protein, acidic, cysteine-rich (osteonectin) SPARC J03040 (osteonectin) SGNE1 Y00757 1 (7B2 protein) SFI FNRP1 1/29091					SEC24 related gene family, member D (S.	1
SEC63L AJ011779 SEC63 protein ' SFRP1 AF056087 secreted frizzled-related protein 1 at SPP1 secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1) secreted protein 1, early T-lymphocyte activation 1) secreted protein, acidic, cysteine-rich secreted protein, acidic, cysteine-rich (osteonectin) SPARC J03040 (osteonectin) SGNE1 Y00757 1 (7B2 protein) SFI FNRP1 1/29091	2211	32770_at	SEC24D	AB018298	cerevisiae)	KIAA0755 protein
SFRP1 AF056087 secreted frizzled-related protein 1 secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1) secreted protein, acidic, cysteine-rich secreted protein, acidic, cysteine-rich (osteonectin) SPARC J03040 (osteonectin) SGNE1 Y00757 1 (782 protein) SEI FNRP1 (129091 selenuum binding protein 1	2212	34349_at	SECeal	AJ011779	SEC63 protein	SEC63 protein
at SPP1 AF052124 activation 1) SPARC J03040 (seteonectin) SGNE1 Y00757 1 (7B2 protein) Selenium binding protein 1	2213	32521_at	SFRP1	AF056087	secreted frizzled-related protein 1	secreted frizzled related protein
at SPP1 AF052124 activation 1) SPARC J03040 (osteonectin) SGNE1 Y00757 1 (7B2 protein) SFI FNRP1 (129091 selenum binding protein 1					secreted phosphoprotein 1 (osteopontin,	
at SPP1 AF052124 activation 1) SPARC J03040 (esteonectin) SGNE1 Y00757 1 (782 protein) SFI FNRP1 1/29091 selenum binding protein 1					bone sialoprotein I, early T-lymphocyte	
SPARC J03040 (osteonectin) SPARC J03040 (osteonectin) SGNE1 Y00757 1 (7B2 protein) SEI FNRP1 (129091 selenum binding protein 1	2214		SPP1	AF052124	activation 1)	osteopontin
SPARC J03040 (osteonectin) SCARE Y00757 1 (7B2 protein) SET ENRP1 1/29091 Selenium binding protein 1					secreted protein, acidic, cysteine-rich	secreted protein, acidic, cysteine-rich
SGNE1 Y00757 1 (7B2 protein) SGI 1/29091 selenium binding protein 1	2215	671_at	SPARC	J03040	(osteonectin)	(osteonectin)
SEI ENRP1 179091 selenium binding protein 1	2216	34265 at	SGNE1	Y00757	secretory granule, neuroendocrine protein (1 (782 protein)	
	2217	37405 at	SELENBP1	U29091	selenium binding protein 1	selenium-binding protein

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2218 39078	39078_at	SPS2	U43286	selenophosphate synthetase 2	selenophosphate synthetase 2
22193	2219 34363_at	SEPP1	211793		selenoprotein P
				sema domain, immunoglobulin domain	
000	77 2 24	CENTRA	000000	(Ig), short basic domain, secreted,	oomanborin F
222	2220 311 g al		ADOUGEO		
				sema domain, immunoglobulin domain	
2221 376_at	176_at	SEMA3C	AB000220		semaphorin E
				sema domain, immunoglobulin domain	
				(lg), short basic domain, secreted,	:
2222	2222 35666_at	SEMA3F	U38276		semaphorin III family homolog
2223	2223 38826_at	2-Sep	2-Sep D50918		septin 2
				,	phosphotyrosine independent ligand for the
2224 4	2224 40898_at	SQSTM1	U46751	sequestosome 1	Lck SH2 domain p62
	!	1		serine (or cysteine) proteinase inhibitor,	
2225	2225 34789_at	SERPINB6	S69272	clade B (ovalbumin), member 6	cytoplasmic antiproteinase
				serine (or cysteine) proteinase inhibitor,	serine (or cysteine) proteinase inhibitor,
				clade E (nexin, plasminogen activator	clade E (nexin, plasminogen activator
2226	2226 38125_at	SERPINE1	M14083	inhibitor type 1), member 1	inhibitor type 1), member 1
				serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member	
2227	2227 39167 r at	SERPINH2	D83174	2	collagen binding protein 2
				serine palmitoyltransferase, long chain	
2228	2228 38818_at	SPTLC1	Y08685	base subunit 1	serine palmitoyltransferase, subunit I
Ŀ				serine threonine kinase 39 (STE20/SPS1	
2229	2229 40966_at	STK39	AF099989	homolog, yeast)	Ste-20 related kinase SPAK
2230	2230 41737_at	SRRM1	AF048977	serine/arginine repetitive matrix 1	Ser/Arg-related nuclear matrix protein
2231	2231 36019_at	STK19	L26260	serine/threonine kinase 19	RP protein
			-	serine/threonine kinase 24 (STE20	
2232	2232 40473_at	STK24	AF024636	homolog, yeast)	STE20-like kinase 3
				serine/threonine kinase 3 (STE20	
2233	2233 32142_at	STK3	U26424	homolog, yeast)	MST2
2234	2234 32784 at	PRP4	AB011108	serine/threonine-protein kinase PRP4 homolog	KIAA0536 protein
533	05101 <u>-</u> at	F 18.1	2011120	Selection	



Serum response factor (c-fos serum response element-binding transcription factor) J03161 factor) J03161 factor) J03161 serum response element-binding transcription factor) J03161 factor) AF059617 serum-inducible kinase X91257 seryl-tRNA synthetase X91257 seryl-tRNA synthetase X91257 seven in absentia homolog 2 (Drosophila) V18007 seven in absentia homolog 2 (Drosophila) V18007 seven in absentia homolog 2 (Drosophila) Seven transmembrane domain protein seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7) U52427 seven transmembrane domain protein seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7) U52427 seven in absentia homolog 2 (Drosophila) Seven transmembrane domain protein seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7) U52427 seven transmembrane domain protein X18004 seven in absentia homolog 2 (Drosophila) SH3 domain binding glutamic acid-rich protein AB005047 sex comb on midleg-like 2 (Drosophila) SH3-domain binding glutamic acid-rich protein AB007960 SH3-domain GRB2-like endophillin B1 SHC (Src homology 2 domain containing) U73377 transforming protein 1 SH018356 sialyttransferase 9 (CMP-Nathase) AB018356 sialyttransferase 9 (CMP-Nathase) AB018356 sialyttransferase 9 (CMP-Nathase) AB018356 sialyttransferase GM3 synthase) SH357652 (homologous Ath RNA binding protein) X12791 signal recognition particle 14kD U51920 signal recognition particle 54kD						
SRF J03161 factor) serum response factor (c-fos serum response element-binding transcription in tesponse element-binding element e		¥	8	C		'n
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SRF Juga161 factor) Serum response factor (c-fos serum serum response factor (c-fos serum serum response factor (c-fos serum serum-inducible kinase SNK AF059617 Serum-inducible kinase SARS X91257 Serum-inducible kinase SET M93651 Serum-inducible kinase SET M93651 Serum-inducible kinase SET SIAH1 U76247 Seven in absentia homolog 1 (Drosophila) SIAH2 U76248 Seven in absentia homolog 2 (Drosophila) Seven in absentia homolog 2 (Drosophila) SIAH2 U76248 Seven in absentia homolog 2 (Drosophila) Seven in absentia homolog 2 (Drosophila) Seven in absentia homolog 3 (Drosophila) Seven in absentia homolog 4 (Drosophila) Seven in absentia homolog 5 (Drosophila) Seven in absentia homolog 6 (Drosophila) Seven in absentia homolog 6 (Drosophila) Seven in absentia homolog 7 (Drosophila) Seven in absentia homolog 7 (Drosophila) Seven in absentia homolog 8 (Drosophila) Seven in absentia homolog 9 (Droso						response element-binding transcription
SRF J03161 factor) response element-binding transcription in the sponse in the sponse element-binding transcription in the sponse in the	2235	40109 at	SRF	J03161		factor)
SRF J03161 factor) SRF J03161 factor) SNR AF059617 serum-inducible kinase SARS X91257 serum-inducible kinase SET M93651 sarociated) Seven in absentia homolog 2 (Drosophila) Seven transmembrane domain protein Seven transform sarociated SH337192 SH3 domain binding glutamic acid-rich SH38GR AF042081 SH3 domain binding glutamic acid-rich SH3GLB1 AB005047 sassociated SH3-domain binding protein SHC SH3-domain binding protein SHC SH3-domain sarociated SHC ST SH3 synthase SHC1 U73377 transforming protein SHC1 SH3-domain protein SHC1 SH3-domain protein SHC1 SH3-domain containing SHC1 AB018356 signal recognition particle 14kD signal recognition particle 54kD s						serum response factor (c-fos serum
SRF J03161 factor) Servim-inducible kinase SNK AF659617 Servim-inducible kinase SNK AF659617 Servim-inducible kinase SIARS X91257 Servim-inducible kinase SET M93651 associated) associated associated associated associated AF0248 Seven in absentia homolog 1 (Drosophila) at SIAH2 U76248 Seven in absentia homolog 2 (Drosophila) Seven transmembrane domain protein Seventh argest subunit; Human RNA polymerase il seventh subunit (rpb-7) Seventh argest subunit; Human RNA Polymerase il seventh subunit (rpb-7) SH360M2 Seventh argest subunit; Human RNA SH337192 Seventh argest subunit; Human RNA SH386R AF042081 SH3 domain binding glutamic acid-rich SH386R AF042081 SH3 domain binding glutamic acid-rich SH36LB1 AE007960 SH3-domain binding glutamic acid-rich SH36LB1 AB007960 SH3-domain binding protein 1 SH3778 AB018356 Signal protein 1 Signal protein 1 Signal protein 1 Signal protein 1 Signal protein particle 14kD Al525652 Alf Synthase Signal recognition particle 14kD Al525652 Alf Synthase Signal recognition particle 54kD SRP54 U51920 Signal recognition particle 54kD Signal recog						response element-binding transcription
at SNK AF059617 serum-inducible kinase serum-inducible kinase at SARS X91257 seryl-tRNA synthetase seryl-tRNA synthetase at SET M93651 associated) seven in absentia homolog 1 (Drosophila) at SIAH1 U76247 seven in absentia homolog 2 (Drosophila) seven in absentia homolog 2 (Drosophila) at NIFIE14 Y18007 seven transmembrane domain protein at NIFIE14 Y18007 seven transmembrane domain protein at NIFIE14 Y18007 seven transmembrane domain protein at SCML2 Seven transmembrane domain protein at SH337192 seven transmembrane domain protein at SH38GR A1337192 seven transmembrane domain protein at SH38GR A1337192 sig	2236	1409_at	SRF	J03161		factor)
at SARS X91257 seryl-tRNA synthetase at SET M93651 associated) at SIAH1 U76247 seven in absentia homolog 1 (Drosophila) at SIAH2 U76248 seven in absentia homolog 2 (Drosophila) at SIAH2 U76248 seven transmembrane domain protein at NIFIE14 Y18007 sevent transmembrane domain protein at NIFIE14 Y18007 sevent transmembrane domain protein at SCML2 Y18007 sevent transmembrane domain protein at SIABGR sevent transmembrane domain protein at SCML2 Y18004 sevent transmembrane domain protein at SH3BGR Al337192 sevent transmembrane domain protein at SH3BGR Al337192 sevent transmembrane domain protein at SH3BGR Al337192 sevent transmembrane domain protein at SH3BGR Al30730 signal protein file2-like alphalin B1 at SHC13 AB07300 signal peptidase complex day	2237		SNK	AF059617	serum-inducible kinase	serum-inducible kinase
at SET translocation (myeloid leukemia- associated) at SIAH1 U76247 seven in absentia homolog 1 (Drosophila) at SIAH2 U76248 seven in absentia homolog 2 (Drosophila) at NIFIE14 Y18007 seventh largest subunit, Human RNA polymerase II seventh subunit (rpb-7) at Db-7 U52427 gene, complete cds. seventh largest subunit, Human RNA polymerase II seventh subunit (rpb-7) at SH3BGR AI337192 SH3 domain binding glutamic acid-rich protein at SH3BGR AR042081 protein at SH3BL AR0507960 SH3-domain binding glutamic acid-rich protein like at SH3GLB1 AR005047 sassociated sasociated) at SHGL AR005047 Sassociated sasociated AB018356 Signal peptidase complex (18KD) at SPC18 AR018356 sialyltransferase 9 (CMP- NeuAc:lactosylcearmide alpha-2.3- signal recognition particle 14kD at SRP14 Al357653 signal recognition particle 14kD at SRP34 U51920 signal recognition particle 14kD at	2238	34849 at	SARS	X91257	seryl-tRNA synthetase	seryl-tRNA synthetase
at SET M93651 associated) at SIAH1 U76247 seven in absentia homolog 1 (Drosophila) at SIAH2 U76248 seven in absentia homolog 2 (Drosophila) at NIFIE14 Y18007 seventh largest subunit; Human BNA polymerase II seventh subunit (rpb-7) at U52427 gene, complete cds. at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) At SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) At SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) At SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) At SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) At SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) At SH36GRL AF042081 sh33 domain binding glutamic acid-rich protein At SH36GRL AF042081 SH3-domain binding glutamic acid-rich protein I the protein I the standard sex complete acid-rich associated) At SH36GRL AF042081 SH3-domain binding glutamic acid-rich acid-rich ac		•			SET translocation (myeloid leukemia-	SET translocation (myeloid leukemia-
at SIAH1 U76247 seven in absentia homolog 1 (Drosophila) at SIAH2 U76248 seven in absentia homolog 2 (Drosophila) at NIFIE14 Y18007 seventh targest subunit; Human RNA polymerase II seventh subunit (rpb-7) at DE2427 gene, complete cds. at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) Al337192 SH3 domain binding glutamic acid-rich protein SH3 domain binding glutamic acid-rich protein like at SH3BP5 AB005047 associated) SH3-domain binding glutamic acid-rich protein Is at SH3GLB1 AB005047 associated) SH3-domain binding protein 5 (BTK-SH3-domain containing) at SHC1 AB007960 SH3-domain binding protein 5 (BTK-SH3-domain containing) SHC1 at SHC1 AB018356 sightlransferase 9 (CMP-Nation Bacognition particle 14kD at SRP14 Al357653 signal peptidase complex (18kD) <	2239	40189_at	SET	M93651	associated)	associated)
at SIAH2 U76248 seven in absentia homolog 2 (Drosophila) seven transmembrane domain protein seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7) gene, complete cds. at Pb-7 V18004 sex comb on midleg-like 2 (Drosophila) SH36RL2 Y18004 sex comb on midleg-like 2 (Drosophila) SH36RL2 A1337192 protein SH36RL AF042081 protein like SH38RP5 A8005047 associated) at SH36RL1 A8005047 associated) sasociated SHC1 U73377 transforming protein 1 sialyltransferase 9 (CMP- NeuAc:lactosylceramide alpha-2,3-at SRC18 AB018356 sialyltransferase; GM3 synthase) signal recognition particle 14kD signal recognition particle 19kD signal recognition particle 19kD signal recognition particle 19kD signal recognition particle 54kD	22.40	32160 at	SIAH1	1176247	seven in absentia homolog 1 (Drosophila)	hSIAH1
at SIAH2 U76248 seven in absentia homolog 2 (Drosophila) at NIFIE14 Y18007 seven transmembrane domain protein at NIFIE14 Y18007 seventh largest subunit; Human RNA polymerase II seventh subunit (pb-7) gene, complete cds. at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) SH337192 SH3 domain binding glutamic acid-rich potein SH3 domain binding glutamic acid-rich potein SH3 domain binding glutamic acid-rich at SH3BP5 AB005047 SH3-domain binding glutamic acid-rich at SH3BP5 AB007960 SH3-domain binding protein 5 (BTK- at SHC1 AB007960 SH3-domain dRB2-like endophilin B1 at SHC1 U73377 transforming protein 1 at SPC18 AB01836 sialyltransferase; GM3 synthase) at SRP14 AI357653 signal peptidase complex (18kD) <	25.5					
at NIFIE14 Y18007 seven transmembrane domain protein at Phb-7 seventh largest subunit, Human RNA polymerase I seventh subunit (rpb-7) at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) at SH3BGR AI337192 protein at SH3BGRL AF042081 protein AF042081 protein like SH3 domain binding glutamic acid-rich B SH3 domain binding glutamic acid-rich SH3 domain binding glutamic acid-rich at SH3BBS AB005047 associated) at SH3GLB1 AB005047 associated) at SHC1 AB007960 SH3-domain GRB2-like endophilin B1 at SHC1 AB007960 SH3-domain GRB2-like endophilin B1 at SHC1 AB007960 SH3-domain GRB2-like endophilin B1 at SHC1 AB018356 SH3-domain GRB2-like endophilin B1 at SHC1 AB018356 SH3-domain pinding protein 5 (BM) at	2241	33799_at	SIAH2	U76248	seven in absentia homolog 2 (Drosophila)	hSIAH2
at rpb-7 bolymerase II seventh RNA polymerase II seventh subunit (rpb-7) gene, complete cds. SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) SSABGR AI337192 SH3 domain binding glutamic acid-rich protein SH3 domain binding glutamic acid-rich protein SH3BGRL AF042081 protein like SH3BGRL AB005047 associated) at SH3GLB1 AB005047 associated) at SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 associated) at SHC1 U73377 transforming protein 1 siaplytransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-at SPC18 AI357653 signal recognition particle 14kD at SRP14 AI357653 signal recognition particle 19kD at SRP14 AI525652 (homologous Alu RNA binding protein) at SRP54 U51920 signal recognition particle 19kD at SRP54 U51920 signal recognition particle 54kD	2242	39088_at	NIFIE14	Y18007	seven transmembrane domain protein	seven transmembrane domain protein
at pb-7 U52427 gene, complete cds. at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) at SH3BGR AI337192 Protein at SH3BGRL AF042081 protein like at SH3BFS AB005047 SH3-domain binding glutamic acid-rich protein like at SH3BFS AB005047 SH3-domain binding protein 5 (BTK-stanger) at SH3GLB1 AB005047 SH3-domain binding protein 5 (BTK-stanger) at SHG05047 SH3-domain containing) at SHC (Sr homology 2 domain containing) SHC (Sr homology 2 domain containing) SHC (Sr homology 2 domain containing) at SPC18 AB018356 sialyltransferase 9 (CMP-nordinger) at SPC18 AB018356 sialyltransferase; GM3 synthase) at SRP14 AI357653 signal recognition particle 14kD at SRP19 X12791 signal recognition particle 54kD at SRP54 U51920 signal recognition particle 54kD					seventh largest subunit; Human RNA	
at SCML2 Y18004 sex comb on midleg-like 2 (Drosophila) at SH3BGR AI337192 SH3 domain binding glutamic acid-rich protein at SH3BGRL AF042081 protein like at SH3BP5 AB005047 associated) at SH3GLB1 AB007960 SH3-domain binding protein 5 (BTK-SH3GLB1 at SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 at SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 at SHC1 L073377 transforming protein 1 at SHC1 L073377 transforming protein 1 at SPC18 AB018356 sialyltransferase 9 (CMP-NeuAcilactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) at SPC18 AI357653 signal peptidase complex (18kD) at SRP14 AI525652 (homologous Alu RNA binding protein) at SRP54 U51920 signal recognition particle 54kD	2243		mb-7	U52427	gene, complete cds.	RNA polymerase II seventh subunit
at SH3BGR AI337192 Protein at SH3BGRL AF042081 protein at SH3BGRL AF042081 protein like at SH3BP5 AB005047 associated) at SH3GLB1 AB007960 SH3-domain binding protein 5 (BTK-associated) at SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 at SHC1 U73377 transforming protein 1 sighttransferase 9 (CMP-associated) NeuAc:lactosylceramide alpha-2,3-asialyltransferase; GM3 synthase) at SPC18 AB018356 sighal peptidase complex (18kD) at SRP14 AI357653 signal recognition particle 14kD at SRP14 AI525652 (homologous Alu RNA binding protein) at SRP19 Signal recognition particle 14kD at SRP54 U51920 signal recognition particle 54kD	2244		SCML2	Y18004	sex comb on midleg-like 2 (Drosophila)	SCML2 protein
at SH3BGR AI337192 protein at SH3BGRL AF042081 protein like at SH3BGRL AR005047 associated) at SH3GLB1 AR007960 SH3-domain binding protein 5 (BTK-SH36LB1 at SH3GLB1 AR007960 SH3-domain GRB2-like endophilin B1 at SHC1 U73377 transforming protein 1 at SHC1 U73377 sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) at SPC18 AB018356 sialyltransferase; GM3 synthase) at SRP14 AI525652 (homologous Alu RNA binding protein) at SRP19 X12791 signal recognition particle 14kD at SRP54 U51920 signal recognition particle 54kD					SH3 domain binding glutamic acid-rich	
at SH3BGRL AF042081 protein like at SH3BGRL AB005047 associated) at SH3GDF960 SH3-domain binding protein 5 (BTK-associated) at SH3GDF960 SH3-domain GRB2-like endophilin B1 at SHC1 U73377 transforming protein 1 at SHC1 U73377 transforming protein 1 at SIAT9 AB018356 sialyltransferase; GMP-nearide alpha-2,3-sialyltransferase; GM3 synthase) at SPC18 AI357653 signal recognition particle 14kD at SRP14 AI525652 (homologous Alu RNA binding protein) at SRP19 signal recognition particle 14kD at SRP54 U51920 signal recognition particle 54kD	2245	36040_at	SH3BGR	Al337192	protein	
at SH3BGRL AF042081 protein like at SH3BP5 AB005047 associated) at SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 at SHC1 U73377 Itansforming protein 1 at SHC1 U73377 Itansforming protein 1 at SIAT9 AB018356 sialyltransferase 9 (CMP-Nord-Clactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) at SPC18 AB018356 sialyltransferase; GM3 synthase) at SRP14 AI357653 signal peptidase complex (18kD) at SRP14 AI525652 (homologous Alu RNA binding protein) at SRP19 X12791 signal recognition particle 19kD at SRP54 U51920 signal recognition particle 54kD					SH3 domain binding glutamic acid-rich	SH3 domain binding glutamic acid-rich-like
at SH3BP5 AB005047 associated) at SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 at SHC1 U73377 transforming protein 1 sialyltransferase 9 (CMP- NeuAc:lactosylceramide alpha-2,3- sialyltransferase; GM3 synthase) at SPC18 AB018356 sialyltransferase; GM3 synthase) at SRP14 Al357653 signal peptidase complex (18kD) signal recognition particle 14kD at SRP19 X12791 signal recognition particle 19kD at SRP54 U51920 signal recognition particle 54kD	2246		SH3BGRL	AF042081	protein like	protein
at SH3BP5 AB005047 associated) at SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 at SHC1 U73377 transforming protein 1 at SHC1 U73377 transforming protein 1 at SIAT9 AB018356 sialyltransferase 9 (CMP-Nou-Ciactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) at SPC18 AB018356 sighal peptidase complex (18kD) at SRP14 AI357653 signal recognition particle 14kD at SRP14 AI525652 (homologous Alu RNA binding protein) at SRP19 X12791 signal recognition particle 19kD at SRP54 U51920 signal recognition particle 54kD					SH3-domain binding protein 5 (BTK-	
at SH3GLB1 AB007960 SH3-domain GRB2-like endophilin B1 at SHC1 U73377 transforming protein 1 at SHC1 L73377 transforming protein 1 at SIAT9 AB018356 sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) at SPC18 AB018356 sighal peptidase complex (18kD) at SRP14 AI357653 signal recognition particle 14kD at SRP19 X12791 signal recognition particle 19kD at SRP54 U51920 signal recognition particle 54kD	2247	38968_at	SH3BP5	AB005047	associated)	SH3 binding protein
at SHC1 U73377 transforming protein 1 at SHC1 U73377 transforming protein 1 at SIAT9 AB018356 sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) at SPC18 AB018356 signal peptidase complex (18kD) at SRP14 AI525652 (homologous Alu RNA binding protein) at SRP19 X12791 signal recognition particle 19kD at SRP54 U51920 signal recognition particle 54kD	2248		SH3GLB1	AB007960	SH3-domain GRB2-like endophilin B1	SH3-containing protein SH3GLB1
SHC1 U73377 transforming protein 1					SHC (Src homology 2 domain containing)	-
SIAT9	2249		SHC1	U73377	transforming protein 1	pegshc
NeuAc:lactosylceramide alpha-2,3- SIAT9					sialyltransferase 9 (CMP-	
SIAT9 AB018356 sialytransferase; GM3 synthase) SPC18 AI357653 signal peptidase complex (18kD) SRP14 AI525652 (homologous Alu RNA binding protein) SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD					NeuAc:lactosylceramide alpha-2,3-	
SPC18 At357653 signal peptidase complex (18kD) SRP14 At525652 (homologous Alu RNA binding protein) SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD	2250	34256_at	SIAT9	AB018356	sialytransferase; GM3 synthase)	GM3 synthase
SRP14 A1525652 (homologous Alu RNA binding protein) SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD	2251	39139_at	SPC18	Al357653	signal peptidase complex (18kD)	
SRP14 Al525652 (homologous Alu RNA binding protein) SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD					signal recognition particle 14kD	
SRP19 X12791 signal recognition particle 19kD SRP54 U51920 signal recognition particle 54kD	2252	41194_at	SRP14	AI525652	(homologous Alu HNA binding protein)	6
SRP54 U51920 signal recognition particle 54kD	2253	35231_at	SRP19	X12791	signal recognition particle 19kD	signal recognition particle 19kU
	2254	36060_at	SRP54	U51920	signal recognition particle 54kD	signal recognition particle

K.3.2

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	∢	В	ပ	O	U
2255	2255 33837 at	SRP72	AF069765	signal recognition particle 72kD	signal recognition particle 72
2256		SRP9	AF070649	signal recognition particle 9kD	
				ptor	signal recognition particle receptor ('docking
2257	2257 36679_at	SRPR	X06272		protein')
				signal transducer and activator of	
2258	2258 AFFX-HUMISGF STAT1	STAT1	M97935	transcription 1, 91kD	transcription factor ISGF-3
				signal transducer and activator of	
2259	2259 32860 g at	STAT1	M97935	transcription 1, 91kD	transcription factor ISGF-3
				signal transducer and activator of	
2260	2260 32859 at	STAT1	M97935	transcription 1, 91kD	transcription factor ISGF-3
				signal transducer and activator of	
2261	2261 33338 at	STAT1	M97936	transcription 1, 91kD	
				signal transducer and activator of	
				transcription 3 (acute-phase response	
2262	2262 39708_at	STAT3	L29277	factor)	DNA-binding protein
				signal transducing adaptor molecule (SH3	
2263	2263 160_at	STAM	U43899	domain and ITAM motif) 1	STAM
L				similar to Drosophila ash2 gene; Homo	
				sapiens ASH2L gene, complete cds,	
2264	2264 35804 at	ASH2L	AB022785	similar to Drosophila ash2 gene.	
2265	2265 41552 g_at	RER1	AW044624	similar to S. cerevisiae RER1	
2266		RER1	AW044624	similar to S. cerevisiae RER1	
2267	2267 33632 g at	DIM1	AF023612	similar to S. pombe dim1+	Dim1p homolog
				similar to SW:GOLI_DROME Q06003	
2268	2268 35083_at	G1L	AL031670	GOLIATH PROTEIN	ring finger protein 24
2265	2269 37178 at	na	M74089	similar to TB1	-
				similar to Wiskott-Aldrich syndrome	
2270	2270 40787_at	WIRE	U90911	protein interacting protein	
227	2271 34705_at	ВЕТЗ	AJ224335	similar to yeast BET3 (S. cerevisiae)	hBET3 protein
2272	2272 39131_at	UPF3A	N36842	similar to yeast Upf3, variant A	
227	2273 41277_at	SAP18	AW021542	sin3-associated polypeptide, 18kD	
227	2274 33859_at	SAP18	U96915	sin3-associated polypeptide, 18kD	sin3 associated polypeptide p18
227	2275 40992_s_at	SAP30	AF055993	sin3-associated polypeptide, 30kD	mSin3A associated polypeptide p30
	1 0000	2	X01868	sine oculis homeobox homolog 1	sine oculis homeobox (Drosophila) homolog
777	2276 40004 at	SIVI	000167	(Diosopima)	

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	А	8	၁	O	Ů
				fascin homolog, sea urchin)	
2277	2277 39070_at	SNL	U03057		actin bundling protein
2278	2278 39086_g_at	SSBP1	AA768912		
2279	2279 32668_at	SSBP2	AL080076	2	hypothetical protein
2280		SSA2	M25077	Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-A/Ro)	60kD Ro/SSA autoantigen
					Conference A33/20 C/103
2281	2281 35295_g_at	SSA2	M25077	_	OUKU HO/SSA autoantigen
		-		Sjogren syndrome antigen B (autoantigen	Sjogren syndrome antigen B (autoantigen
2282	2282 38450_at	SSB	X69804	La)	La)
2283	2283 37715_at	SNW1	AF045184	SKI-interacting protein	nuclear receptor coactivator NCoA-62
2284	2284 37389_at	IMAGE145052	Al346580	small acidic protein	
				small nuclear ribonucleoprotein 70kD	
2285	2285 40875_s_at	SNRP70	X06815	polypeptide (RNP antigen)	hU1-70K-like protein (216 AA)
				small nuclear ribonucleoprotein	
2286	2286 38679_g_at	SNRPE	AA733050	polypeptide E	
				small nuclear ribonucleoprotein	
2287	2287 37337_at	SNRPG	AI803447	polypeptide G	
				small nuclear ribonucleoprotein	
2288	2288 34842_at	SNRPN	U41303	polypeptide N	small nuclear ribonuleoprotein particle N
				small nuclear RNA activating complex,	
2289	35247_at	SNAPC5	AI557062	polypeptide 5, 19kD	
L				SMART/HDAC1 associated repressor	
2290	2290 32172_at	SHARP	AL096858	protein	hypothetical protein
				SMC1 structural maintenance of	
2291	2291 32849_at	SMC1L1	D80000	chromosomes 1-like 1 (yeast)	
				SMT3 suppressor of mif two 3 homolog 1	
2292	2292 38738_at	SMT3H1	X99584	(yeast)	SMT3A protein
				SMT3 suppressor of mif two 3 homolog 2	
2293	2293 41185_f_at	SMT3H2	AI971724	(yeast)	
2294	2294 38288_at	SNAI2	U69196	snail homolog 2 (Drosophila)	
				soc-2 suppressor of clear homolog (C.	
2295	2295 38659_at	SHOC2	AB020669	elegans)	KIAA0862 protein
2296	2296 40928 at	WSB1	W26496	SOCS box-containing WD protein SWiP-1	



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2297	2297 36609_at			solute carrier family 1 (glial high affinity glutamate transporter), member 3	glutamate transporter
2298	2298 35320_at	SLC11A2	AB004857	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 NRAMP2	NRAMP2
2299	2299 33143_s_at	SLC16A3	U81800	solute carrier family 16 (monocarboxylic acid transporters), member 3	monocarboxylate transporter
2300	2300 39260_at	SLC16A4	U59185	solute carrier family 16 (monocarboxylic acid transporters), member 4	solute carrier family 16 (monocarboxylic acid transporters), member 4
2301	2301 36979 at	SLC2A3	M20681	solute carrier family 2 (facilitated glucose transporter), member 3	solute carrier family 2 (facilitated glucose transporter), member 3
2302	2302 32084_at	SLC22A5	AF057164	solute carrier family 22 (organic cation transporter), member 5	organic cation transporter OCTN2
2303	2303 38122_at	SLC23A1	D87075	solute carrier family 23 (nucleobase transporters), member 1	
				solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator),	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator),
2304	2304 32822_at	SLC25A4	302966	member 4	member 4
2305	2305 37740 r at	SLC25A5	J02683	solute carrier farmiy 25 (milochondra) carrier; adenine nucleotide translocator), member 5	solute carrier rannily 23 (mitocriordinal carrier, adenine nucleotide translocator), member 5
2306	2306 40436 g_at	SLC25A6	103592	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	
2307	2307 40435 at	SLC25A6	103592	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	
2308	2308 37675_at	SLC25A3	X60036	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	phosphate carrier protein
2309	2309 33901_at	SLC29A1	U81375	solute carrier family 29 (nucleoside transporters), member 1	equilibrative nucleoside transporter 1
2310	2310 40364_at	SLC31A1	U83460	solute carrier family 31 (copper transporters), member 1	high-affinity copper uptake protein

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7		SI C3142	1102464	solute carrier family 31 (copper	nitative conner untake protein
3	2311 04/49 at	SECSING	003401	OMD ciplic prid	שימיים בסלקבי מדימים ביים
2312	2312 37895 at	SLC35A1	D87969	transporter), member 1	CMP-sialic acid transporter
				solute carrier family 35 (UDP-N-	
2313	38208 at	SLC35A3	AB021981	transporter), member 3	UDP-N-acetylglucosamine transporter
				solute carrier family 4, sodium bicarbonate	-
2314	34936_at	SLC4A7	AB012130	cotransporter, member /	sodium bicarbonate cotransponerz
2315	34166 at	SI C6A7	580071	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	brain-specific L-proline transporter
				solute carrier family 7 (cationic amino acid	solute carrier family 7 (cationic amino acid solute carrier family 7 (cationic amino acid
2316	2316 32186_at	SLC7A5	M80244	transporter, y+ system), member 5	transporter, y+ system), member 5
					tion original circles / L'ilimphatine of the
			1	solute carrier family / (callonic arnino acid	solute carrier family / (callonic arrino acid solute carrier famility / (callonic arrino acid
2317	2317 39533_at	SLC7A6	D87432	transporter, y+ system), member 6	transporter, y+ system), member 6
				solute carrier family 9 (sodium/hydrogen	
				exchanger), isoform 1 (antiporter, Na+/H+,	_
2318	2318 32681_at	SLC9A1	568616	amiloride sensitive)	Na+/n+ exchanger INDE-1 Isoloffit
				solute carrier family 9 (sodium/hydrogen	
2319	2319 36542_at	SLC9A6	AF030409	exchanger), isoform 6	sodium-hydrogen exchanger 6
2320	2320 39097_at	NOS	X63753	SON DNA binding protein	SON DNA-binding protein
2321	2321 32857_at	SOS2	L13858	son of sevenless homolog 2 (Drosophila)	guanine nucleotide exchange factor
2322	2322 41462 at	SNX2	AF065482	sorting nexin 2	sorting nexin 2
2323	2323 39360_at	SNX3	AF034546	sorting nexin 3	sorting nexin 3
2324	2324 40605_at	SNX4	AA524345	sorting nexin 4	
2325	2325 37808_at	SNX7	AL049989	sorting nexin 7	hypothetical protein
				Source: H.sapiens genes for histones	
2326	2326 33352_at	H2A	X57985	H2B.1 and H2A.	histone H2A
2327	2327 36112_r_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2
2328	2328 36111_s_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2



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				Source: Homo sapiens chromosome 10	
2320	0320 1173 n at	,	HG172-HT3924	clone RP11-96B5, WORKING DRAFT SFOUFNCE 8 unordered pieces.	
2	5			Source: Homo sapiens Chromosome 16	
			-	BAC clone CIT987SK-44M2, complete	i
2330	2330 40617_at	44M2.1	AC004381	sequence.	hypothetical protein FLJ20274
				Source: Homo sapiens clk2 kinase	
				(CLK2), propin1, cote1,	
		-		glucocerebrosidase (GBA), and metaxin	
				genes, complete cds; metaxin	
				pseudogene and glucocerebrosidase	
				pseudogene; and thrombospondin3	
2331	2331 33740_at	COTE1	AF023268	(THBS3) gene, partial cds.	chromosome 1 open reading frame 2
				Source: Homo sapiens hJTB gene,	
2332	2332 41834_g_at	HJTB PAR	AB016492	complete cds.	jumping translocation breakpoint
				Source: Homo sapiens hJTB gene,	
2333	2333 41833_at	HJTB PAR	AB016492	complete cds.	jumping translocation breakpoint
				Source: Homo sapiens mRNA for	
2334	2334 32335_r_at	UbC2	AB009010	polyubiquitin UbC, complete cds.	polyubiquitin UbC
				Source: Homo sapiens mRNA for	
2335	2335 32334_f_at	UbC2	AB009010	polyubiquitin UbC, complete cds.	polyubiquitin UbC
				Source: Human CCAAT-box-binding	
2336	2336 32194_at	CBF	M37197	factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
				Source: Human CCAAT-box-binding	
2337	2337 229_at	CBF	M37197	factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
				Source: Human Chromosome 16 BAC	
				clone CIT987SK-A-101F10, complete	
2338	2338 41791_at	101F10.3	AC002550	sequence.	hypothetical protein
			-	Source: Human Chromosome 16 BAC	
				clone CIT987SK-A-211C6, complete	
2339	2339 41488_at	A-211C6.1	AC002394	sequence.	hypothetical protein A-211C6.1
				Source: Human Chromosome 16 BAC	
			,	cione CI1987SK-A-362G6, complete	
2340	2340 35742_at	A-362G6.1	U95740	sequence.	hypothetical protein A-362G6.1

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				Source: Human Chromosome 16 BAC	
				clone CIT987SK-A-61E3, complete	
2341 41733_at	733_at	61E3.1	AC003007		Unknown gene product (partial)
_				Source: Human DNA sequence from	
				clone RP4-742C19 on chromosome 22,	
2342 36894 at	894 at		AL031846	complete sequence.	
H				Source: Human mRNA for HLA class I	
343 37	2343 37383 f at	HLA class I - locus	us X58536	locus C heavy chain.	HLA class I heavy chain
-				Source: Human N-	
				acetylglucosaminyltransferase i (GlcNAc-	acetylglucosaminyltransferase f (GlcNAc- mannosyl (alpha-1,3-)-glycoprotein beta-1,2-
2344 39778	1778_at	GLYT1 GLCNAC-	5-1M55621	TI) mRNA, complete cds.	N-acetylglucosaminyltransferase
2345 41573 at	573 at	SP3	X68560	Sp3 transcription factor	
_				spastic ataxia of Charlevoix-Saguenay	
2346 32102_at	102_at	SACS	AB018273	(sacsin)	KIAA0730 protein
				spastic paraplegia 4 (autosomal dominant;	
2347 35171_at	1171_at	SPG4	AB029006	spastin)	KIAA1083 protein
2348 39	1423 f at	SPOP	AJ000644	type POZ protein	SPOP
2349 38	2349 38924 s_at	SSH3BP1	AF001628	ing protein 1	interactor protein AbIBP4
2350 33886 at	3886_at	SSH3BP1	AF006516	spectrin SH3 domain binding protein 1	e3B1
2351 39556_at	1556_at	SPTBN1	M96803	spectrin, beta, non-erythrocytic 1	beta-spectrin
-					
2352 34	2352 34304_s_at	SAT	AL050290	spermidine/spermine N1-acetyltransferase	
				sphingomyelin phosphodiesterase 1, acid	
2353 32574_at	2574_at	SMPD1	X59960	lysosomal (acid sphirlgomyelinase)	sphingomyelin phosphodiesterase
				spinocerebellar ataxia 1	
				(olivopontocerebellar ataxia 1, autosomal	
2354 36	2354 36142_at	SCA1	X79204	dominant, ataxin 1)	ataxin-1
				spinocerebellar ataxia 2	
				(olivopontocerebellar ataxia 2, autosomal	
2355 36	2355 36998_s_at	SCA2	Y08262	dominant, ataxin 2)	ataxin 2
-				splicing factor 30, survival of motor neuron	
2356 31	8040_at	SPF30	AF107463	related	splicing factor
2357 30	2357 36973_at	SF3B2	U41371	splicing factor 3b, subunit 2, 145kD	spliceosome associated protein



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				splicing factor proline/glutamine rich	
9358	0358 36004 a at	CEDO	A1807895	(polypyrimidine tract binding protein	
	200ct 1 - 8 - ct			dei- de- ((((((((((
				spiicing ractor proline/glutamine rich (polypyrimidine tract binding protein	
2359	2359 40638_at	SFPO	X70944		PTB-associated splicing factor
					splicing factor, arginine/serine-rich 1 (splicing
2360	2360 36098_at	SFRS1	M72709	ctor)	factor 2, alternate splicing factor)
2361	140_s_at		U68063		transformer-2 beta
2362	2362 32183_at	SFRS11	M74002	splicing factor, arginine/serine-rich 11	arginine-rich nuclear protein
				splicing factor, arginine/serine-rich 2,	
2363	2363 35258_f_at	SFRS2IP	AF030234	interacting protein	splicing factor Sip1
2364	2364 40457_at	SFRS3	AF038250	splicing factor, arginine/serine-rich 3	
2365	2365 36991_at		L14076		pre-mRNA splicing factor
2366	2366 40453_s_at	SFRS5	U30826	splicing factor, arginine/serine-rich 5	SRp40-1
2367	2367 40262 at	SBP46	AE031166	Solicing factor argining/sering-rich 46kD	SBn46 splicing factor
0366	0360 36030 24		D78130	Т	and and and an and an an an an an an an an an an an an an
0003	33033 at		200	squalette epokicase	מלמשוטום להסיים מה
				squamous cell carcinoma antigen	
2369	2369 39047_at		AB020880	recognised by T cells 3	squamous cell carcinoma antigen SARI-3
2370	41784_at	DKFZp564B0769		SR rich protein	hypothetical protein
2371	2371 36091_at	SCAP2	AF051323	src family associated phosphoprotein 2	Src-associated adaptor protein
2372	41354_at	STC1	U25997	stanniocalcin 1	stanniocalcin precursor
2373	2373 32043_at	STC2	AF098462	stanniocalcin 2	stanniocatcin-related protein
2374	2374 41295_at	STARD7	AL041780	START domain containing 7	
2375	2375 38800_at	STMN2	D45352	stathmin-like 2	
2376	41823 at	STAU	AJ132258	staufen. BNA binding protein (Drosophila)	staufen protein
2377	2377 38669_at	SLK	D86959	Ste20-related serine/threonine kinase	KIAA0204 protein
				stem cell growth factor; lymphocyte	
2378	2378 37147_at	SCGF	AF020044	secreted C-type lectin	lymphocyte secreted C-type lectin precursor
2379	2379 36913_at	SLBP	U75679	stem-loop (histone) binding protein	histone stem-toop binding protein
				steroid sulfatase (microsomal),	steroid sulfatase (microsomal), arylsulfatase
2380	2380 38034_at	STS	M16505	arylsulfatase C, isozyme S	C, isozyme S

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					steroid-5-alpha-reductase, alpha polypeptide
				polypeptide 1 (3-oxo-5 alpha-steroid delta	1 (3-oxo-5 alpha-steroid delta 4-
2381	2381 589_at	SRD5A1	M32313	4-dehydrogenase alpha 1)	dehydrogenase alpha 1)
2382	2382 33369_at	SC4MOL	AI535653	sterol-C4-methyl oxidase-like	
				sterol-C5-desaturase (ERG3 delta-5-	
2383	2383 33421_s_at	SC5DL	AB016247	desaturase homolog, fungal}-like	sterol-C5-desaturase
2384	2384 40419 at	EPB79	X85116	stomatin: H sapiens epb72 gene exon 1.	band 7 integral membrane protein
2385	2385 33322 i at	SFN	X57348	stratifin	stratifin
	::			stress-associated endoplasmic reticulum	
2386	2386 37035_at	SERP1	AI557272	protein 1, ilbosoffie associaced inclinitions protein 4	
					stromal cell derived factor receptor 1 isoform
					b; stromal cell derived factor receptor 1
2387	2387 35747_at	SDFR1	AF035287	stromal cell derived factor receptor 1	isoform a
2388	2388 32666_at	SDF1	U19495	stromal cell-derived factor 1	intercrine-alpha
2389	2389 33834 at	SDF1	L36033	stromal cell-derived factor 1	pre-B cell stimulating factor homologue
2390	2390 41627 at	SDF2	D50645	stromal cell-derived factor 2	SDF2
				succinate dehydrogenase complex,	succinate dehydrogenase flavoprotein
2391	2391 34826_at	SDHA	L21936	subunit A, flavoprotein (Fp)	subunit
				succinate dehydrogenase complex,	
				subunit C, integral membrane protein,	
2392	34385_at	SDHC	U57877	15kD	integral membrane protein CII-3
_				succinate dehydrogenase complex,	
2393	2393 40467_at	SDHD	AB006202	subunit D, integral membrane protein	cytochrome b small subunit of complex II
				succinate-CoA ligase, ADP-forming, beta	ATP-specific succinyl-CoA synthetase beta
2394	2394 40893_at	SUCLA2	AF058953	subunit	subunit
2395	2395 35832_at	KIAA1077	AB029000	sulfatase FP	KIAA1077 protein
2396	2396 33712 at	SULT4A1	N63574	sulfotransferase family 4A, member 1	
2397	34814 at	UBA2	AL041443	SUMO-1 activating enzyme subunit 2	
				superkiller viralicidic activity 2-like (S.	
2398	2398 37998_at	SKIV2L	U09877	cerevisiae)	helicase-like protein
L				superoxide dismutase 1, soluble	superoxide dismutase 1, soluble
2396	2399 36620_at	SOD1	X02317	(amyotrophic lateral sclerosis 1 (adult))	(amyotrophic lateral sclerosis 1 (adult))
2400	2400 40069_at	SVIL	AF051850	supervillin	supervillin
240		GHRF GRF	AL031659	supported by FGENESH	growth hormone releasing hormone

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2402 33297_at 2403 34825_at 2404 1640_at 2405 37745_at 2406 37805_at 2407 31855_at 2408 31869_at 2409 40213_at 2410 40961_at	CBF-B HAP2 NF- AL031778 TTRAP AL031775 ST13 U17714 ST5 U15780 STPUL AF060567 SRPVL AF060567 SRPX U61374 KIAA0640 AB014540 SMARCA1 M88163	AL031778 AL031775 U17714 U15780	E, GENSCAN	nuclear transcription factor Y, alpha, isoform
2403 34825_at 2404 1640_at 2405 37745_s_at 2406 37805_at 2407 31855_at 2408 31869_at 2409 40213_at 2410 40961_at	ST13 ST5 SRPUL SRPVL SRPX KIAA0640 SMARCA1	AL031775 U17714 U15780		
2404 1640_at 2405 37745_s_at 2406 37805_at 2407 31855_at 2408 31869_at 2409 40213_at 2410 40961_at	ST13 ST5 SRPUL SRPX KIAA0640 SMARCA1	U17714 U15780	Supported by GENSCAN	TRAF and TNF receptor-associated protein
2406 37745 s at 2406 37805 at 2406 37805 at 2407 31855 at 2409 40213 at 2410 40961 at	ST13 ST5 SRPUL SRPX KIAA0640 SMARCA1	U17714 U15780	nicity 13 (colon	
2405 37745_s_at 2406 37805_at 2407 31855_at 2408 31869_at 2409 40213_at 2410 40961_at	ST5 SRPUL SRPX KIAA0640 SMARCA1	U15780		putative tumor suppressor ST13
2406 37805_at 2407 31855_at 2408 31869_at 2409 40213_at 2410 40961_at	SRPUL SRPX KIAA0640 SMARCA1		suppression of tumorigenicity 5	p82
2407 31855_at 2408 31869_at 2409 40213_at 2410 40961_at	SAPX KIAA0640 SMARCA1 SMARCA2	AF060567		sushi-repeat protein
2407 31855_at 2408 31869_at 2409 40213_at 2410 40961_at	SMARCA1	,	sushi-repeat-containing protein, X	
2409 40213 at 2410 40961 at	KIAA0640 SMARCA1 SMARCA2	U61374		
2409 40213_at	SMARCA1 SMARCA2	AB014540	_	KIAA0640 protein
2409 40213_at	SMARCA1 SMARCA2		SWI/SNF related, matrix associated, actin	
2409 40213_at	SMARCA1 SMARCA2		dependent regulator of chromatin,	
	SMARCA2	M88163	\neg	transcription activator
- 1	SMARCA2		SWI/SNF related, matrix associated, actin	
.,	SMARCA2		dependent regulator of chromatin,	
		X72889	subfamily a, member 2	HBRM
			SWI/SNF related, matrix associated, actin	
			dependent regulator of chromatin,	
2411 32579_at	SMARCA4	U29175	$\overline{}$	transcriptional activator
			SWI/SNF related, matrix associated, actin	
		_	dependent regulator of chromatin,	
2412 39132_at	SMARCA5	AB010882	subfamily a, member 5	hSNF2H
2413 34753_at	SYBL1	X92396	synaptobrevin-like 1	synaptobrevin-like 1
2414 41692_at	SYNJ1	AB020717	synaptojanin 1	KIAA0910 protein
2415 38075_at	SYPL	X68194	synaptophysin-like protein	synaptophysin-like protein
2416 36452 at	KIAA1029	AB028952	synaptopodin	KIAA1029 protein
				synaptosome associated protein of 23
2417 32178_r_at	SNAP23	AJ011915	synaptosomal-associated protein, 23KU	Kilodaltons, Isotorm A
	. !		syndecan 2 (heparan sulfate proteoglycan	
2418 39757_at	SDC2	J04621	1, cell surface-associated, fibroglycan)	
2419 32092_at	SDC3	AB007937	syndecan 3 (N-syndecan)	KIAA0468 protein
2420 38110_at	SDCBP	AF000652	syndecan binding protein (syntenin)	syntenin
	STX12	AL035306	syntaxin 12	hypothetical protein
2422 38381_at	STX3A	U32315	syntaxin 3A	syntaxin 3

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2423	2423 38774_at	STX7		syntaxin 7	syntaxin 7
2424		STX8	AF036715	syntaxin 8	syntaxin 8
2425	at			inding protein 1	hUNC18b
2426		STXBP3	D63506	syntaxin binding protein 3	unc-18homologue
				Synthetic construct chimeric DNA-binding	
2427	2427 33315_at		M29204	factor mRNA, complete cds.	chimeric DNA-binding factor
				TAF7 RNA polymerase II, TATA box	
				binding protein (TBP)-associated factor,	
2428	2428 192 at	TAF7	U18062	55 kD	TFIID subunit TAFII55
				TAF9 RNA polymerase II, TATA box	
				binding protein (TBP)-associated factor,	
2429	2429 193_at	TAF9	U21858	32 kD	TAFII32 precursor
				TAFII20; contains homology to histone	
				H2B; TFIID subunit; TAFII15; contains	
				homology to histone H2B; TFIID subunit;	
				Human TFIID subunits TAF20 and TAF15	
2430	2430 37620_at	TAF12; TAF2J; TA	TAU57693	mRNA, complete cds.	TAF20; TAF15
2431	2431 32166_at	TLN1	AB028950	talin 1	KIAA1027 protein
2432	2432 39765_at	TLN2	AB002318	talin 2	
2433	41168_at	TAPBP	AF029750	TAP binding protein (tapasin)	tapasin
2434	2434 39779_at	TARBP1	U38847	TAR (HIV) RNA binding protein 1	TAR RNA loop binding protein
2435	32241_at	TARDBP	AL050265	TAR DNA binding protein	hypothetical protein
2436	39416_at	TIP-1	U90913	Tax interaction protein 1	Tax interaction protein 1
				Tax1 (human T-cell leukemia virus type I)	
2437	2437 498_at	TAX1BP1	U33821	binding protein 1	tax1-binding protein TXBP151
				Tax1 (human T-cell leukemia virus type I)	
2438	2438 35279_at	TAX18P1	U33821	binding protein 1	tax1-binding protein TXBP151
2439	2439 36702_at	TBX19	AJ010277	T-box 19	TBX19 protein
2440	2440 32196_at	TIP120A	AB020636	TBP-interacting protein	KIAA0829 protein
2441	2441 34791_at	TCP1	X52882	t-complex 1	t-complex 1
				t-complex-associated-testis-expressed 1-	
2442	2442 36921_at	TCTE1L	U02556	like	t-complex-associated-testis-expressed 1-like
				t-complex-associated-testis-expressed 1-	1-complex-associated-testis-expressed 1- 1-complex-associated-testis-expressed 1-like
2443	2443 946_at	TCTEL1	D50663	like 1	

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	A	8	O	Q	Ш
				TEIG; EGRa; Homo sapiens TGFb inducible early protein and early growth	
				response protein alpha genes, complete	GFb inducible early protein; early growth
244	2444 38374_at	TIEG; EGHA; KLF AF050110		cds.	response protein alpha
				telomeric repeat binding factor (NIMA-	telomeric repeat binding factor 1, isoform 2;
2445	2445 32255_i_at	TERF1	U40705	interacting) 1	telomeric repeat binding factor 1, isoform 1
2446	2446 32134 at	TES	AL050162	testis derived transcript (3 LIM domains)	hypothetical protein
				testis enhanced gene transcript (BAX	testis enhanced gene transcript (BAX
2447	33988_at	TEGT	X75861	inhibitor 1)	inhibitor 1)
2448		TETRAN	L11669	tetracycline transporter-like protein	tetracycline transporter-like protein
2449		TSPAN-3	M69023	tetraspan 3	
2450		TTC1	U46570	tetratricopeptide repeat domain 1	tetratricopeptide repeat protein
2451	# H	TTC3	D83077	tetratricopeptide repeat domain 3	TPRD
2452	2452 224 at	TIEG	S81439	TGFB inducible early growth response	zinc finger transcription factor
				TGFB-induced factor (TALE family	
2453	2453 38805_at	TGIF	X89750	homeobox)	TGIF protein
				The AAs encoded by bases 5728-5736	
				and 5917-5926 may be ASN-linked	
				glycosylation sites; insulin-like precursor;	
				Homo sapiens growth factor-binding	
				protein-3 precursor (IGFBP3) gene,	
2454	2454 37319 at	IGFBP3	M35878	complete cds.	growth factor-binding protein-3 precursor
				The AAs encoded by bases 5728-5736	
				and 5917-5926 may be ASN-linked	
				glycosylation sites; insulin-like precursor;	
	4			Homo sapiens growth factor-binding	
				protein-3 precursor (IGFBP3) gene,	
2455	2455 1586_at	IGFBP3	M35878	complete cds.	growth factor-binding protein-3 precursor

Fig. al

	A	8	O	O	Ш
2456 342	342_at	P1; M6S1; NF	JF D12485	The first in-frame ATG codon is located at nucleotides 17-19, followed by a second ATG codon 52 codons downstream. And the second ATG codon is potential initiation point for translation of NPPase.; Human mRNA for nucleotide pyrophosphatase, complete cds.	NPPase
2457 2458	2457 36992_at 2458 34768_at	TXN	A1653621 AL080080	thioredoxin thioredoxin domain-containing	hypothetical protein
2459	2459 31508_at	TXNIP TXNRD1	S73591 X91247	thioredoxin interacting protein	brain-expressed HHCPA78 homolog VDUP1 thioredoxin reductase (NADPH)
2461	2461 32214_at	TXNL	AF003938	thioredoxin-like, 32kD	thioredoxin-like protein
2462	2462 38473_at	TARS	M63180	threonyl-tRNA synthetase	threonyl-tRNA synthetase
2463	2463 659_g_at	THBS2	L12350	thrombospondin 2	thrombospondin 2
2464	2464 658_at	THBS2	L12350	thrombospondin 2	G/T mismatch-specific thymine DNA
2465	2465 40865_at	TDG	U51166	thymine-DNA glycosylase	glycosylase
2466	2466 31557_at	TMSB4X	M17733	thymosin, beta 4, X chromosome	thymosin, beta 4
2467	2467 32654 g at	SMAP	AW020536	thyroid hormone receptor coactivating protein	
2468	2468 39699_at	TRIP12	D28476	thyroid hormone receptor interactor 12	thyroid hormone receptor interactor 12
2469	2469 41251_at	TRIP3	L40410	thyroid hormone receptor interactor 3	thyroid receptor interactor
2470	39341_at	TRIP6	AJ001902	thyroid hormone receptor interactor 6	TRIP6
2471	37348_s_at	TRIP7	AA845349	thyroid hormone receptor interactor 7	
2472	2472 41625 at	TRAP240	AB011165	thyroid hormone receptor-associated protein, 240 kDa subunit	KIAA0593 protein
2473	2473 34323_at	TRIP15	AF084260	thyroid receptor interacting protein 15	signalosome subunit 2
2474	33852 at	TIA1	M77142	TIA1 cytotoxic granule-associated RNA binding protein	TIA1 protein, isoform 1; TIA1 protein, isoform 2
2475	2475 41763_g_at	TIAL1	D64015	TIA1 cytotoxic granule-associated RNA binding protein-like 1	T-cluster binding protein
2476	2476 36655_at	TJP2	L27476	tight junction protein 2 (zona occludens 2)	tight junction protein 2 (zona occludens 2) tight junction protein 2 (zona occludens 2)
2477	2477 37801_at	176	AF112972	TJ6 protein	901

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2478	35238_at	TRAF5	AB000509	TNF receptor-associated factor 5	TRAF5
2479	2479 33243_at	GG2-1	AF099935	TNF-induced protein	MDC-3.13 isoform 2
2480	2480 40310_at	TLR2	AF051152		TolVinterleukin-1 receptor-like protein 4
2481	2481 1030_s_at	TOP1	007806		DNA topoisomerase I
2482	2482 36571_at	TOP2B	09089X	topoisomerase (DNA) II beta (180kD)	DNA topoisomerase II
2483	2483 32233_at	TOR1B	AF007872	torsin family 1, member B (torsin B)	torsinB
2484	2484 32219_at	TLK1	D50927	tousled-like kinase 1	KIAA0137 protein
2485 35321	35321_at	TLK2	AB004884	tousled-like kinase 2	PKU-alpha
				TRAF family member-associated NFKB	
2486	2486 39742_at	TANK	U59863	activator	I-TRAF
2487 40051	40051_at	KIAA0057	D31762	TRAM-like protein	TRAM-like protein
2488	2488 1073_at	TCEA1	M81601	transcription elongation factor A (SII), 1	transcription elongation factor SII
				transcription elongation factor A (SII)-like	
2489	2489 38317_at	TCEAL1	M99701		transcription elongation factor A (SII)-like 1
				(SIII),	RNA polymerase II elongation factor SIII,
2490	2490 1399_at	TCEB1	L34587		p15 subunit
				(SIII),	RNA polymerase II elongation factor-like
2491	41759_at	TCEB1L	247087	polypeptide 1-like	protein
				transcription elongation regulator 1	
2492	2492 39426_at	TCERG1	AF017789	(CA150)	putative transcription factor CA150
				transcription factor 12 (HTF4, helix-loop-	
2493	2493 33348_at	TCF12	M80627	helix transcription factors 4)	helix-loop-helix protein
				transcription factor 3 (E2A immunoglobulin	
2494	2494 1373_at	TCF3	M31523	enhancer binding factors E12/E47)	
				transcription factor 8 (represses	
2495	2495 33440_at	TCF8	U19969	interleukin 2 expression)	ZEB
				transcription factor AP-4 (activating	
2496	2496 39638_at	TFAP4	S73885	enhancer binding protein 4)	AP-4
2497	2497 37757_at	TFDP1	L23959	transcription factor Dp-1	E2F-related transcription factor
2498	2498 32578_at	TCFL4	AW005997	transcription factor-like 4	
				transcription factor-like 5 (basic helix-loop-	_
2499	2499 35614_at	TCFL5	AB012124	helix)	transcription factor-like 5
2500	2500 35749_at	TADA3L	AF069733	transcriptional adaptor 3-like	ADA3-like protein



	d, gamma- g protein		hyroid									(Camurati-	(Camurati-	(Camurati-	(Camurati-	(Camurati-	(Camurati-	(Camurati-	(Camurati-	(Camurati-	(Camurati-	(Camurati-	(Camurati-	(Camurati-	(Camurati-	(Camurati-	(Camurati-
	KIAA1080 protein; Golgi-associated, gamma- adaptin ear containing, ARF-binding protein 2	hypothetical protein	silencing mediator of retinoid and thyroid	hormone action	KIAA0127 gene product		Tob	Tob transducin (beta) like 1 protein	Tob transducin (beta) like 1 protein transferrin receptor (p90, CD71)	Tob transducin (beta) like 1 protein transferrin receptor (p90, CD71) transformer-2 alpha	Tob transducin (beta) like 1 protein transferrin receptor (p90, CD71) transformer-2 alpha TSC-22	Tob transducin (beta) like 1 protein transferrin receptor (p90, CD71) transformer-2 alpha TSC-22 transforming growth factor, beta 1 (Camurati-	Tob transducin (beta) like 1 protein transferrin receptor (p90, CD71) transformer-2 alpha TSC-22 transforming growth factor, beta 1 (Engelmann disease)	Tob transducin (beta) like 1 protein transferrin receptor (p90, CD71) transformer-2 alpha TSC-22 transforming growth factor, beta 1 tengelmann disease)	Tob transducin (beta) like 1 protein transferrin receptor (p90, CD71) transformer-2 alpha TSC-22 transforming growth factor, beta 1 transforming arowth factor arow	Tob transducin (beta) like 1 protein transformer-2 alpha TSC-22 transforming growth factor, beta 1 Engelmann disease) TGF-betalIR alpha	Tob transducin (beta) like 1 protein transformer-2 alpha TSC-22 transforming growth factor, beta 1 Engelmann disease) TGF-betalIR alpha	Tob transducin (beta) like 1 protein transformer-2 alpha TSC-22 transforming growth factor, beta 1 Engelmann disease) TGF-betalIR alpha TGF-betalIR alpha transforming growth factor induced	Tob transferrin receptor (p90, CD71) transformer-2 alpha TSC-22 transforming growth factor, beta 1 (Camura Engelmann disease) TGF-betalIR alpha TGF-betalIR alpha transforming growth factor induced protein	Tob transducin (beta) like 1 protein transformer-2 alpha TSC-22 transforming growth factor, beta 1 Engelmann disease) TGF-betalIR alpha TGF-betalIR alpha transforming growth factor induced	Tob transducin (beta) like 1 protein transformer-2 alpha TSC-22 transforming growth factor, beta 1 tensforming growth factor, beta 1 tensforming growth factor induced transforming growth factor induced transforming growth factor induced	Tob transducin (beta) like 1 protein transferrin receptor (p90, CD71) transformer-2 alpha TSC-22 transforming growth factor, beta 1 tensforming growth factor, beta 1 tensforming growth factor induced transforming growth factor induced transforming growth factor induced TACC1	Tob transducin (beta) like 1 protein transferrin receptor (p90, CD71) transformer-2 alpha TSC-22 transforming growth factor, beta 1 tensforming growth factor induced transforming growth factor induced	Tob transducin (beta) like 1 protein transferrin receptor (p90, CD71) transformer-2 alpha TSC-22 transforming growth factor, beta 1 tensforming growth factor, beta 1 tensforming growth factor induced transforming growth factor induced	Tob transducin (beta) like 1 protein transferrin receptor (p90, CD71) transformer-2 alpha TSC-22 transforming growth factor, beta 1 tensforming growth factor induced transforming growth factor induced	Tob transducin (beta) like 1 protein transformer-2 alpha TSC-22 transforming growth factor, beta 1 tensforming growth factor, beta 1 tensforming growth factor induced transforming growth factor induced TGF-betalIR alpha TACC1 TACC1 TACC1 TACC2 protein smooth muscle protein transgelin 2 hTGN48	Tob transducin (beta) like 1 protein transformer-2 alpha TSC-22 transforming growth factor, beta 1 Engelmann disease) TGF-betalIR alpha TACC1 TACC1 TACC2 TACC1 TACC2 TACC1 TACC2 TACC1 TACC2 TACC1 TACC2 TACC1 TACC2 TACC1 TACC2 TACC1 TACC1 TACC1 TACC1 TACC2 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC1 TACC2 protein
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2	Transcriptional coactivator P15 like	transcriptional co-activator with PDZ binding motif (TAZ)	transcriptional co-repressor; Human silencing mediator of retinoid and thyroid hormone action (SMRT) mRNA, complete		transcriptional regulator interacting with the PHS-bromodomain 2	FRRR2 1	יוברים ביים ביים	sta)-like 1	transducin (beta)-like 1 transferrin receptor (p90, CD71)	transducio (Deta)-like 1 transferrin receptor (p90, CD71) transformer-2 alpha (htra-2 alpha)	transducin (beta)-like 1 transferrin receptor (p90, CD71) transformer-2 alpha (htra-2 alpha) transforming growth factor beta-stimulated	transducin (beta)-like 1 transferrin receptor (p90, CD71) transferrining growth factor beta-sprotein TSC-22 transforming growth factor, beta-transforming growth factor, beta-	ransducin (beta)-like 1 ransducin (beta)-like 1 ransformer-2 alpha (htra-2 alpha (ransforming growth factor beta protein TSC-22 ransforming growth factor, beta (camurati-Engelmann disease)	alpha (htra-2 alpgrowth factor better) growth factor better) growth factor, better) growth factor, better) gelmann disease growth factor, between factor, betw	transducin (beta)-like 1 Iransducin (beta)-like 1 Iransformer-2 alpha (htra-2 alpha) Iransforming growth factor beta-stimulate protein TSC-22 Iransforming growth factor, beta 1 (Camurati-Engelmann disease) Iransforming growth factor, beta 1 Iransforming growth factor, beta receptor (70-80kD)	ransducin (beta)-like 1 transducin (beta)-like 1 transformer-2 alpha (htra-2 alpha) transforming growth factor beta-stimulate protein TSC-22 transforming growth factor, beta 1 (Camurati-Engelmann disease) transforming growth factor, beta receptor transforming growth factor, beta receptor transforming growth factor, beta receptor	ata)-like 1 eptor (p90, CD7 alpha (htra-2 alprayment) factor bett growth factor, better growth factor, better growth factor, better	transformer-2 alpha (htra-2 alpha) Iransformer-2 alpha (htra-2 alpha) Iransforming growth factor beta-stimulate protein TSC-22 Iransforming growth factor, beta 1 (Camurati-Engelmann disease) Itansforming growth factor, beta receptor II (70-80kD) Iransforming growth factor, beta receptor transforming growth factor, beta receptor II (70-80kD) Iransforming growth factor, beta receptor II (70-80kD) Iransforming growth factor, beta receptor II (70-80kD)	alpha (htra-2 alpha (htra-2 alpha (htra-2 alprowth factor better	transformer-2 alpha (htra-2 alpha) transforming growth factor beta-stimulate protein TSC-22 transforming growth factor, beta 1 (Camurati-Engelmann disease) transforming growth factor, beta 1 (Camurati-Engelmann disease) transforming growth factor, beta receptor II (70-80kD) transforming growth factor, beta receptor II (70-80kD) transforming growth factor, beta receptor transforming growth factor, beta receptor transforming growth factor, beta receptor transforming growth factor, beta-induced, 68kD transforming, acidic coiled-coil containing protein 1	transformer-2 alpha (htra-2 alpha) Iransformin eceptor (p90, CD71) Iransforming growth factor beta-stimulate protein TSC-22 Iransforming growth factor, beta 1 (Camurati-Engelmann disease) Iransforming growth factor, beta receptor II (70-80kD) Iransforming growth factor, beta receptor II (70-80kD) Iransforming growth factor, beta-induced, 68kD Iransforming, acidic coiled-coil containing protein 1 Iransforming, acidic coiled-coil containing transforming, acidic coiled-coil containing transforming, acidic coiled-coil containing	alpha (htra-2 alpha (htra-2 alpha (htra-2 alprowth factor beta gelmann disease growth factor, be growth factor, be acidic coiled-coil	alpha (htra-2 alpha (htra-2 alpha (htra-2 alpha (htra-2 alprowth factor, beingelmann disease growth factor, begrowth factor, beacidic coiled-coileacidic coiled-coileacidic coiled-coileacidic coiled-coileacidic coiled-coileacidic coiled-coileacidic coileacidic alpha (htra-2 alpha (htra-2 alpha (htra-2 alpha (htra-2 alpha) gelmann disease growth factor, be growth factor, be growth factor, be acidic coiled-coil	ransducin (beta)-like 1 ransducin (beta)-like 1 ransducin (beta)-like 1 ransforminer-2 alpha (htra-2 orming growth factor, be (htransforming growth factor, be (htransforming, acidic coiled-coil protein 1 transforming, acidic coiled-coil protein 2 transgelin transgelin transgelin transgelin transgelin 2 transgelin 2	ransformer 2 alpha (htra-2 alpha) ransformer 2 alpha (htra-2 alpha) ransforming growth factor beta-stimulated brotein TSC-22 ransforming growth factor, beta 1 (Camurati-Engelmann disease) ransforming growth factor, beta receptor II (70-80kD) ransforming growth factor, beta receptor II (70-80kD) ransforming growth factor, beta-induced, 68kD transforming, acidic coiled-coil containing protein 1 transforming, acidic coiled-coil containing protein 2 transgelin transgelin transgelin transgelin transgelin transgelin transgelin transgelin 2 transgelin 2 transgelin 2 transgelin 2 transgelin 2	ransducing the standard of the	
	Transcriptiona	transcriptional co-a binding motif (TAZ)	transcriptional silencing medi hormone actio	cds.	transcriptional regulator in the PHS-bromodomain 2	transducer of ERBB2, 1		transducin (beta)-like 1	transducin (be transferrin rec	transducin (be transferrin rec transformer-2	transducin (bete transferrin receptransformer-2 transforming graps	transducin (be transferrin rec transformer-2 transforming g protein TSC-2 transforming g	transducin (be transferrin rectransferrin rectransforming grotein TSC-2 transforming g (Camurati-Eng	transducin (be transferrin rec transformer-2 transforming g protein TSC-2 transforming g (Camurati-Eng transforming g	transducin (be transferrin rec transforming g protein TSC-2 transforming g (Camurati-Eng transforming g	transducin (be transferrin rectransferrin rectransforming g protein TSC-2 transforming g (Camurati-Engransforming g II (70-80kD)	transducin (be transferrin rec transforming g protein TSC-2 transforming g (Camurati-Eng transforming g II (70-80kD) transforming g II (70-80kD)	transducin (be transferrin rec transferrin rec transforming g protein TSC-2 transforming g (Camurati-Eng transforming g II (70-80kD) transforming g II (70-80kD) transforming g 68kD	transducin (be transferrin rec transferrin rec transforming g protein TSC-2 transforming g (Camurati-Eng transforming g II (70-80kD) transforming g II (70-80kD) transforming g 68kD	transducin (be transferrin rec transforming g protein TSC-2 transforming g (Camurati-Eng transforming g II (70-80kD) transforming g II (70-80kD) transforming g fransforming g fransforming g transforming g fransforming g	transducin (be transferrin recutansferrin recutansforming grown transforming g (Camurati-Eng transforming g II (70-80kD) transforming g II (70-80kD) transforming g II (70-80kD) transforming g II (70-80kD) transforming ge	transducin (be transferrin rec transforming g protein TSC-2 transforming g (Camurati-Eng transforming g II (70-80kD) transforming g II (70-80kD) transforming g 68kD transforming g fransforming g transforming g transforming g	transducin (be transferrin rec transferring g protein TSC-2 transforming g (Camurati-Eng transforming g II (70-80kD) transforming g 68kD transforming g 68kD transforming g fransforming g fransforming g fransforming g fransforming g fransforming g fransforming g fransforming g fransforming g fransforming g	transducin (be transferrin rec transforming g protein TSC-2 transforming g (Camurati-Eng transforming g II (70-80kD) transforming g 68kD transforming, gencein 1 transforming, protein 1 transforming, gransforming, protein 2 transforming, transforming, transforming, transforming, transforming,	transducin (be transferrin rec transferrin rec transforming g protein TSC-2 transforming g (Camurati-Eng transforming g II (70-80kD) transforming g II (70-80kD) transforming g BkD transforming, protein 1 transforming, protein 2 transgelin transgelin 2 transgelin 2 transgelin 2 transgelin 2	transducin (be transferrin rec transferrin rec transforming g protein TSC-2 transforming g (Camurati-Eng transforming g II (70-80kD) transforming g II (70-80kD) transforming g E8kD transforming, protein 1 transforming, protein 2 transforming, protein 3 transforming, pro	transducin (beta)-like 1 transferrin receptor (pg transformer-2 alpha (ht transforming growth fac protein TSC-22 transforming growth fac (Camurati-Engelmann transforming growth fac II (70-80kD) transforming growth fac II (70-80kD) transforming growth fac II (70-80kD) transforming acidic co protein 1 transforming, acidic co protein 1 transgelin transg
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O	RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN)	(VCP); Human homolog of spiQ01853ITERA_MOUSE	TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE)	(15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN)	(VCP) pirllS25197 transitional endoplasmic reticulum ATPase - mouse	gil55217 (Z14044) murine valosin-	containing protein; 99% identical to	mouse, rat, and pig nomologs; A-ray cross complementing gene 9; Putative DNA	repair protein; Hypothetical 96.6 kDa	putative membrane protein; Most similar	to hypothetical proteins in fission and	budding yeast, and C. elegans:	(AB004539) OHF YLL031c	[Schizosaccharomyces pombe] producing	hypothetical protein (AL021766)	[Schizosaccharomyces pombe]; probable	membrane protein YLL031c - yeast	(Saccharomyces cerevisiae)	gniiPiDie245463 (Z73136) ORF YLL031c	(Saccharomyces cerevisiae); (AF003137)	C27A12.9 [Caenorhabditis elegans];	Hypothetical 38.8 kDa putative membrane	protein; Most similar to hypothetical	proteins: PIDIe2/6130 (2810/2) F30A10.5 ERA_HUMAN; XHCC9; P1.11659_3; Caenorhabditis elenans snlD72655 VR28 D1.11659_4-1211659_5	translation factor suit homolog		
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2525	41051_at	TSNAX	X95073	translin-associated factor X	Translin associated protein X
2526	2526 32831 at	TIMM17A	AA453183	translocase of inner mitochondrial membrane 17 homolog A (yeast)	
2527		PEND	IN D13641	translocase of outer mitochondrial membrane 20 (yeast) homolog	mitochondrial outer membrane protein 19
25.28	2528 37050 r at	TOMM34	A1130910	translocase of outer mitochondrial membrane 34	
25.20	2520 32853 at	TOMMZOA	AB018262	translocase of outer mitochondrial membrane 70 homolog A (veast)	KIAA0719 protein
2	1700		Ve2670	translocating chain-associating membrane	TBAM protein
2531	2530 347 90_at	TI OC1	D87127	translocation protein 1	translocation protein-1
2532	2532 950_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2533	2533 41531_at	TM4SF1	A1445461	transmembrane 4 superfamily member 1	
2534	2534 39362_r_at	TM4SF6	AF043906	transmembrane 4 superfamily member 6	T245 protein
2535	32083_at	TM7SF1	AF027826	Iransmembrane 7 superfamily member 1 (upregulated in kidney)	putative seven pass transmembrane protein
2536	2536 38835_at	TM9SF1	U94831	transmembrane 9 superfamily member 1	multispanning membrane protein
2537	2537 34307 at	TM9SF2	U81006	transmembrane 9 superfamily member 2	p76
2538	2538 37955 at	TMEM4	AB015631	transmembrane protein 4	type II membrane protein
2539	2539 37445_at	TMEMS	AB015633	transmembrane protein 5	type II membrane protein
2540	2540 36128_at	TMP21	L40397	transmembrane trafficking protein	
2541	2541 38982 at	RAP1	W28865	TRF2-interacting telomeric RAP1 protein	
2542	2542 39382_at	TRIM2	AB011089	tripartite motif-containing 2	KIAA0517 protein
2543	2543 36825_at	TRIM22	X82200	tripartite motif-containing 22	gpStaf50
2544	2544 38537_at	TRIM32	U18543	tripartite motif-containing 32	zinc-finger protein
2545	2545 32635_at	TRIM33	AB029036	tripartite motif-containing 33	KIAA1113 protein
2546	2546 33107_at	TRIM37	AB020705	tripartite motif-containing 37	KIAA0898 protein
2547	2547 40461_at	TIX1	AB007855	triple homeobox 1	
2548	2548 36791_g_at	TPM1	M19267	tropomyosin 1 (alpha)	tropomyosin 1 (alpha)
2549	2549 36790_at	TPM1	M19267	tropomyosin 1 (alpha)	tropomyosin 1 (alpha)

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2550	36792_at	TPM1	224727	tropomyosin 1 (alpha)	tropomyosin isoform
2551	2551 32313_at	TPM2	M12125	tropomyosin 2 (beta)	tropomyosin 2 (beta)
2552	2552 32777_at	WRB	Y12478	tryptophan rich basic protein	congenital heart disease 5 protein
2553	2553 38121_at	WARS	X59892	tryptophanyl-tRNA synthetase	471 aa polypeptide (gamma2)
				Tu translation elongation factor,	
2554	2554 39867_at	TUFM	S75463	mitochondrial	P43
2555	2555 31944_at	TULP3	A1028290	tubby like protein 3	
2556	2556 32272_at	K-ALPHA-1		tubulin, alpha, ubiquitous	tubulin, alpha, ubiquitous
2557	2557 39332_at	TUBB	AF035316	tubulin, beta polypeptide	
2558	2558 39331_at	TUBB	X79535	tubulin, beta polypeptide	beta tubulin
2559	2559 33346_r_at	TUBG1	M61764	tubulin, gamma 1	gamma-tubulin
2560	2560 36176_at	TBCC	U61234	tubulin-specific chaperone c	cofactor C
2561	2561 35159_at	TBCE	U61232	tubulin-specific chaperone e	cofactor E
2562	2562 37007_at	TDE1	U49188	turnor differentially expressed 1	tumor differentially expressed 1
				tumor necrosis factor receptor	
2563	2563 34892_at	TNFRSF10B	AF016266	superfamily, member 10b	TRAIL receptor 2
				tumor necrosis factor receptor	
				superfamily, member 12 (transfocating	
2564	2564 41190_at	TNFRSF12	U83598	chain-association membrane protein)	death domain receptor 3 soluble form
				tumor necrosis factor receptor	
2565	2565 1563_s_at	TNFRSF1A	M58286	superfamily, member 1A	turnor necrosis factor receptor
				tumor necrosis factor receptor	
2566	2566 35150_at	TNFRSF5	X60592	superfamily, member 5	CDw40
				tumor necrosis factor receptor	
2567	2567 37643_at	TNFRSF6	X63717	superfamily, member 6	APO-1 cell surface antigen precursor
				tumor necrosis factor, alpha-induced	
2568	2568 36988_at	TNFAIP1	M80783	protein 1 (endothelial)	B12 protein
		-		tumor necrosis factor, alpha-induced	
2569	2569 38631_at	TNFAIP2	M92357	protein 2	B94 protein
				tumor necrosis factor, alpha-induced	
2570	2570 595_at	TNFAIP3	M59465	protein 3	A20
2571	2571 40076_at	TPD52L2	AF004430	tumor protein D52-like 2	hD54+ins2 isoform
2572	2572 1711 at	TP53BP1	U09477	turnor protein p53 binding protein, 1	p53-binding protein
2573	2573 34822_at	TP53BP2	U58334	turnor protein p53 binding protein, 2	Bbp/53BP2
2574	2574 38568 at	TP53BPL	U82939	tumor protein p53-binding protein	p53 binding protein

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2575	2575 31584 at	TPT1	X16064	tumor protein, translationally-controlled 1	tumor protein, translationally-controlled 1
				essing subtransferable	ğ
2576	s at	1SSC3	AF001294		
2577	2577 147_at	TSG101	U82130	tumor susceptibility gene 101	tumor susceptibility protein
2578	2578 40328_at	TWIST	X99268	rosopnila)	B-HLH DIVA binding protein
2579	2579 2086_s_at	TYRO3	D17517		Sky
2580	2580 35246_at	TYRO3	U18934	TYRO3 protein tyrosine kinase	receptor tyrosine kinase
				tyrosine 3-monooxygenase/tryptophan 5-	tyrosine 3-monooxygenase/tryptophan 5-
				monooxygenase activation protein, beta	monooxygenase activation protein, beta
2581	2581 32324_at	YWHAB	X57346	polypeptide	polypeptide
				tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, theta	
2582	2582 409_at	YWHAQ	X56468	polypeptide	14.3.3 protein
				tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, theta	
2583	2583 32530_at	YWHAQ	X56468	polypeptide	14.3.3 protein
				tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, zeta	
2584	2584 1235 at	YWHAZ	M86400	polypeptide	phospholipase A2
2585	32718 at	TPST1	AF038009	tyrosylprotein sulfotransferase 1	tyrosylprotein sulfotransferase-1
2586	2586 35172 at	TPST2	AF049891	tyrosylprotein sulfotransferase 2	tyrosylprotein sulfotransferase-2
2587	38977_at	YARS	U89436	tyrosyl-tRNA synthetase	tyrosyl-tRNA synthetase
				U2(RNU2) small nuclear RNA auxillary	
2588	2588 36517_at	U2AF1	M96982	factor 1	U2 snRNP auxiliary factor small subunit
2589	2589 32858_at	UBN1	Al341565	ubinuclein 1	
2590	2590 34824_at	UBQLN2	AB015344	ubiquilin 2	ubiquilin 2
				ubiquinol-cytochrome c reductase (6.4kD)	
2591	2591 38451_at	Uach	T58471	subunit	
				ubiquinol-cytochrome c reductase binding	
2592	2592 39427_at	UQCRB	T79616	protein	
2503	2503 40854 24	I IOCBC3	104973	ubiquinol-cytochrome c reductase core	ubiquinol-cytochrome c reductase core
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				ubiquinol-cytochrome c reductase hinge	
2594	2594 36104_at	UQCRH	AA526497	protein	
2595	2595 1366_i_at	UBC	M26880	ubiquitin C	ubiquitin C
2596	2596 1367_f_at	UBC	M26880	ubiquitin C	ubiquitin C
				ubiquitin carboxyl-terminal esterase L1	ubiquitin carboxyl-terminal esterase L1
2597	2597 36990_at	UCHL1	X04741	(ubiquitin thiolesterase)	(ubiquitin thiolesterase)
2598	2598 811_at	UFD1L	U64444	ubiquitin fusion degradation 1-like	ubiquitin fusion-degradation 1 like protein
2599	2599 40623_at	UBE38	AI749193	ubiquitin protein ligase	
				ubiquitin protein ligase E3A (human	
				papilloma virus E6-associated protein,	E6-associated protein E6-AP/ubiquitin-
2600	2600 41205_at	UBE3A	U84404	Angelman syndrome)	protein ligase
2601	2601 34383_at	USP1	AB014458	ubiquitin specific protease 1	ubiquitin specific protease
2602	2602 37683_at	USP10		ubiquitin specific protease 10	
2603	2603 162_at	USP11	U44839	ubiquitin specific protease 11	UHX1 protein
		•		ubiquitin specific protease 14 (tRNA-	
2604	2604 36982_at	USP14	U30888	guanine transglycosylase)	tRNA-Guanine Transglycosylase
2605	2605 39866_at	USP22	AB028986	ubiquitin specific protease 22	KIAA 1063 protein
2606	2606 35847_at	USP24	AB028980	ubiquitin specific protease 24	KIAA1057 protein
				ubiquitin specific protease 4 (proto-	
2607	2607 1357_at	USP4	U20657	oncogene)	ubiquitin protease
				ubiquitin specific protease 5 (isopeptidase	
2608	2608 34405_at	USP5	U47927	Τ)	isopeptidase T
				ubiquitin specific protease 7 (herpes virus- herpesvirus associated ubiquitin-specific	herpesvirus associated ubiquitin-specific
2609	2609 37672_at	USP7	Z7 2499	associated)	protease (HAUSP)
2610	2610 39794_at	USP8	D29956	ubiquitin specific protease 8	ubiquitin specific protease 8
				ubiquitin specific protease 9, X	
2611	2611 32572_at	USP9X	X98296	chromosome (fat facets-like Drosophila)	ubiquitin hydrolase
				ubiquitin-activating enzyme E1C (UBA3	
2612	2612 40066_at	UBE1C	AF046024	homolog, yeast)	UBA3
				ubiquitination factor E4A (UFD2 homolog,	ubiquitination factor E4A (UFD2 homolog,
2613	36579_at	UBE4A ·	D50916	yeast)	yeast)
				ubiquitination factor E4B (UFD2 homolog,	
2614	2614 41339_at	UBE4B	AF043117	yeast)	ubiquitin-fusion degradation protein 2
2615	2615 36959_at	UBE2V1	U49278	ubiquitin-conjugating enzyme E2 variant 1 UEV-1	UEV-1

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				conjugating enzyme E2A (RAD6	ubiquitin-conjugating enzyme E2A (RAD6
2616	2616 890_at	UBE2A	M74524	homolog)	homolog)
				ubiquitin-conjugating enzyme E2D 1	
2617	2617 37826_at	UBE2D1	AF020761	(UBC4/5 nomolog, yeast)	
				ubiquitin-conjugating enzyme E2D 2	
2618	2618 38705_at	UBE2D2	AI310002	(UBC4/5 nomolog, yeast)	
				ubiquitin-conjugating enzyme E2D 2	
2619	2619 832_at	UBE2D2	U39317	(UBC4/5 homolog, yeast)	UbcH5B
				ubiquitin-conjugating enzyme E2D 3	
2620	2620 39083_at	UBE2D3	U39318	(UBC4/5 homolog, yeast)	UbcH5C
				ubiquitin-conjugating enzyme E2D 3	
2621	2621 504_at	UBE2D3	U39318	(UBC4/5 homolog, yeast)	UbcH5C
				ubiquitin-conjugating enzyme E2E 3	
2622	2622 34850_at	UBE2E3	AB017644	(UBC4/5 homolog, yeast)	ubiquitin-conjugating enzyme E2
				ubiquitin-conjugating enzyme E2G 2	
2623	2623 32236_at	UBE2G2	AF032456	(UBC7 homolog, yeast)	ubiquitin conjugating enzyme G2
				ubiquitin-conjugating enzyme E2I (UBC9	
2624	2624 38480_s_at	UBE2I	U66867	homolog, yeast)	ubiquitin conjugating enzyme 9
				ubiquitin-conjugating enzyme E2I (UBC9	
2625	2625 838_s_at	UBE21	U45328	homolog, yeast)	ubiquitin-conjugating enzyme
2626	2626 223_at	UBEZL3	581003	ubiquitin-conjugating enzyme E2L 3	L-UBC
2627	2627 40505_at	UBEZL6	AA883502	ubiquitin-conjugating enzyme E2L 6	
				ubiquitin-conjugating enzyme E2N	
2628	2628 36604_at	UBEZN	D83004	(UBC13 homolog, yeast)	ubiquitin-conjugating enzyme E2 UbcH-ben
2629	2629 457_s_at	UBL1	U67122	ubiquitin-like 1 (sentrin)	SUMO-1
2630	2630 155_s_at	UBL1	U61397	ubiquitin-like 1 (sentrin)	ubiquitin-homology domain protein PIC1
2631	2631 40839_at	UBL3	AL080177	ubiquitin-like 3	hypothetical protein
2632	2632 37336_at	UBXD2	D87684	UBX domain-containing 2	KIAA0242 protein
				UDP-Gal:betaGlcNAc beta 1,4-	
2633	2633 40960_at	B4GALT1	D29805	galactosyltransferase, polypeptide 1	beta-1,4-galactosyltransferase
			-	UDP-Gal:betaGlcNAc beta 1,4-	
2634	2634 34177_at	B4GALT2	AF038660	galactosyltransferase, polypeptide 2	beta-1,4-galactosyltransferase
				UDP-Gal:betaGlcNAc beta 1,4-	
2635	2635 39445_at	B4GALT3	AF038661	galactosyltransferase, polypeptide 3	beta-1,4-galactosyltransferase
				UDP-glucose ceramide	
2636	2636 40215_at	UGCG	D50840	glucosyltransferase	ceramide glucosyltransferase

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2637	35214_at	навп	AF061016	UDP-glucose dehydrogenase	UDP-glucose dehydrogenase
2638	2638 37373 at	UGP2	U27460	UDP-qlucose pyrophosphorylase 2	uridine diphosphoglucose pyrophosphorylase
				UDP-N-acetyl-alpha-D-	
				acetylgalactosaminyltransferase 1	UDP-GalNAc:polypeptide N-
2639	2639 38041_at	GALNT1	U41514	(GalNAc-T1)	acetylgalactosaminyltransferase
				UDP-N-acetylglucosamine-2-epimerase/N-	UDP-N-acetylglucosamine-2-epimerase/N-UDP-N-acetylglucosamine-2-epimerase / N-
2640	2640 36515_at	GNE	AJ238764	acetylmannosamine kinase	acetylmannosamine kinase
				UDP-N-acteylglucosamine	UDP-N-acetylglucosamine
2641	2641 41242_at	UAP1	AB011004	pyrophosphorylase 1	pyrophosphorylase
2642	2642 34827_at	ULK1	AF045458	unc-51-like kinase 1 (C. elegans)	serine/threonine kinase ULK1
2643	2643 37315 f at	BM036	A1057607	uncharacterized bone marrow protein BM036	
				uncharacterized hypothalamus protein	
2644	2644 35750_at	HT010	AL049948	HT010	
				uncharacterized hypothalamus protein	
2645	2645 41058 g_at	HT012	AI760162	HT012	
				uncharacterized hypothalamus protein	
2646	2646 41057_at	HT012	AI760162	HT012	
			!	unnamed protein product; Human gene	;
2647	2647 38610_s_at	KRT10, KPP	X14487	for acidic (type I) cytokeratin 10.	Keratin 10
2648	2648 34402_at	UNRIP	AB024327	unr-interacting protein	WD-40 repeat protein
0.40	24272 24	1000	A B000340	upstream regulatory element binding	upstream regulatory element binding protein
2650	2650 37686 s at	- CNI	YOSOOR	uracil-DNA glycosylase	uracil-DNA glycosylase
				uridine monophosphate synthetase	uridine monophosphate synthetase (orotate
				(orotate phosphoribosyl transferase and	phosphoribosyl transferase and orotidine-5'-
2651	2651 33815_at	UMPS	J03626	orotidine-5'-decarboxylase)	decarboxylase)
				•	dermatan/chondroitin sulfate 2-
2652	2652 41859_at	UST	AB020316	uronyl-2-sulfotransferase	sulfotransferase
				UV Radiation Resistance Associated	
2653	2653)39429 at	UVRAG	X99050	Besistance Associated Gene.	p63 (processed form)

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					v-abl Abelson murine leukemia viral
					oncogene homolog 1 isoform a; v-abl
		-		v-abl Abelson murine leukemia viral	Abelson murine leukemia viral oncogene
2654	2654 39730_at		X16416		homolog 1 isoform b
2655	2655 35779_at	VPS45A	AJ133421	vacuolar protein sorting 45A (yeast)	vacuolar protein sorting
				VAMP (vesicle-associated membrane	
2656	2656 38801_at	VAPA	AI742846	protein)-associated protein A (33kD)	
				•	vascular cell adhesion molecule 1, isoform a
					precursor; vascular cell adhesion molecule
2657 583	583_s_at	VCAM1	M30257	vascular cell adhesion molecule 1	1, isoform b precursor
2658 1953	1953_at		AF024710	vascular endothelial growth factor	vascular endothelial growth factor
2659	36100_at	VEGF	AF022375	vascular endothelial growth factor	vascular endothelial growth factor
					VEGF related factor isoform VRF186
2660	2660 37268_at	VEGFB	U43368	vascular endothelial growth factor B	precursor
2661	2661 159 at	VEGFC	U43142	vascular endothelial growth factor C	vascular endothelial growth factor related protein
				÷	
				Homo sapiens voltage dependent anion	
2662	2662 36102 at	VDAC3: HD-VDAC	 AF038962	channel protein mRNA, complete cds.	voltage dependent anion channel protein
2663	2663 40147 at		U18009	vesicle amine transport protein 1	vesicle amine transport protein 1
2664	2664 33930 at	RA410	AB020724	vesicle transport-related protein	KIAA0917 protein
				vesicle-associated membrane protein 2	
2665	2665 32254_at	VAMP2	AL050223	(synaptobrevin 2)	
				vesicle-associated membrane protein 3	
2666	2666 35783_at	VAMP3	H93123	(cellubrevin)	
2667	2667 40103_at	VIL2	X51521	villin 2 (ezrin)	villin 2
2668	2668 34091_s_at	NIM	Z19554	vimentin	vimentin
					vinculin isoform VCL; VCL isoform meta-
2669	2669 36601_at	VCL	M33308	vinculin	VCL
2670	2670 39091 at	AWL	AF070523	vitamin A responsive: cxtoskeleton related	JWA protein
	ı			vitamin D (1,25- dihydroxyvitamin D3)	vitamin D (1.25- dihydroxyvitamin D3)
2671	2671 1388_g_at	VDR	J03258		receptor
		9		v-Ki-ras2 Kirsten rat sarcoma 2 viral	
2672	2672 1940_at	KHAS2	M54968	oncogene homolog	K-ras oncogene protein
				•	

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2673	2673/41504 s at	МАЕ	AF055376	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	short form transcription factor C-MAF
				v-maf musculoanoneurotic fibrosarcoma	
2674	2674 32835 at	MAFF	AA725102	oncogene homolog F (avian)	
2675	2675 40198 at	VDAC1	L06132	voltage-dependent anion channel 1	voltage-dependent anion channel
2676	2676 37696_at	VDAC2	L06328	voltage-dependent anion channel 2	voltage-dependent anion channel
2677	2677 171_at	VBP1	U56833	von Hippel-Lindau binding protein 1	VHL binding protein-1
				v-raf-1 murine leukemia viral oncogene	
2678	2678 38743_f_at	RAF1	X06409	homolog 1	
				v-ral simian leukemia viral oncogene	
				homolog B (ras related; GTP binding	v-ral simian leukemia viral oncogene
2679	2679 32776_at	RALB	M35416	protein)	homolog B
				v-rel reticuloendotheliosis viral oncogene	-
				homolog A, nuclear factor of kappa light	
				polypeptide gene enhancer in B-cells 3,	
2680	2680 36645_at	RELA	L19067	p65 (avian)	NF-kappa-B transcription factor subunit
				v-rel reticuloendotheliosis viral oncogene	
				homolog A, nuclear factor of kappa light	
				polypeptide gene enhancer in B-cells 3,	
2681	2681 1295_at	RELA	L19067	p65 (avian)	NF-kappa-B transcription factor subunit
				v-yes-1 Yamaguchi sarcoma viral	v-yes-1 Yamaguchi sarcoma viral oncogene
2682	2682 1674_at	YES1	M15990	oncogene homolog 1	homolog 1
				v-yes-1 Yamaguchi sarcoma viral related	v-yes-1 Yamaguchi sarcoma viral related
2683	2683 1402_at	LYN	M16038	oncogene homolog	oncogene homolog
2684	2684 1058_at	WASF3	Se9790	WAS protein family, member 3	
2685	2685 38736_at	WDR1	AL050108	WD repeat domain 1	hypothetical protein
2686	2686 41430_at	WDR7	AB011113	WD repeat domain 7	KIAA0541 protein
100		000	7		C coopings cooliforing of colimic statement
/907	2067 30009 at	CLOSS	Ar091092	Weakly shillial to glutatino le peroxidase z	weakly similar to glutaninone perchidase z
2688	2688 36909_at	WEET	X62048	WEE1+ nomotog (5. pombe)	weer lyrosine kiliase
					eukaryotic translation initiation factor 4H,
,				Williams-Beuren syndrome chromosome	Isotorm 1; eukaryotic translation mitiation
2689	2689 41212_r_at	WBSCR1	D26068	region 1	lactor 4H, isolorm 2
2690	2690 41635_at	WTAP	D14661	Wilms' tumour 1-associating protein	Wilms' tumour 1-associating protein
2691	2691 31862 at	WNTSA	120861	wingless-type MMTV integration site family, member 5A	wingless-type MMTV integration site family, member 5A precursor
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Wolf-Hirschhorn syndrome candidate 2 protein formin binding protein 21 oxidoreductase putative RNA binding protein RBP56 XPAC protein				radrome candidate 2 ng protein 2 ng protein 4 (formin ining oxidoreductase ining adapter with a stosum, group A stosum, group C in 1; putative ATP(GTP)-	yndrome candidate 2 ng protein 2 ng protein 2 ng protein 4 (formin nining oxidoreductase nining adapter with a ntosum, group A ntosum, group C in 1; putative ATP(GTP)-	Wolf-Hirschhorn syndrome candidate 2 prote WWW domain binding protein 2 WWW domain binding protein 4 (formin binding protein 21) WWW domain containing adapter with a coiled-coil region xeroderma pigmentosum, complementation group A xeroderma pigmentosum, complementation group C XPAC XPAC is a pinding protein 1; putative ATP(GTP)-binding protein ATP(ATP) ATP(ATP) ATP(ATP)	Wolf-Hirschhorn syndrome candidate 2 WW domain binding protein 2 WW domain binding protein 4 (formin binding protein 21) WW domain containing oxidoreductase WW domain-containing adapter with a coiled-coil region xeroderma pigmentosum, complementation group A xeroderma pigmentosum, complementation group C XPA binding protein 1; putative ATP(GTP)-hinding protein	Wolf-Hirschhorn syndrome candidate 2 WW domain binding protein 2 WW domain binding protein 4 (formin binding protein 21) WW domain containing adapter with a coiled-coil region xeroderma pigmentosum, complementation group A xeroderma pigmentosum, complementation group C XPA binding protein 1; putative ATP(GTP)-binding protein	Wolf-Hirschhorn syndrome candidate 2 WW domain binding protein 2 WW domain binding protein 4 (formin binding protein 21) WW domain containing oxidoreductase WW domain containing adapter with a coiled-coil region xeroderma pigmentosum, complementation group A xeroderma pigmentosum,	AF101434 Wolf-Hirschhorn syndrome candidate 2 AL049981 WWV domain binding protein 2 WWV domain binding protein 4 (formin AF071185 binding protein 21) U13395 WWV domain containing adapter with a U51334 coiled-coil region xeroderma pigmentosum, D14533 complementation group A xeroderma pigmentosum, Complementation group C	AE101434 Wolf-Hirschhorn syndrome candidate 2 AL049981 WW domain binding protein 2 WW domain binding protein 4 (formin AF071185 binding protein 21) CU13395 WW domain containing adapter with a U51334 coiled-coil region Xeroderma pigmentosum, COMPLESS COMPLEMENTATION GROUP A Xeroderma pigmentosum, COMPLEMENTATION GROUP A Xeroderma pigmentosum, COMPLEMENTATION GROUP A XERODERMENTATION GROUP A XER	WHSC2 AF101434 Wolf-Hirschhorn syndrome candidate 2 WBP2 AL049981 WW domain binding protein 2 WW domain binding protein 4 (formin WWOX U13395 WW domain containing adapter with a WAC U51334 coiled-coil region xeroderma pigmentosum, xPA D14533 complementation group A xeroderma pigmentosum,	2 AF101434 Wolf-Hirschhorn syndrome candidate 2 AL049981 WW domain binding protein 2 WW domain binding protein 4 (formin AF071185 binding protein 21) C U13395 WW domain containing adapter with a U51334 coiled-coil region Xeroderma pigmentosum, D14533 complementation group A Xeroderma pigmentosum,
	nin Hase	n 2 n 4 (formin doreductase apter with a	g protein 2 g protein 4 (formin ning oxidoreductase ning adapter with a osum, oup A osum, oup C	binding protein 2 binding protein 4 (formin in 21) containing oxidoreductase- containing adapter with a gion igmentosum, ation group A igmentosum, ation group C igmentosum, ation group C ignoredian 1; putative ATP(GTP)-	domain binding protein 2 domain binding protein 4 (formin ng protein 21) domain containing oxidoreductase domain-containing adapter with a d-coil region derma pigmentosum, plementation group A derma pigmentosum, plementation group C binding protein 1; putative ATP(GTP)	WW domain binding protein 2 WW domain binding protein 4 (formin binding protein 21) WW domain containing oxidoreductase WW domain-containing adapter with a coiled-coil region xeroderma pigmentosum, complementation group A xeroderma pigmentosum, complementation group C XFA binding protein 1; putative ATP(GTP) binding protein				AL049981 AF071185 U13395 U51334 D14533	AE049981 AF071185 (U13395 U51334 D14533	WBP2 AL049981 WBP4 AF071185 WWOX U13395 WAC U51334 XPA D14533	WBP2 AL049981 WBP4 AF071185 at WWOX U13395 WAC U51334 XPA D14533
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	1786_at	TSGA	AB018285	zinc finger protein	KIAA0742 protein
2710 39977	9977_at	ZNF-U69274	U69274	zinc finger protein	zinc finger protein
2711 40140_at)140_at	ZFP103	D76444) ()	zinc finger protein 103 homolog
2712 36295_at	3295_at	ZNF134	U09412	zinc finger protein 134 (clone pHZ-15)	zinc finger protein ZNF134
2713 32192_g	2192_g_at	ZNF144	D13969	zinc finger protein 144 (Mel-18)	Mel-18 protein
2714 36928	3928_at	ZNF146	X70394	zinc finger protein 146	zinc finger protein
2715 41532	1532_at	ZNF151	Y09723	zinc finger protein 151 (pHZ-67)	Miz-1 protein
2716 32628	2628_at	ZNF161	D28118	zinc finger protein 161	DB1
2717 41436_at	1436_at	ZNF198	AJ224901	zinc finger protein 198	ZNF198 protein
2718 40724_at	724_at	ZNF200		zinc finger protein 200	zinc finger protein
2719 35368_at	5368_at	ZNF207		zinc finger protein 207	zinc finger protein 207
2720 41542_at	1542_at	ZNF216	AF062346	zinc finger protein 216	zinc finger protein 216 splice variant 1
2721 840_at	t0_at	ZNF220	U47742	zinc finger protein 220	monocytic leukaemia zinc finger protein
2722 39762	9762_at	ZNF262	AB007885	zinc finger protein 262	zinc finger protein 262
2723 34299	4299_at	ZNF278	AL096880	zinc finger protein 278	hypothetical protein
2724 39005_s	9005_s_at	ZNF294	AB018257.	zinc finger protein 294	KIAA0714 protein
2725 37	2725 37860_at	ZNF337	AL049942	zinc finger protein 337	hypothetical protein
				zinc finger protein 36, C3H type, homolog	
2726 4(2726 40448_at	ZFP36	M92843	(mouse)	zinc finger transcriptional regulator
2727 38740	8740_at	ZFP36L1	X79067	zinc finger protein 36, C3H type-like 1	butyrate response factor 1
2728 36	2728 36046_at	ZNF363	AL050144	zinc finger protein 363	hypothetical protein
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2/314	2/31 40510_at	ZFK	AI/4350/	Zinc finger KivA binding protein	
2732 3	2732 39751_at	ZDHHC3	AF052182	zinc finger, DHHC domain containing 3	
				zinc metalloproteinase (STE24 homolog,	,
2733 33	33912_at	ZMPSTE24	Y13834	yeast)	farnesylated-proteins converting enzyme 1
2734 36521	6521_at	DZIP1	AB023213	zinc-finger protein DZIP1	KIAA0996 protein
2735 3	2735 35995_at	ZWINT	AF067656	ZW10 interactor	ZW10 interactor Zwint
2736 706_at	06_at		HG4582-HT4987		
2737 9	2737 960_g_at		HG2463-HT2559		
2738 956_at	56_at		HG1980-HT2023		
2739 955_at	55_at		HG1862-HT1897		
2740 3.	2740 324_f_at		HG1515-HT1515		

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၁	HG1800-HT1823	HG2639-HT2735	HG1112-HT1112	HG3543-HT3739	HG2036-HT2090	HG162-HT3165	HG2855-HT2995	HG2855-HT2995	AL038340	HG3044-HT3742	HG4322-HT4592	HG4322-HT4592	HG1112-HT1112	HG1322-HT5143		AL031282		AL031282
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	2741	2742	2743	2744	2745	2746	2747	2748	2749	2750	2751	2752	2753	2754		2755	L	2756

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